

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7283	21184	A	7343	306	164	IYMLYFTIYITLIYIHTHTHTHLYLDKYI YL*CVHCFL**AYMICQR
7284	21185	A	7344	442	8	SQMSKLTWFRVAHAHWPSTLGGQGR IT*VREFETSLGNTARPNLYWN
7285	21186	A	7345	3	248	HELSSLSPFFFKNEKGS*VAHAGL KLLTSSDPPT*ASQSARITGISHCARPL LSHFLAYLALPCHQNRLCTGHLPT
7286	21187	A	7346	2	246	HELYQSILLSPLFFKNDIGSR*IAHAGL QLLT*SDPPT*ASQSARITGISHCARPL LSHCLAYLALTCHQNRLCTGHLPT
7287	21188	A	7347	1	130	GTRLLKRLTQETRLNPGRGCREPSLHY CTPTWARQSQTVAHN*KRLTQETRLNPG GRGCREPSLHYCTPTWARQSQTVAHN
7288	21189	A	7348	516	288	FFETESRFTTGTGVQCDLGPLQLPPG FKGFSCSLSS*DYRCLPPHPANCFIF SRDGVSPC*LGWSQTPDLK
7289	21190	A	7349	417	148	STSVVQAGVQWHDHGLLPGPRLK*S SHLSLPHG*DYRHILSCLANF*NIPVEA GFRHTAGLEPLGSSDLPASASQSAGIT GMSHLA
7290	21191	A	7350	143	2	TQKFKTSLSWDYRRVSAHVANFCIFSK DRVSPY*PGWSRTPDPA
7291	21192	A	7351	189	37	EAIIVRRII*NLFFFFFF*RWGLTVLPK LVSNSWAQAILSPQPSKVLRLQA
7292	21193	A	7352	131	2	KSRGLTVAHACNPSTLGGRGHWIT*SRE FKTSRANMVKPRPA
7293	21194	A	7353	1	106	GTRGQCLTMLPRLVLNYAQMILPPWPP *VLGLQV
7294	21195	A	7354	939	653	KGNFIFLRQSFTLVAQAGVQWRDLGSPQ PPPPGSK*FSCSLRSSWDYRHGPPHPA NFAFLVEMGFLHVGQAGLELPT*GDPPT SASQSAGITGR
7295	21196	A	7355	270	26	EARFLGLLRDIAQLCPGWSAAV*S*LT AASTSWAQVKASTHLSLNN*D*ARATM PG*LKKYVFF*RQGLAILPRLRVF
7296	21197	A	7356	329	206	HHLANF*TFCDRGLTMLARLNSWPQAI LLPQPPKVLGLQM
7297	21198	A	7357	128	253	MRPDTVAHTCNPSTLGGQGRIT*THEF ETSLGDMMKPYLYK
7298	21199	A	7358	2	108	AREGGGQCCEP*WRHCTAAWVTEQDP VSKTIKK
7299	21200	A	7359	1	340	GTRERNWHLA*ALHTHTHTHTRHTHTH THFSFPANS*RDTFVIF*QSLLEIMTS FSPSLGLKCSFSQQPSGLLSSIAGERDS RIHAGENTVSMCLHNRLKAELRSVISLR V
7300	21201	A	7360	385	1	SVGPSKPCAGYNLLVCHLLRPLEKRSIR VGVT*FSRCHLSPLSLTRKANSLTPCTS WMRRCLILLRLTLGVPHPMSCTHCPTLP SEMNLGPQLEMQKSPIFCVAHAGSPRLE LFLFGHLGSTPNLPSC
7301	21202	A	7361	234	29	LSTEPKGSKALKFNVTLLLNIAF*CNSG CNSNL*S*QY*RVIQSHLSQTLWLTP VIPALWEAEAGG
7302	21203	A	7362	68	339	DRDIANKPAWQLCQSRILYLAQLQFIDQ GELLPDFRIHYKVI*TCTAWH*RRNRLI DQWNRADIPDLNPCQAWRLTPVILVLWE ADVGG

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7303	21204	A	7363	168	2	CFYSTHAHIFKELRQRPGAVAHAYNLSTLGGRGGRLT*GQKFETSLANMVKPHSC
7304	21205	A	7364	399	62	QPGQYGKHPVLIKNSKIPFWDGPPVVPNAREG*A*KMVEPGKVRVQSAQIKALEFNLGPKKKVPFKKKNPWLAKGGGLRPEIPAFGKASKGGSPPRSRILRPPGFLLPYPAHF
7305	21206	A	7365	289	76	VCDVLRERSAQLSRKCSGII*AHCNVS IAGSSNCHASALRVPGSTGVWVESERGDVDRFEAYGSRGYVCA
7306	21207	A	7366	364	182	QWHDHCNFKLLGSSNPPTLAP*VAGTAGTCHCAWLI*FLTWKIGFKTSLKIIIVLLGYFWF
7307	21208	A	7367	155	2	ELGTRKREGWEKSATVAHACNPSSLGGRGRWIT*GPEFPTSMANMMKAHPRA
7308	21209	A	7368	342	184	LSLPSSWDRRYTPPRLANFFKFFFKR*S LTMPLRLYRPFYITTHQTINSAMTF
7309	21210	A	7369	2	211	AREPKCL*TDEWINKMQYIDAVEYHLAIKLEILTHATTWMNLENMLIGRS*TQKATCCVIPFMDSIYV
7310	21211	A	7370	190	344	YKNVTVKRILTWPSSTVAHACNPSTLGGQGGFRFG*GQEFETSLGKIARPCLY
7311	21212	A	7371	24	254	KPQGIGAHAASSQHYGRPRREDHLSLGV* DQPGQHGEIPSLQKKKKKGLPGRGGVCLKPWFLKILGEKNVWVLTPKG
7312	21213	A	7372	43	358	DSNLNYSLFFHGEADLGTQVLTHPSTTAMFYFVHYCQSP*ILYGTINT*PPVHKNP IHIKTPSPCLQASTAINLQLSHINCNSKATPHPLGYQQTYPPPLTVHST
7313	21214	A	7373	2	288	IHIILAFSTSLGILVYRSHLIASLLCLHGIILSLTIIAPLIPLNTHSLAPIGPIAILVIAA*QAAVGLALLVSI STTYGLNYVHNLALLQCCN
7314	21215	A	7374	335	1	VQWNDFGSLQNPFGVSEFFFWLSLPPNLF GFKGPPPRPGPFLKF**KPGFSALTRMVSLSRPRDSAPLAPPKAGVSRINPRARAP FFFVFVFCFHFFLLSGEKKSLAHKGGI
7315	21216	A	7375	399	91	RIFFFPFSLKAPPHRQKPTDFPPTKKPLVFSIPPPIFPKFLKKNPFSPWEVFLFLSFFQKDAFFGPGV*KGNFFFFKGPPLTQNSPQGVPPKKKKKKKKKN
7316	21217	A	7376	377	131	YLYIKFYNFIIILFYIFIFNIF*FNMFNLLFYIFYILINFNIIILIIINFFYFILLIILNIIILYIIIIYFIKNIKT
7317	21218	A	7377	2	156	FHHVV*AGLELLGSSNPPTWAFQSAETTGVSHHAQLPHFILRKQELLSLGL
7318	21219	A	7378	319	59	DTKMNSQDILYSIQSNRT*W*LIKRO*T KQKSAPRNGNEVP*THQSTATTLSQQPSTSKQDPPAAK*L*FAEGRLLAPPSNNVF
7319	21220	A	7379	308	12	FSPTISNFNYKSNPSPLIYLFQ*PITQLIPTNISTNTPLNL*FYLRLIYSTSISLLPISNNVLIK*QFEHTKPTFPLPTLIALTLLLLPISPILIIIL
7320	21221	A	7380	11	169	RRDLAMVPRLFSSSPGLK*SLHLGFPEHWDYSHEPPSWLLFFFLITEGYFF
7321	21222	A	7381	300	2	KFFPPPGFFFKGFFSPL*SHQKKTQIFFGEFFWGFKKFFLFFFPGGFFFFFFFFFFF FFFFFFFF

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						FF*INSLFIQNSFLT
7322	21223	A	7382	163	160	PGTSNDEIQRRNSRNRTSPIAER*GLSL LPRLEWMGSNEAHSNLELQGSNNPPASA SKSTMITGVSHCA*PRLEWMGSNEAHSN LELQGSNNPPASASKSTMITGVSHCA
7323	21224	A	7383	1	183	VCVCVCVCVCVCIKWDSYSAIKKNELVA FVVTWKRLETIILSEVSQE*NTIYHMS LICGS
7324	21225	A	7384	2	196	KIQMWPGVVAHACYPNTLGGQDGRTA*G QEFQTS LGNIARPCLYQQQQQQQPRCS LTYDGDKS
7325	21226	A	7385	3	192	RNLSSLQPPPPGLK*WSCSLPSSWDYR REPPCPANCFMLCEFFRTNGVFPCSPGV YFEPRN
7326	21227	A	7386	266	198	TMLSGFLRSAGLTMTIS*PHDPPASASQS AGITGVSHRARPLVLFRLDSLYSGTQAG VPWRDLSSLQSRLEAQMRFCEP
7327	21228	A	7387	164	311	SKQQKGLSGVAHPCNPSTLGGGRGRWIN* GQEFETSMASMVKPCLSLLKL
7328	21229	A	7388	3	218	EIMSFATWMQLEANILSTLSHE*IAKY CMLSLLSGAKHWLNMNIEVGTGDTDRDYL GCTYPSSTEQLGYY
7329	21230	A	7389	521	58	SDCGLTPIAQTGVHWHHLLSSLQP*LPWL G*FSLHSLPSSWDYKYVPPCPASFLYF LVETGFCHVAQDGLELLDSNNPPSSASQ SAGITGMSGCAGLRRF*KLRSWRYLVLL AMQVNEQGTSQAGEAVSEADAGQGCCCG LCLHRLISQQYALP
7330	21231	A	7390	169	322	APGNFKTN*RNKGFWAGNTLGVSVKNMK NGAWWLTSPVLPALWEAEAGGSP
7331	21232	A	7391	1	353	GTSPHYGSFHHQKDVTKGGSQSRPRER VLGSHARKNSLPVHEVKAYLL*KYLSIL RATHILISPDGCWVPFIAQSYIFLSSC GFFLLFFLLLLTSLFCSWHLIISFLALF VIPLY
7332	21233	A	7392	372	3	IQAGACCAECIPSKGIRWNPSIVEGLHS DMSWSLCLFLSGAISVLCNFRLSGSSDS PMSA*QAARTAVIRHHTRLIFCIFSRRDR ETGFHHVGQENLLMLLQLFSGLGFSIS ATLLTLMLLV
7333	21234	A	7393	362	176	ARMECSGAI*AGLRGSSDSLASAS*EAG YTGKCGHAQ*TFVFLVEVRFHHVGQNAI NIRTS
7334	21235	A	7394	2	304	ARADCCARNE*GSVGMGPSEPGVGYNLL VFRFLRPLEKHSIRVGETRFSRCCLSQL CLARTGNSLTPTCTSWVRQCLALLRLMLG ALHPLSCTQRPTSHSE
7335	21236	A	7395	256	3	MYAARYWNKAKITTESLRHWAGHGGSH PYNPSTLGG*GGQIS*AHKFETSLGNMV KPHLSKNKQTNKQTNKQTNISWSWCTCL
7336	21237	A	7396	346	2	RDHFYRESHSLITYICLENVKSNLKCGE GPLNFTFHLQRKNCNLGHTRSPGGVYHV GRTEATGPIKRRNGLGAVAHTSNPSNL GGQGGWIT*GQEFKTSLSLPRWLTPVIP LV
7337	21238	A	7397	2	242	RRYSYDPDAYTT*NILSSVGSFISLTAV ILIIIFMT*EA*KKKKKKKKKKKKGGPF KKTLLGGPKFNRRMEGKNFSLKGG

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7338	21239	A	7398	1	289	TKLLGLYYTLLQASNDKSPFSIFDGIY GSTFFVTTGFHGLHVIIGSTILTI*FIR QLIFHFTSKHHFGLEADA*YWHLADARR HSESIHQCCSL
7339	21240	A	7399	346	40	IIIFTNKIYIKINKRLKLFIIKILDLYI I*IFFFRK*FTFKQ*K*IIININKIYIN NIK**IFIYLF*FFFFFFFFFFFFLFFFF FFFFFFFFFFFFFFFFFFFFLKK
7340	21241	A	7400	1	334	NSCRRQRLDLLLLPITL*LPQLIGYIE KSTRYECGFHPISPARVPSIKFFLVAI TFLFDLQIALLLPLP*ALQTTNLPPLIV MSSLLLIILALNLAYE*LPKGLD*AE
7341	21242	A	7401	2	302	HTINLLGERYVLATTY**STMTLLLTGL TVLHTGLYSVYLMTTTQWG*LTPLINM KP*FTR*DTLVFIHLSPIILLSLNPDII TGVVLVLLSYELYLLT
7342	21243	A	7402	57	338	TTHNVIGYIEASTAYESGCDPISPARVP FSIKFFLVAITFLLFDLBIALLPLP*A LQTTNLPPLIGMSSLLLIILALSLAYE* LQKGLD*AE
7343	21244	A	7403	407	68	QEELVDPLTTVREQCEQLENCVKAR*RL *LCDERVSSRSHSEEDCEDLDFDLHAR DHCVFLLIYLINLKYMCALT
7344	21245	A	7404	494	154	SLFIFYLYLIFLF**FFHYFFYFLLSI FSEKLLFFFLHFFHMFLLFFSPENK IFFPKIPPRFFLPLF**KFFFLPFKF LSPLGFFF*SPPFFFFFFFFFFFFFFFFF F
7345	21246	A	7405	1	400	NPGRFLSTSNSSLYERTREIRPTSQSAF PRK*YHLKKKKKKKKKKKKKKKKKKK KKGGLPLKKPRGQK*TGGEKKKFPKR GGKKKPPGKF*KKTFFWGGKKMGKTPQK KINPLGKKKIFKGRGKTPPL
7346	21247	A	7406	2	257	RASLCHPGWSAVV*SWLIAALTSWLKQF SHLNSLKCWDYRHEPHLA*LRFEHRHS GSSICTLNR*ILLSFPILSIRYKNGLIL Y
7347	21248	A	7407	259	47	YVFFFLFLLFFIRLQSVSPFFFFFFFFF FFFFFFFFFFFFFFFVK*SPIEMFSFVV LYLLRQVSI SIAYTLFG
7348	21249	A	7408	3	248	VTFL*CDVEIAVLIPLP*ALPTTNLALI DMSSLLLIILALRLAYE*LRGGLD*AE EHQATHSAYERAPPL
7349	21250	A	7409	2	350	RSGMPRRYSYDPDAYTT*NILGSVGAFI CLTAGILIFMI*EAFASKRKVLIVEQP SINLE*LYGCPPPYHTFEPPVIKSRHI RKESNPPKLVSQPHGLHDFKKKLGTI TEKN
7350	21251	A	7410	2	232	LDQTYAKIHFTIVFIGVDLTLLPQHFLG LSGMPRRYSYDPDAYTT*NILSSVGSFI ALTAAILIIFMI*EAFAKKF
7351	21252	A	7411	2	321	TSLLAVALLIIMTL*LPQLNRYIEKSTPY ECGFDPICPRVPFSIKFFLVAITFLLF DLETALLPLP*SLQTTNLPPLIAMSSLL LIILDLNLAYE*LQKGLD*AE
7352	21253	A	7412	2	194	SIECFVLPITLLCDLEIALLLPLP*AL QTSNLPPLIVMSSLLLIILALNLAYE*L QKGLD*AD



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7353	21254	A	7413	1	197	LYTTYFVTKTLLLTSLFL*GRTAYPRLR YDQLIHLL*KNFLPLTLALLI*HVSIPIT TISSIPPQT
7354	21255	A	7414	1	185	STPLP*ALQTTNLPLIVMSSLLLIIL LSLAYE*LQKGLD*AEKKKGA AVLKDP SGGPS
7355	21256	A	7415	347	228	LE*LYGCPPPYHTFEPPVYIKSRKRKE SNPPKLVSSQPHGLHDFFKHIKNYRKNK RKEGLASVKENDRGP
7356	21257	A	7416	1	296	HAYDHASQNLNGYIEQSTPYECGFDPIS RARVPFCIKVFLVAITFLLFDLEIALLL PLP*ALQATANLPLIGMSSLLLIILALS LAYE*LHKGLD*AE
7357	21258	A	7417	3	202	TCSI*HVLVRMT*LIYDLEIALL*PVP* ALQSTNLPLISMTSLLLIILALSMAYE *LQGLD*AE
7358	21259	A	7418	1	321	SNLTLALVLTITTS*LPQLSGCVGECTP YECGICRILNARALCCMQIFLKAITFLL FDLEIALLLPLP*ALQTTNLPLIDMSSL LLIIILALS LAYE*LQKGLD*AE
7359	21260	A	7419	1	212	RTRGIIIFRPLSQSLY*LLAANLVILT*I GGQPVSYPTIIGQVAVLYFTTILILI PTICLIENKILKWA
7360	21261	A	7420	2	257	GRVGRVGYSTIAFFLQAITVLVLDLESA LLLALP*SLQTTNLSLIVMSSLLLIIL ALS LAYE*LPLGLD*AEYWGEMMTTLD A
7361	21262	A	7421	367	269	HCDLKLGGSSDPPASAS*VAWITGTCHH TKLS
7362	21263	A	7422	2	116	ALQTTNLPLIVMSSLLLIILALRLAYE *LQKGLD*AE
7363	21264	A	7423	2	336	KPECGREGILPCCSSSAWPEGSFRPFQM NLGSFLSFFLFFFEKGLFLCPPV*S PYGKSNLLEPSASRFQFFCLGPLNNWD YRLFPPFPNGFVFKNRVFPFWPSLV
7364	21265	A	7424	3	154	LFL*IRTAYPRFRYDQLIHLL*ENFLPL TVALLI*HVSIPITISSIPPQT
7365	21266	A	7425	3	154	LFL*IRTAYPRFRYDQLIHLL*ENFLPL TLALLI*HVSIPITISSIPPQT
7366	21267	A	7426	1	314	INTLLTLLLIITL*LPQLNGYIN*STP YECGFDPISPARVPFSIKFFLIATFLL FDLEIALLLPLP*ALQATNLPLIDMPSL LLIIILALS LAYE*LHQGLY
7367	21268	A	7427	1	331	ILIINTLLALLLIITF*LPQLNGYIEK STPYECGFDPISPARVPFSIKFFLVAIT FLLFDLEIALLLPLP*ALQTTNLPLIVM TSLLLIILALRLDYE*LQGLD*AD
7368	21269	A	7428	2	373	SDRNHIIHALVITILLGLYFTLLQASEY FESAFTISDGIYGSTFFVATGFHGLHVV IGSTFLTICFIRQLIFHFTSKHHFGFEA AA*YWHIVDVAGLFLHVSIRGGSYNHQ IIPSVAQESTPA
7369	21270	A	7429	378	63	PSFFPPFP*NEFFPPRPLFSPGGFPFP FPPQKGPFPKIPPGFFSPFWEKFFF PPPPLILPPRFFFNPPPPFFFFFFFFFF FFFFFFFFFFFFFDFLGGSC
7370	21271	A	7430	1	109	QTTNLPLIVMSSLLLIILALS LAYE*L QKGLD*AE

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7371	21272	A	7431	358	290	FLLVIPNLFHFHFLIYIITISIVPNVSFFH IIYILSIFFPFIIFILLSSFNFILFFF FITSFPFFVFFFFFFFFFFFFFFFFFFFF FFFFSFFFFFFFF*FFFTN
7372	21273	A	7432	1	95	PTRPPTRPHNSLQL*TPGLKQSYPRLP SWD*RHMPSPHPANFRKFF*RWHLCPGW S*TPGLKQSYPRLPSSWD
7373	21274	A	7433	1202	870	HNIFKIRPHCRLTHRGKFFYWGLLVTPV FSPSLRPSFLPSFLPSFLPS*LPSFLPS FLFLSYSFCPLSFLCLRCIPHSAFFWG NPROVQENCIVITTIYRYSFTALHQL
7374	21275	A	7434	163	1	SVYVKRIGLGRVAYTCNPSTVGGQDG*I T*GQEFETILAKRREPLFLACFLFLI
7375	21276	A	7435	148	362	NDDNSVEFGIRLHKGLGTVAHTYKPSL GGQGGHIA*AQEFMTSLGHMT*SSLYHK LTEYGWRDTASLLMC
7376	21277	A	7436	61	233	GGDLRHWPSDSFFLSLSFFF*NKNGGG LALLPRLDLNSWSQAILPLKPPNALGLQ A
7377	21278	A	7437	44	242	FVCLFLFFFKEKESTFQHDLSLQPPLP RFKRFSCLSLPSTWDYRLAPQCLANF*I F**KSGFTFG
7378	21279	A	7438	119	300	YCVSLIIFIFIYIFILLIFKFLFITL NYISFLFFYF*H*FYF*KNFIFVFPFGY FPRP
7379	21280	A	7439	1	221	LKLQHHDPPTISLVITRNWKQPKCPNVQ QIVH*SAIKRNELLIHAKTWMNLRGIML SEICQPQKILYLEIPFI
7380	21281	A	7440	35	345	FSFCCVCVCVCVSLPKHAIIEMLNQTHP YVPKGVAYLPEREPFIVPMDDELTA*YE DYRTHESAQEPSEPHQLSRRSLPH*PGH ATRDHSPPTDSWGRRTSH
7381	21282	A	7441	3	384	VIHL*AGAVIIGSRSKSTNALAHFLRQG TPTPVILVLGIIETMNLIIQPVALAERL TDNITAGHLLMHLIVSATLAILTINLTS TLIMFTVLILLTILQIAVALMHAYVFAL LVCLYLHDDAYDHGG
7382	21283	A	7442	15	277	GLAILPRLVPNSWPKVILQVWPPKMLG* QA
7383	21284	A	7443	21	694	NGGLNAHLASASEFDHSGVQLIEREEI CIFYEKINIQEKMKLNGEIEIHLLEEKI QFLMKKIAEKQRQICVTQKLLPAKRSLD ADLAVLQIQFSQCTDRIKDLEKQFVKPD GENRARFLPGKDLTEKEMIQKLDKLELQ LAKKEEKLEKDFIYEQVSRLTDRLCSE TSCKQDITLLFTKKMNGYSRRIKNATEK MMALCA*LSMKQAPTIELQKEVQGERRP
7384	21285	A	7444	141	428	DRSLLEAGDGRIAGDFFFF*TGTFNFAV AKVQWGIHSSLHP*PGLKQSSYLNLG SYHHWLRPHALFFFLKNRGSFLCPGWFG TGFRGTTFWGAK
7385	21286	A	7445	35	343	GYSIIGCPKFLDEKIFDSGHEKERKINS LLF*KKKKKKKKKKKKKKRGLLKK TSGGPKIKRGGGIKNFPIKGGVKTSGE FFGKKPFFGGEKFWELP
7386	21287	A	7446	403	193	EYIKQGAE*NNQPKLHAHRKRLTWKETP RCIHEGIAPAIMNSDCLVFDTSIAQLFA ENGNLGINVTISM

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7387	21288	A	7447	411	110	LTDSLINIVYR*KMSYIS*TNSA*VYLY IFCIYIYIYIYIRRIYSIYRC*YIYYG PAHIVLVYSSSYILVYVESHKYGYIMGL NILSYIFIYSYFSACS
7388	21289	A	7448	1	380	PTRPQKLKKNCNGVSNGLCFFGGGQFL IWGFFFFFCILIEGGLNSKNYELKSLIK TYGAKKAEIEHTEN*KNRETLLEAAQL AIKVTNPNAMLRTVEHDYAMYMHNFWLN KLNCHKVAISCKQ
7389	21290	A	7449	200	437	VQSNNNKNFKRRRL*PGVVAHTCNPSTL GGQARRIS*AQELTGLNNLMRPNYNYK FINVLDDVHGVTSPPVSQYKKVC
7390	21291	A	7450	405	3	PPRFFGGFFFPYPLKFFFPKGFNFEGG FFPIFFPPKKKFFFKNSPGGFFLPPFLG KIFFFLPPFKFGPPRGFF*RAPLFFFFF FFFFFFFFFFFFFFFFFFFFFLQRINF ARPGTPLSRVPLRGALPPSA
7391	21292	A	7451	2	348	PRVRPRVRYKLQTKRCDTLPS*GHSHV SLRNTTFDALKS*DTDSLSPKLECHGV NTPNCNLRLPSLSDYPASLSREAWIAST RLRAWEIFVFLAQMRQDYCMNPGGGGCN ELK
7392	21293	A	7452	1	168	LVHDGHAGLKLSTSGDRPA*AYQSAGIT GVRPLGPPTYYYFRTASFMTFICEFATV
7393	21294	A	7453	184	260	SSRGGLASRSSR*STLLGLPKCWDYRC MPPSLANFFNF*INFCFW*RRSLGM LRLVNS*MQAILPLRRLQGIHFAQT QTFSL
7394	21295	A	7454	405	64	FFFFFFNF*KKKI*DVEAKIFFKIFFFF SGLKIFWGGGFQNAAPPQKFFFF*KIKSF FELNFFF*KNIFFFVAGVFFLLNFFER GAPLFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFF
7395	21296	A	7455	368	2	SQSFGRPRWENRLGPEQHIKISRYRPAQ VHACHPSTLGGGRWIT*QGEFKGSTHL GLPKYWDYMEPLLLVYIQCFHRTFCN KAAIHCFKPEQLLYNKTSYFKESYKVK ALVACKPTRP
7396	21297	A	7456	2	183	TERDSVSKNKYIYIHTHTHTHTYICVHG VIYVYI*SLLLIYNIAIYILYHVFIYLL IFKA
7397	21298	A	7457	281	127	YNFCIFM*RCGFNNVVGQSGLKVLLRGYS PASASQIAGITGVSSQCAQPVAYS
7398	21299	A	7458	2	194	TSVRKYF*YPFITITDRYGSTWVATGL HGLHVIIGSTFLTICLIRQLIFHFTSYH HFGSEAAG*YWHFVEPARLFLYVCIY** GSTWVATGLHGLHVIIGSTFLTICLIR QLIFHFTSYHFGSEAAG
7399	21300	A	7459	22	319	GGSVTGAYHRILDHNRQIFLA*GGSVT GAYHRILDHNRQIFLALLISMLGLYF TLLQASKYFECPTICDGIYGSTFFVAT GFHGLHVIIGSTFLTICWIRQLILHFTS RHHFGLEAAA*YWHFVDVV*LFLVSIY **GSVTGAYHRILDHNRQIFLALLISM LLGLYFTLLQASKYFECPTICDGIYGS TFFVATGFHGLHVIIGSTFLTICWIRQL ILHFTSRHHFGLEAAA
7400	21301	A	7460	1	222	TILLGLYFTLLQA*EYFKATFTTYDGIY

<b>SEQ ID NO: of nucleotide sequence</b>	<b>SEQ ID NO: of peptide sequence</b>	<b>Meth od</b>	<b>SEQ ID NO: in USSN 09/515,126</b>	<b>Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence</b>	<b>Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence</b>	<b>Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)</b>
						GSTFFAATGFHGLHDIIGSAFLTICFIRQLIFHFTSEHHFGFEAAA*YWHFVDAT*LCMVYSII**GSTFFAATGFHGLHDIIGSAFLTICFIRQLIFHFTSEHHFGFEAAA
7401	21302	A	7461	3	246	LNYSLFFTHGEANLGTQTQVLTHPSTTAMYFVHYCQQPP*ILYGTINT*PPVVHKNPICKKKKKKKKKKKKKKKKKKKRGGG
7402	21303	A	7462	2	155	SRSRAALLPLP*ALQTTNLPLIVMSSLLLIIILALSLAYE*LQKGLD*AE
7403	21304	A	7463	1	136	PTRPAPSHLLYCKNIKKLFPSGTANEALIADI FLRCKKKKFVK**VLKASEE*N GCKHLHGMM*NSAVCTVFWLKQIMNSD**KVNTQ*KKKKKKKKKKKKKKKKKKKKKKKKKKKKKGGENNK*KNIKKLFPSGTANEALIADI FLRCKKKKFVK
7404	21305	A	7464	166	192	NIN*MWYMHTVECYSDFKRKELIHATTWMNLEDIMVSEISQSQDKCYCMILHIEYKLYIHM
7405	21306	A	7465	416	55	LFFLRRLGYFFLPNIRVFFFLSTLFFFFFFVWGFFFFGRFFFFFFFFPPPQVCFFFIF*GIFFFFLEK*KNMFFFFFFFFLWGPPPPFFFSGAPLFFFFFFFFFFFFFFFFFFFFFFFFLKANTKKMF
7406	21307	A	7466	295	84	IWGNVTLLQLVSLCFCLFLFH*GFFCCC CCLFLFLFVCLFVCWFLNLKPSIKCLLPFSLSLGCAEIPSSF
7407	21308	A	7467	142	258	PGTVAHTCNPNSTAGQGGRIP*GHEFKTNLANMVKLHLY
7408	21309	A	7468	3	192	PSEYFESPFTISDGIYGSTFFVATGFHGLHVIIGSTFLTICFIRQLIFHFTSKHHFGFEAAA*YWHFVDVV*LFLYVSIY**GSTFFVATGFHGLHVIIGSTFLTICFIRQLIFHFTSKHHFGFEAAA
7409	21310	A	7469	2	110	GRVGKHHFGEFAAA*YWHFVDVV*LFLYVSIY**GS
7410	21311	A	7470	380	8	TPQKRKKLKKAGEGVFP PPPKKTTPPPPIFIYFIFFFFFIYFFFFFFFFFYMSFYSHIMIQRHFLNF*ESFYSCISILQ*L FKFFSFLGGLIKL
7411	21312	A	7471	1	107	PTRPHHFGFEAAA*YWHFVDVV*LFLYVSIY**GS
7412	21313	A	7472	2	360	VNTLLALLLITMTF*LPQLNGYIEKSTPYECGLDPISPARVPFSIKLFLVAITFLLDLEIALLLPLP*ALQTTNLPLRAMSSLLVVIILALGLAYE*LQRGLD*AEWLHSLTQPTNNN
7413	21314	A	7473	423	167	VKVHKCF LPGVAPHAFNPSTLGGRGRI A*AQEFKTSLGNIVRPPSDTCNP IVLGLQA
7414	21315	A	7474	1	73	IKPE*YFLFAYTILRSPNKLGGV
7415	21316	A	7475	131	3	ISWGAEWLTRVIPAL*EAESGVSRGQEIETILANTVKPDAW
7416	21317	A	7476	2	103	PRVRSTGFSSIAHITRDVNYG*IIRYLHANGAK
7417	21318	A	7477	2	325	NTLLALLLIITTF*LPQLIGYIEKSTPYECGFDPI SPARVPFSIKFLVAITFLLDLEIALLLPLP*ALQTTNLPLIVMSSLLIIILALSLAYE*LQKGLTERDT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7418	21319	A	7478	423	170	FFSFFFFFFFFFFFEIDKNVYLIM*CTNPQEKRNLLFCFLVMVSPVCITPHTYICVCVCVIYIYIYIYIYIYIYPIFSCCD
7419	21320	A	7479	433	50	RVFFFFFFTPEKKTFFFPQBIYLFFSPFFL*NFFFSPPKPLFLFLGGFAPNFPPPKKVFFLKFPDGGFFFSPPFKKKKFFFFPRFFFAPPRFFF*GPPSFFFFFFFFFFFFFFFFFLTVKTRGRGFRGFCGQI
7420	21321	A	7480	401	337	FFFFFFGKFFFPQEFTVFFPPFPFKIFFSLRLFFWGGAQFFPPQK*VFFSKFPRWFFFPPLFRKKKFFFP*FLAPQGGFFLKGPPIFFFFFFFFFFFFFPI*VGGRVGNNPNPNTNYLPN
7421	21322	A	7481	1	84	KNFLPLTLALL*HVSIPITISSIPPQT
7422	21323	A	7482	562	412	LFSEHVSGTMAHTCNPSTLTG*GRIT*GLEFKTSLGNTVRSHRYRKKKIA
7423	21324	A	7483	12	233	DIHFHTSKHYFGFEAAA*YWHFVDVVRLFLYASII**GSL
7424	21325	A	7484	385	56	GNFPTPKKNFFPYFYLISFFFFPKKLKFF*EIFPIFPPPKFLFLPNNFVLFFFFFLFWBFFFSFLWFFFFFFFFFFFFFFFFFFFFFFFFFF*KTEFYFVNSNFQHTK
7425	21326	A	7485	424	6	FFFFSESGSLIREDPGAGALYDGR*LUVVTG*TLFVGVIYVIEIARGNRLCD
7426	21327	A	7486	16	129	FXXRXRLIXKEPSINLE*LYGCPPPYHTFEFPPVYIKS
7427	21328	A	7487	183	387	IASGLDIFLLLLLETGSHSVTQAGVQWHNHDLSQPRLTGLK*SSRRSPRGSWDYRVLLCHPGWSAEA
7428	21329	A	7488	351	169	EKKIFFFSPPRGYGPFFFLKAPPHIFFFFFFFFFFFFFFFFFFRGGGDHKNFFFFFFFFWGFLKNFPLFFFFPRV*I*IFFFFFFFFFFFFFFFFFFLGGGGTIKIFFFFGGF
7429	21330	A	7489	47	212	THASALFL*IRTAYPRFRYDQLIHLL*KNFLPLTLALL*HVSIPITISSIPPQT
7430	21331	A	7490	98	273	TSGSCCSAHILAFKP*AGMATFITKSL*CHTHTHTHTHTHTHTHYMIYTHMHTYIF
7431	21332	A	7491	70	405	LYGCPPPYHTFEFPPVYI*EAFASKRKVLIVEEPSINLE*LYGCPPPYHTFEFPPVYIKSRQKRKESNPPKLVSSQPHGLHDFKKKKKKKKKKKKGGGPKKPRGGPNLTGGGKKNFFFFRGGEKKPPGGFWKKTFLFLGGGKLGTPPPRRF
7432	21333	A	7492	22	208	RSSLPARPTRAVALIIFMI*EAFASKRLVLIVBEPINLE*LYGCPPPYHTFEFPPVYIKSYV
7433	21334	A	7493	2	204	KLPETVKKKKKKKFSFRSIVMLLLYLFSL*SLSFLLYSLLFFLPLLSFYIYSFLCFPLCKTATTEH
7434	21335	A	7494	2	104	TTLLLSRT*NKLT*LTPLIPSTLLSLGGLPPLTG
7435	21336	A	7495	291	160	PRHF*IFVEMGSHYVAQAGLKLVAASNLLAWASQSAGVTGVSHGSLITSC
7436	21337	A	7496	422	180	LGAPQGVF*KGPPFSPSSSSSYSSSSSSPS*QNIFNKIFLVCFLVETESVTQGVQWRDLGSLQLPPGFKRFTIITH
7437	21338	A	7497	244	296	FFFFFFFFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFFG GNF*FYK*LLGNRDGVCPLPPSSYL
7438	21339	A	7498	1	410	PTRPDQLIHLL*KNFLPLTLALLI*HVS IPITISSIPPYT
7439	21340	A	7499	51	478	PQKYTLIMKICITIPPGKGRFPVEMLAGG NENTRCLIEERSYKYHYSLIKLGLQQQC IFSSLLYKYNMIYCLMLCYIYIFIFY DMYYRQYSVLYYKLYNVMLI*YIILYL FMCI*KYIYFIFM*YKYIFIYLYLY*YK YIFYIYLCVYKNIYTLNININILYTY IYININIIY
7440	21341	A	7500	3	110	FTSKHHFGFEAAA*YWHFVDEV*LFLYV SIY**GS
7441	21342	A	7501	168	327	APCYKATVIKTI*Y*YKHRYTEQWSRTK NPDINPYICGQMIIFLQLKSLHKI
7442	21343	A	7502	400	159	NNFSPLRNLQGFFGPLKFFPMGFQAGPPG *GFSSFFLRSNFFLDVFRGKY*TFGF*DF FYCPSPNEVLGEPPLMGCKPKGFP
7443	21344	A	7503	401	257	TSQKKKKKKKKTTPKKKKKNREKPPKKKR GTRGEPFKTGGGKEKKKFPPKKKKKGK PP*PQLVKRGGREKKKKNLWKKKGAF*K KKKKKKKNPKKKKKKPGKTPKKKKGDPG GTF
7444	21345	A	7504	44	344	LLASLANLALPPTINLLGELSVLVTFPS *SNITLLLTGLNIVTALYSLYIFTTQ WGLTHHINNIKPSFTRENTLMFIHLSP ILLLSLNPDIITGFSS
7445	21346	A	7505	286	252	I*FAFHVHGQAGLEFLTSDLPASASQSA RITSVSQHAWPVHNIIFYSL
7446	21347	A	7506	3	213	RELPLGKRFFLLSLSWD*WRMPHSHA TFCIFCRDEVLPCCPAGLLILLVWNLKN CCCYHHHRYYYCY
7447	21348	A	7507	400	20	SLPQKKVSLKLKSAVQLVMF*DRFSLC HPGWRA*GQSGVTTASSLRAR*SSCLTW EYRPSPLPLADFLFW*RRGLPI*PRVVS NS*GQVGLLHQPSKMLKFSSLSPCARPL FFFFNRSTNLRVQS
7448	21349	A	7508	349	227	SDFLTSANPPASASKSFGITGVSHHTRP *PRFLKVNLIYSEMEVYN*ASFRHVD*G GLELLTL*FTHLGLPKLWDYRREPPHPA LTKIFKGKPYIQ
7449	21350	A	7509	371	21	FLVETGFHHVG*AGLEPLASSNLPASAS QTAGITGMSHCAQPNPGLLNKTMLAVA TEQWVGVMWPSVFGHITARPEGKRLSDC LHSDTNVCVVCVCSGLIFVCFETGCRFA LQPG
7450	21351	A	7510	330	14	DKVCSVTQARVQWHDHGSLLFLSSGLRQ SSHLSLLSSWDHRHMPPGMAFFFYF**R LRSHYVAQAGLKLASSNPPTLTCSAG ITGVSHNTWPKALFVSVDLKH
7451	21352	A	7511	417	33	APPCGGGPPKRIFGFSRKRKGKPPPPKR FF*KNKPPKGGGKKSPPPPKNFFPKKN LGPKKKKSFGWGRFAPPRAPGGGVFNFP FKAGGEKFFSRGEINPRGAGKKKGFFL GKKNTKKKT*PKKKDL
7452	21353	A	7512	81	296	CLREGASHSAAQAGLHWDHSSSLHP*NP GLRGSSRLNLLSIWDYRCVPPSLANFES CLLKIILGSPFFPKNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7453	21354	A	7513	412	279	KKYTGQLGVVAHAYNPSTLGSQGRRI* AQFETSLGNTGRPCLH
7454	21355	A	7514	74	126	KT*DWVPKGAPLQGPVF*NSTFRPRVRN RGPPWP RP GPPTVWKG*NKKN*PAPRGSN PPFFFPGNPGPFKLRGWPGSS*GSFQNC KKAQAG*APT*KPGPPPPQNKV
7455	21356	A	7515	332	20	GERQVGSYFFMNTERLFGMTKKF*KWIV SMVAQHSSSISGVWVFRQELAFPLSPD WQVDYESYTWKLDPGSEETQTLVREYF SWEGAFQHVKGAFNQGKIFK
7456	21357	A	7516	1	167	RTRGQRFTVLARIVLIS*HCDLPASASQ SAGITGVSHCTRPGLSFLYTPTAKHST
7457	21358	A	7517	2	223	GRMEEMGSHYVA*AGLEFLGASDLPA*A PQRAKILLLLGGHKPGLTILPRLSSNSW PHVKWPRWPLKALGLRG
7458	21359	A	7518	151	476	SLGKFAVSFSFSLK*RRALAVLPRLCS NSWP*AVLLPWLPRVGIAGMSYHTQPDY HFQARAVAEILGLVSTQHSSVTGLPVEN SFRAGHGGPRLQSQHFGRLRWADC
7459	21360	A	7519	3	134	CSFRLGAVAHCNVITLGGRRGRIA*AQ EFETCLDNIA RPCLY
7460	21361	A	7520	14	219	APSIHGFGFLYTYIHTHTHTHVYMI*V YIHTHIESIKCQPLTQLQSNKKANRIVF RTQFMLTCYFMR
7461	21362	A	7521	134	334	RKHSC*IFFNFCFYLSLETRSHYVASTG LDLLASSNPPALASQRARITGMSHAPP VLTFRKKSFL
7462	21363	A	7522	406	145	FLKTGFSPFGPFVF*TPPPGFPPPPPPP IFGVPGGGPFAPPLFFFFPQTKHFPPFL NPBSPPPQRGFFRGFFLPAPFFLKTPP FFF
7463	21364	A	7523	3	382	HPQEGGRLTSLE*NTSLRLKKKKKKKK KRGGPFKKNPWGAQI*PGKKKNFFLKR GAKKNHLGNFGKKPYFWGGKKLAKPPKK N*TFKGGKKFLRGKGKKT PKPWLLKIF FSGFYLLKIFPPGP
7464	21365	A	7524	319	106	GTRSCSVT*AGVQWHDHSSLQP*TPWLK RSSWLRNRWDYKHEPPCLNNFYFFCRDG GLLCHPGWSQSPCLK
7465	21366	A	7525	433	228	MQPYNWEVNSSSQLSLSSARQRVTHVLT GNFFIK*ERWDLPLVLPRLVSKSWPQVIF PPWPSKVLKLQV
7466	21367	A	7526	26	351	CRSLVFSLPKPLRFVSILHIQVFSHFD FFFLTGNTOK*RK*TPFIFPA*LFKTPA PKPCMVAHTCSPSYSGGLDGRIA*AQEF RTSLGNKTNP SLEGGRKKKKPSGS
7467	21368	A	7527	438	62	QLSKIHRPPAGGRFFKSGGGFKPFCVVG LPPFGKKANQPTPKNP PPKQKPSGGGLS PMGKPP*FPCSMPSDSPGSVSFSRGVA PAPKDYCPIV*AALIPSKKKKSKPG*V KKGKPNLYSIYNK
7468	21369	A	7528	3	132	FYYL*RRGFVLPRLVLNSWLQVILLPW PPKVLN*AAHHPHG
7469	21370	A	7529	2	628	FFFLPGVVNRVLLMGRGLGEANSREGRG PSQPRGMHGQLEVRGGRSQGDGWHGTL PPWGRIRYRGAPPTFAAPQAPKPFRLLP M*LPGRPSSCLLPETPALSPLPSAEWGG FKLLTGTSETPGPSGSPSVGSANAQAAG

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						ATTIVARGHTPCTRGPLDTHAHSSLRWH AHTRPPPRPLAHEHGTHHAHPHTPGAW VGEQPFQGWGRA
7470	21371	A	7530	63	205	GRPTRPRTRGVKIL*QFEHTKPTPGLPT LIALTTLLLPISPFIIL
7471	21372	A	7531	390	56	KTFFFFNLIAFTEAKSVLLFLLFFETG SRSSAQPGVQWHHQSILQPP*LGSS CLSLLSN*DYRCAPPCQ*SPCLSLKWC DYKREPPHPAKESHMQQSYLIYSLYIA
7472	21373	A	7532	543	335	LAAYGGTCLQS*LFSRLRWEDHLSPGVQ GCNELQLQHCPAWATE*DPVFKEGKKE RVLVKVFS
7473	21374	A	7533	3	145	WCDHGSLEPRSPGLKQSSCLSLPSNWDH SSEPLHTTSMWNF*IFKFLNLK
7474	21375	A	7534	386	106	SWVTDEITMEI*ECVLNDSNTPYQNLW DTEKVVLRKFTALNACMKKSERAIQRH TCVHTHTHTHTHTHTGSKCLLRKYLTLT IQQNIRIN
7475	21376	A	7535	398	2	SLQPLPPRVKCFSSPSPRRWDYRGAPP RGGKFFFGKKEFPVGGGF*FLPPGV LAPPPQKGRISGGSPRRPFFFFFKIR ISYPIIAKQLKLCFLKKKKSIQAIKLY HHQKNPITKSSVFWESQRA
7476	21377	A	7536	2	344	HSKCVPAEVTMAYYIRYLSISSLLHIL ENIVHFFHFHLY*GPNLFFFYFAGTRL IQRSWK*PMII*VHVQIKREGQIFNK* IFCMIGRGG*ITCGQEFETSLVNMVKPC LY
7477	21378	A	7537	116	224	LHTHTHTHTHTHTHTHTQFNKLP*LFIP CGHIPRRY
7478	21379	A	7538	1	383	WHERTHSRITILFQGLETLPLIATF**L LASLANLVLPPTINLLGELFVLVTTF* SNITLLLTGLNILVTALYSLYIFTTQ* GSLTHHINNIKPLFTRENTLMFIHLSPI LLLSLNPDIITGFSS
7479	21380	A	7539	31	332	DNYLSSYSSSGSWMRELILASQIRWEP IVDRTPSHHRTHTHTHTHTHTHTHTV LFRIGPWTHAREPRGHICGN*IRNQSP* KNPRTRGKNLRTPHGW
7480	21381	A	7540	199	15	NNVQIK*QFEHTKPTPFLPTLIALTTLL LPISPFIIL
7481	21382	A	7541	337	157	AEIVPLNSSLGNRVRLH*MESYSVAQAG VQWHDLSGVQPLPPGFKRFSCFSLSSW DSRLYFRCHD
7482	21383	A	7542	28	313	RARIGSDQCLSAGTQVVENKSQISGDFM WNDFRS*SVTRVGVRWRNHGSL*PWIPG LR*SSGFLPNCWDYDRNEVWGGKKEV TCPTVNLQKSQ
7483	21384	A	7543	493	180	GGFRGSWLVRDGGQGVGFCSLPPPSR VKQFFCLRFPRRWGGREGSPRPSYFFFP *EKPRFFFLGRVVLNFLGQGVGPWPSPQ RVGFPGLTGPGRASFFFNLI
7484	21385	A	7544	403	426	FF*KFFITFHTLFFFTFFFTFFFTFFFT FFFTFFFTLAPPGGFFFTFFFTQKIFL KFPQGPEKFPALPFGGGFFFT*GKFPQFFF CFLVFFFTFFFLFLENGVSLYCPGRSRT GLKLSSRLASLRAGITGVSH
7485	21386	A	7545	3	335	RHYSDYPDGYST*NILSSDSLISLTAA



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLMVFMI*EAFAYRRTGLIA*EPSMNL *LYGCPPPYHTFEPPGYIKSRLKRKESN PKLVSQQPHGLHDFFKKKKNRGGPF
7486	21387	A	7546	424	140	RRVKFVGGGAPQGPPPKRGVLPKIPREK VFPPPPG*NGPPGPAFKTPPKKKNISS PPPGNWAPPGLLKGPPIFFFFFFF FFFFFFLNPLK
7487	21388	A	7547	2	348	FCHVAQSGKLKLASSDPPTLASQSARIT GMSHHGGLK*GEFLGPSSNKGALLWEA TWLQSFMSASLFFVKRPPTFVFVFAFV GYRDIYFTASSLIKVIQEGLYTMKCAP LTL
7488	21389	A	7548	2	90	RKQAYTHNTHTHTHTHTHT*KKTGIIHAH KHTHTHTHTHTLKAEQQIRGGK
7489	21390	A	7549	256	405	CELYSGKEMELVFGLFIETGVTRLETIFY KKECSSFFHSQSRGHLQPSILNEWWHI RNPLGLTHFLLL*KTGVAEYKNSLNVVH HPFFLSYAVSFLLQGWSEFAMLSKLGNS *VQARCLPQSPKVLGLKESPOERTVNVS SIRGKKWSWYLDYLFSSQGLQGLKLFIRK SVHSSIPRAEGINCNHQY
7490	21391	A	7550	2	362	ILIMNTLLALLLIITTF*LPQLNGYVEK STPYECGFDPISPARVPLCIKFFLAAIT FLLYELEIALLLPLP*ALQTTNPLPLIGM SSLLLIILALSLAYE*LQKGLD*AELK EEQKTLQC
7491	21392	A	7551	1	317	TTFDNSALLFFWDGGEIEFHSVSQAGVQ WHNLCSL*PQPPGFKQKLILPQIVKENV SKISSQLLFSRVNINISPEQCITPESL QLARIGIFYAAKIHLTKGLRG
7492	21393	A	7552	479	183	YLFHVHTTASHSNGACTGPTVGDIIVSS TL*SMTEQVTMPLASAVSDGTVPVSRTA SRGSEQAESMVSSHEIILEHAGELVI ASPEGQLEVQTVIV
7493	21394	A	7553	454	105	KPPWGNKIRPPLFPGRKVPVPPRF*NPVR GSPPKK*FVFPVGRVLGTGVTPLSPLK TTPLLLWDPLSQPPGVKPENSLYPGK KRFR*PKFPPCPPANGTKRKPPLQKKK QVVL
7494	21395	A	7554	439	1	LLKRCVRKDSPPPQNKIFFFIIKKFVFF FAPY*VRKFYFLTAHFGKRPPQIYIFGP PPVFLIFCFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFNKQVFI ERLLCARHCFRPPPEEKTKNKIEANPN SEGEER
7495	21396	A	7555	323	82	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFR**AYL VRSPLLFLFVFSYF*LI*HVIHRYSVYI ELDVLLTGSKIILI
7496	21397	A	7556	194	412	KMYRTSLGHLVEAKKKKKKKKKKKKK KKKKKKKKKKKKKDSRGGVV*KKFGGG HNTRGVKIIFFSLGG
7497	21398	A	7557	414	219	KGFKKLFPPPVF*FFLCPPPIFLKGFP* GRKPPPKPNPQGGPPFFFTTPPLFFF FFFFFFFF
7498	21399	A	7558	377	25	THVGGVFWGKFFFSRRVFFFFHYHLIQIL SPPQKRPPPKGTPEG*IFPLFKEINFF FF*DDFFAPPPFFFFFLFFFFFFFF

1012

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPPGYFVFLVNGVFPVGPFGFELSPSPS *VAPPASQKGGVSGVSPCPRVWVPFFKK KKKLRGVEQRCTMHLLVYSKNVPVKPQK KSSIGSL
7514	21415	A	7574	2	383	PRVRSTAFSSIAHITRDVNYG*IIRYLH ANGAKKKKKKKKKKKKKRGGALKKKPG GGQKKGGGEEKKNFFFKGGEKKKPGGIFE KKTFFGGGNGAHPPQKKKTPGGKKKIL RGKGGKKPLYPWGEK
7515	21416	A	7575	402	69	KIFFKNSPLWKISHPPTYRGFFPPFPF* NFFFLPGPYFFLGGCSHLGPPPKKGGFFQ KIPPGFLFLSPFFKKKIYLFPPRIFLAPP GVFLKAPPPFFFFFFFFFFFFFFFFFFFF
7516	21417	A	7576	1	119	LTFHFTSKHHFGFEAAA*YWHFVN*V*L FLYVSIY**GS
7517	21418	A	7577	219	69	NDISANTAKKFWKLPRCPTTEGWLNT* LYIHLVEYYATLKVCGDLYVR
7518	21419	A	7578	3	287	HASAQNLNGYIEKSTPYERGFDPISPARV PFFIKFLVAITFLLLELIALLLPLP* ALQTTNPLIVMPSLLLSIILALRLAYE *LQKGL*AE
7519	21420	A	7579	10	125	ALQTTNPLIVMSSLLLIILT*ALQTT NLPLVMSLLLIILTLILAYEGLQKG LN*AE
7520	21421	A	7580	3	299	DAVVRLLDFFD*VELPTEARIRIITTSQ DVLHS*ADPTLGLKTDAPGRNLNQTFTT ATRPGVYQGQCEICGANHSFMPIALLEL VELKIFEIGPVFTL
7521	21422	A	7581	3	116	AFASKRTGLGVEEPSLTLE*LGGGPPP* HTLEEPVNI
7522	21423	A	7582	398	2	RVFPAPKNSLQIFPPLFFFWGSPWKFFF TFPPHFVFWGNGFNPFPAFLFRLEFPF GEKIPLVFFFFFFD*NFVENFFFLSLL FFFGFFFFNM*S*LF*SPANFNV*VTH LFI FMVFFHPDFWSFGPILW
7523	21424	A	7583	288	9	RGSKNLEKNSFPYKVNHNHNGSPLFPHL FFSPRGVGPFFFFFFETRSRSVIQAGVQW HDLSSPPGLK*SSHLSIQSSWDY*RAPP HPANFVYF
7524	21425	A	7584	1	124	RDGGFTMLPRPILLTGLKQSSCISLPK* WDYRCEPLHLASC
7525	21426	A	7585	339	76	THPGHNGISVSPKKKKIPRGGGPPPLFP PLPRVGGGDSL*PRKGGFN*TKPAPFPS SWGKKKELPFSSKKKKKKRKKGSISTPF SRIE
7526	21427	A	7586	205	87	SISLSLSLSHTHTHTHTHTLHSHPRCV PQPIGLPISKWAKVKELIT*R
7527	21428	A	7587	353	256	PHPSVTTLVTSQQYQDPPPAKRL*LAEG SDDC
7528	21429	A	7588	159	195	QICRHRVHINFLMSMGSIMITPPSFLF LNFL*SYVAQAGLKHLSQSDPPASASQS AEIRGMSHNAWPHF*YFVELVHFYINK FVGIELFILTS
7529	21430	A	7589	76	205	RKKPEPEKTCFDNITGNTYPCLSYEH SD*YVVRNT*LCAER
7530	21431	A	7590	218	20	LSLYLASHLWLPKPPHLEWAPSKSSLRL GTVASPCNPSTLGGRGWVT*GQSEST LANMAKPCFY

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7531	21432	A	7591	142	12	QIDYYYLFT*RKGLTLMRLVSNWLHIILLPWPPKVLGLQM
7532	21433	A	7592	2	224	QIIEALLITILLGHYFTLLQA*EYSKAPFTISDGIYGSTFFVTTGFHGLHGIIGSTFLTICYNPQLIFHFTSEHKFGLQAAP*YWLFDVVARLFVFPASIY**GSLFYPPTSLRVLQGSLLHHFRRDLRLNIFCNHRLPRTPRHYWLNVPHYLLQPPTNISLYLRT
7533	21434	A	7593	1	323	HAYGNTLVA*LVVTMTF*LPLVDGYIKKFTPYEGGFEPKSAARVLFSIKVFLVAITFLLSDLQSALLPLP*AVQTTNPLIVMAALLLDIILALSLAYA*LLKGLE
7534	21435	A	7594	1	104	RACVCVCVCVCVCLCLLMKMCVCVCVVCVCVCFCAC*KMCVCVCVCVCVCFCAC
7535	21436	A	7595	383	43	VFISETLCEHVAWSQTTIESLGLGTVAHTLNASTLRG*GRMIA*GQ*SKTRRGNMDSISSHSQTIAQSPHLLGRHQPKWCMCVQAAEAVLKGVETDASFQIQKIPINSLINL
7536	21437	A	7596	2	331	WPPTGITPLNPLEGPPLNTGGLLA*GVSMT*AHHSLGENNRNQVIALVITILLGLYFTLLRASEYFESPFTISDGVDRSTFFVTTGFHGLHVIIGSTLLSIWFIRQLICNFTSKHHFGFKAVA*YWLNFTKYLVPPTNM
7537	21438	A	7597	384	23	LFKTKQYRFLPPFPPLKIFFFPPLKA*IFLGGFSHYFPFPKKGFPKSPWF*IPPPYRKKHFCSTPKNLAPRWF*KRPPHFFIFFF**RWGLAMLPRLFSNS*AQAVLLLQSPEVLGL
7538	21439	A	7598	401	189	RVLPFCFAGWS*TPGLKCTCLGL*KCWDYRREPPCLIRFYLFVYFLRQGLAMLPSLVLSWP*VILLP*SP
7539	21440	A	7599	81	368	KCVIYPFLSITLGKAKYDFFFFLEKELAFFPQGEHQGNL*G*LPPLR*RDPSCLALPRGNGRGAPPSPTNFGFLGGNGVYPGPGGFETPDLK
7540	21441	A	7600	264	25	AVEHPQLRLFCSHY*NNIVEERLGLARTCNCPLEDKAAWIT*RHEFETSLANMVIIFCLDIGSKSFLSMRFSRCLLWKL
7541	21442	A	7601	1	196	WEPVLGETNVNSFNQKYINWPGAVAHTYNAGTLGGGGWIT*GQLEITLSKKVKPSTYFTNTR
7542	21443	A	7602	315	82	TCTQVFIALFITAKKFKLICPLTDNWISRVWYVHTMKHISAIKRKAVIHATMWVKLENIILSEIKQSQKATGCMISFI
7543	21444	A	7603	334	118	PKIKTEGGPPPKKNAGGMYK*KKFILVLAAPHPFPFVFSVFSYFSWFFRFFFFFFFFFFF
7544	21445	A	7604	3	288	DAYTT*NILSSVGSFISLTAVILIFMI*EASSSSSPPGGLRPRAFPVRPPGAGLVF*VSVPPDLQCSSLAGLQVLRFMELARLAPHIRWIIQ
7545	21446	A	7605	354	33	EGRARYTRVPQRPRFHLGLGIFAPQLGK KKKFSFSKKKKKKQLWLGA VSHANNLS TKGG*GRGRSFT*A*EFRTSQKLGT KGN MVKPISTNTFKNERGGAELS QL
7546	21447	A	7606	401	161	YLVSHLLQIILPPALFVVIFFF*DRVLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CGPGWSAVVWSYCSLCLGSSNSPPCQSL PSSWDYRHLWRFLMPRGILCVYV
7547	21448	A	7607	354	50	SGAQDPAGQHGTTPFSQKVPKKVYPAWW CMVVPATQEA*LKKSLEPWRRLFLREA FFVYLGWVLSNGEPPPLGGGGSVFLEAL EKSVGFSSLGFGWVFFF
7548	21449	A	7608	370	115	TIKNICNSWEVKIPRTFGVWKKLIPATL MDDLEGFKTLVEEPTEDV*ITGELEVE PENVIEFLQSHDQTSTDEGLLLMDEQRR W
7549	21450	A	7609	120	358	TTAVYLGHYCQSP*ILNGTVNT*PPVVH KDPILFLTPPCFPHASSAMNLQLSHISC NSKATPHPLGYQQTYPPLTVHMT
7550	21451	A	7610	3	164	HE*ASIP*NTHTHTHTHTHTHTHTFYK EENLSHLWNISCIFLGAHKGKKMN
7551	21452	A	7611	85	324	FRFFAFFFF*KKISFCQAGGQGGILPS LDPPPPGLKKFSGLTPPRSWN*GPCPPP GLIGVFLKKRGFPLVGRGPNLWT
7552	21453	A	7612	268	317	FLENCNPGGGGCSQPKLGPCPPAWGAK *ASLSKKKKKNKN*LSYKAPSYGYKKG
7553	21454	A	7613	101	339	AVPLTMVKIHALWKRVRFHNSKL*LP CDPAISLVSMYPKEMKSVCLKDVCSPRL ITGPLTIAGMWNPPNRSSMDYSG
7554	21455	A	7614	366	208	LELLTSGDLPASASQSAGITGISHRRAP GTLFF*AVNGGCGNQVFLFLRVNLGL
7555	21456	A	7615	30	328	NYCLDFHGETELGTTHFLTHPSTRAMVF EPYCQAL*IL*GVINT*PTVLHRNRSHI KAACLCQARTVVNLQISHINWKY*TPP HPL*YQQTPALEYI
7556	21457	A	7616	39	159	TPGLKQFHLGLPRCWDRHEPPRCPN MYLI*ISF*CV
7557	21458	A	7617	290	91	KMSFLIFFRDMASLCCPGWT*TPGLKQS SCFHLPRSWDHRCTSLHLAVKTFLYYFL KMFYQNVWH
7558	21459	A	7618	37	246	TQQLVYIYRYIDTHTHTHTHTHTHTS HTHYWIYTWKHTLKGPKLF*EKTMGST PIISWKERLSLYRS
7559	21460	A	7619	23	190	IPPQPCPFLLSLFC*IDMSCNMCAVC VCVCVYVCVICDMVLLPFCCKLECSK
7560	21461	A	7620	367	2	FFSPKALIFLGGGGPIFPKKSKFFSKI PPGGFFPLPGFLKPPPPPLF*NPPLKKK NFFFPPEPWAPPRVFFKGPPPPFFFFF FFFFFFFWSSRFLIFPQFFFLNNKIGKK KIFRHLGAG
7561	21462	A	7621	6	25	SVILQSTIIIFIATTNLLGLLPHSLTPPT QLSINLAMAIP*AGAEIIGFRSKIKNAL LAHFLPQGTPTPLIPILVIIETISLLIQ PIALAERLTANITAGHLLMHLIGSTTLA ISTI*LLYNNP
7562	21463	A	7622	383	67	AFLNPGKKPFPFGFKRFFCPPPKKWGK NRGPPPRGKIFFFVFVKTKFFHVGPFG F*ILTSGDPPGQGGGLGGFFFFQIGGT GDLNLSHKSPMPFTINTHNG
7563	21464	A	7623	372	35	TGGFWGVFFFFFFFKQGFPPKSTGGLGP KNPCPKGPRVSPPPPP*NRGPQGPPPP PGKKPFFFFFFFETGFPHVALAGLEL PGSGNLPSTVSQSAGIPGISTWPNGVFQ
7564	21465	A	7624	287	6	LSGVVWDHMINICLFFKKLPCCV*KWL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YQPVAVAHACNPSTLGGDRWIPGGQEF KTTCLSLPKRWHRREPLYLAFCPPFYNG IGCLLIIGF
7565	21466	A	7625	271	277	NRGKGKGTGSLGILEKNPFFGGGPFWANP PP*GLKFWGGVGPKRPPPKRVFFQNSQ GTSFPLPPVLKSGPGLVLKKAPQKEKNI TFQPPGKFGPPRGSLKRAPPFFFFFFFS LRKSSVIEK
7566	21467	A	7626	2	269	LLGELSVLVC*FPPKHTTFLTGLSLILF TGLYSLYILTTFQWGSLSLTHIINLKPLF TPKNTLMFIHLYPILLLSLNPDIKKKK KGGAF
7567	21468	A	7627	397	164	FPPPKKVFFQKNPKKKFSPPRVF*TPPP PFFFLPPPKKKKFFFSPP*IWPPGLIF *KPPPLFFFFFFFFFFFFFFF
7568	21469	A	7628	3	324	DGMNVSTLYGATGSHGLHDIMGSALLTI WYIRQLILHFTSKHHFGFEAAA*YWHFV DVD*LFLCGSIY**GSPGGPKFSRGGKG IAPHWGDD
7569	21470	A	7629	2	246	SGLGTTLS*KNISVLLTGLKILVTGLYS VYIFTATQWGSLSLTHINKIKP*LTRENT LMFIHLCPILLLSLNPDISYPCPTS
7570	21471	A	7630	112	290	LISGKGQWTQMRPLPVLVTLFTDSFSK*K NPSTLGEQCGRIT*GQELETSLGNIVRP HLY
7571	21472	A	7631	248	2	KVPASGKRPEPHWYPYHAVPGCGRIPAT AIWTQKWYQGFPPALSPRLCSGAISAH CYFGFPGPSDSPAAPS*LAGTTGTRP
7572	21473	A	7632	383	106	GWGQCFKPATPALERPNOECFRPGVLN QP*PQNKSPFFFFFFFFKKKYIYICMVV HAYNPSYSGG*GGRIT*AQFKTSLNNT VRPHLYKK
7573	21474	A	7633	435	133	YACLGLPKCWDNRHEPPGLANFCIFSKN RGFPISDRVVINSWPRVFG*PKPPKMG FQTLVQASLGFLILFLKTGFPPFSQHE EQGWDTSSFQHRFFRGK
7574	21475	A	7634	1	209	NAYRIVILCQKLFPLLSGKMNFKKTRCW LGMVAHACSPSTLGG*GGRIA*AQEFGT SLGSILRPCHCKK
7575	21476	A	7635	117	495	STSFIDKVQLRHSFLFFSLFFETKSCSL TQTGVQWHDGSL*PPPPRFK*FSLGLP LSSWDYRHAPRPASFFVFLVEMRFHHV GQAGLELLTSGDPPASASQSAGITGMSH HALAHLVFSSGKS
7576	21477	A	7636	1	241	LEGSSDSPTSASQVAGITGMCHHAQLFF FLAF*LIFNF*FFFGNSFFVFPQAGGHW GIGG*LNPPPPGLKRFSCLTWGG
7577	21478	A	7637	3	93	EAEAGESLEPGDRGCSKLRSCHYTPAWQ QSVTLVSKKETKNTKTSEVPFGVLNLLY KVSINILIFKEIFYQAPLILV*DNPDS TLSSALQPGQSKTVSNKTKQKTVS*PG NRV
7578	21479	A	7638	46	228	GTPHIQPSKSVFNNVHGPGTVAHTRNPN TLEY*GGSIT*GHEFETSLGNIVRLPPP SLQSI
7579	21480	A	7639	1212	1023	KNHSNEWIKKM*YICTMEY*AIRRNEIM AFAAT*MKLETIILSEVTQEWKTKYCMF SLVSGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7580	21481	A	7640	479	318	AEFLNLGDGGCSEPR*HHCTPAWATRAK FHLKRKKK
7581	21482	A	7641	470	172	RNIRPRENQYPVFMVAFFLIANKW*QPK CPSSEAMNKLRCIHTTAVLHSSEEEQP TDTNNSDLRSIAPSWRSQTRAAHRMI PWHSGKGKTPSTENA
7582	21483	A	7642	2	201	AGAPPPAWLP*PCRLISDC*ASNQRDSVG VGPSEPYATVRKYLELLLCQMHHDMCTY RFSIRIVLNL
7583	21484	A	7643	521	385	GGSPLETH*YTSQGGGIPYTDLTGHHPS QGRIQEAPKLTHL
7584	21485	A	7644	331	3	DLVPPKGGGGKKTTPRIKFFPPKGEDFF FFTPHYFVVVFFVFWGGAFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFT*DYIIS F*EERFNKFYRCQSTLVQIGHTSNL
7585	21486	A	7645	88	367	HCSFLLLGKKKKKKKKKKKKKKKKKK KKKKTKKNEYKNLLGGAPP*KPPSGALY KYRRENFIPFSFERVSKYPPRDLCCKNL FWGGLNIPS
7586	21487	A	7646	378	37	FFFPXFFFFFFSPDPXFFFLXFFFXPFF XSFSLPPLPLXXPPPPPLFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFNI*TI VL
7587	21488	A	7647	34	293	TGIPGVISAIFMI*EAFVSRKRVLIGKK PSINLE*LYGCPPPYHTFEPPVYIKSTQ KRKESNPPKLGSSQPHGLHDFKCKKI IK
7588	21489	A	7648	22	106	KNFLPLTLTL*KNFLPLTLTLI*YGS IPITISSIPPQT
7589	21490	A	7649	1	231	PDRITISKDISK*MVLVSKKKKKKQKKK KKKKKKKKKKKGGGPFKKTGGGAPKNP GEEKIIFFLGGGKKNWTGFF
7590	21491	A	7650	79	286	VVSRLVSLRNPCI*IKTCS*AKKKKKK KKKKKKKKKKKWGAFLKIPWGGPIFFG GKFFFFFFGGGY
7591	21492	A	7651	57	375	SGKSEFHRVPQWPGTGADACNPSTLGGR GRWIT*QGEFETSPQGDPISTKKKKKKR GALLKDSLGGPNLPFGNPKVFSFRGGI LKPTWEFWEGTFILGGEKIGPN
7592	21493	A	7652	3	357	LAFLALSKITHASIPVSSPSKSPRS KGTKKKKKKKKKKKRGGPLKKTGPGPK INGKKKKIIFFFKGGEKTPGGILEKKL FLGGCKMGPNPPKKIKPLGEKKNF*GEK GEKKP
7593	21494	A	7653	113	378	MGAFLNLPFLMGGGNPSGPNHGWV LGA GSYLPGKTPPKKSQKGGPPDL*GRGG QCSPGTKPGGGGEKTGLAPPFTKSLGFL LQKK
7594	21495	A	7654	341	147	NFFFSLKPIFFGGFCPIFPPPKSFFS KIPPVVFSPPP*EKIFFPPPLNFAPP RVFFKGPP
7595	21496	A	7655	395	3	FFFFFFFFFFFFFRGKSE*FVLFPVSPAP SLRG
7596	21497	A	7656	2	162	ESKGYTHTHTHTHIYTHIYTHYTPREH *PKKADVAMLIILNKLFFKPRCVALL
7597	21498	A	7657	333	28	LEFFNFNFFSYFLFFS*RVWGPERRPPP LKKAV*KFFLFDIFLFFFFFI GLGFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFLEHIRLLMFVTFSSHR
7598	21499	A	7658	1	137	HSSIGDRVRPCLKKKKKKKKKKKKKKKK KKKKKKKKKKKKGGGLF*EKKKKKKKKK KKKKKKKKKKKKGGGLF
7599	21500	A	7659	236	32	IIFLIKFLYF*FIFI*F*FFLTFFYFKR LKILFFFFFFFFFFFFFFFFFFFF*KNFIK NIIYFFIFYLFYLLKFFIYIKTFLFLKI
7600	21501	A	7660	301	65	KAPPKIFWFFFFVFFVFFVSYIFFFFFF FLFFFFFFFFFFFFFFFFFFFFF*FWKS LAAT*FLRGFETF*LAYILKTT
7601	21502	A	7661	70	273	KHSPPHKPSD*NTLTKKKKKKKKKKK KKKKKKKKKKKKKKKKGGGALIKNPWG GPIHRGGEKFFFSFLRRD
7602	21503	A	7662	1	353	ILIINTLLALLLIITFGLPQLSGCLQK STPYEGGSDPISPARGRFSKGLPLQAMT FLL*ELEIAL*PLP*ALQTTNLPIDM GCLLLNIIILCLSLAYE*LP*GLDCSRYH SQRIQ
7603	21504	A	7663	1	131	FIRQLIFHFTSKHHFGFEAAA*YWHFVD VA*LFLYVSIY**GS
7604	21505	A	7664	2	192	PLSQSLY*LLAADLLILT*IGGQPVSY FTIIGQVASVLYFTTILILIPTISLIEN KILKWAY
7605	21506	A	7665	356	2	TFFFLSSPGSGSGSPTPARPKKNPPPWG GGLPLFSRRGALFPKNFFWGGYPFFFLF *KKPPFFPPGPQSPVTSKDVVPLRM PPPRPHVRPLGLPKKSFSSPRWEKQVKK TKKRAA
7606	21507	A	7666	312	2	GFFFFFFFFFFFFL*DRVLLLLPRLECNG VISAH
7607	21508	A	7667	1	233	FWLSSNAEFDSANSCECLEVQRMIDQD SFPTYHYFDMYVCIYV**RSLAVSPGLV SNSWPQAILQPQPQSLGLQE
7608	21509	A	7668	174	295	IFFLPFCGEHSLAVLRLVLNSWTQAIL PPLPP*ILGLQA
7609	21510	A	7669	183	330	NKFKLYWSPVAMAHACNPRTHRGWIT* CEEFETLANMVNMVVKPLY
7610	21511	A	7670	3	319	TSNTLLALLLIITF*LPQLNGYIEKST PYESGFDPISPARVPFYIKFFLVAITFL LFDLEIALLLPLP*AVQTTNLPILVMSS LLLIILPLALAYE*LQKGLD
7611	21512	A	7671	1	313	ARGERERERERERERERERESGGGGP TQTDCKGRNT*RGREIYRESE*DDRPP FLPTYRVNLQRPVGLRLKAGDKTFCL ILTLARDYVWPDYRMKRAHDM
7612	21513	A	7672	3	91	TRRERERDR*REREREREREIIFREKNSQ S
7613	21514	A	7673	1	115	DELANLFII*KAGFPVLRLVLNSWLQV ILLPWPPRLN
7614	21515	A	7674	3	232	TRRERERERERERERERERERERE RYRE*DRERERERERDCVWGGVISLSR AVALSGAPAVGRQTRERISR
7615	21516	A	7675	1	234	ARGERERERERERERERERERERE REIERERERLTQRERERERGRGVHAPL AIERG*KPQGGFWWKEERVKKEPLGKLL
7616	21517	A	7676	1	262	ARGERERERERERERERERERERE RERERERERERERERARAPQNL*ERWAH



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPPAPGVSLSWREHTRGGPPWGKKEGGW GRLGHPPPSILRAKGG
7617	21518	A	7677	214	2	QQASVAQAGVKWPDLCSLQSMPPRFK*F SCLSLSSWDYGPPPPCAGLHIWRRNVT LALQGLPTTSLALV
7618	21519	A	7678	3	341	HERHELEELIKTLFFFFFRKKNHLCKP GGKKRGPIWFLKKFFSPQKKPPPPPPF LREIGAMAPQPGGGLLI*NKTPFRPRGQ GGPKPPTPGKPNPPPPKGNFPL*GNP QPPGSPTPPPPQKVIFPFEHQHA
7619	21520	A	7679	1	357	GTRINTLLALLLIITTF*LPQLTGYIKK STPYECGFDPISPARVPFSIKFFLVAIT FLLLDLEIALLLPLP*ALQTTNLPIDM SSLLLIILTLSLAYE*LQKGLD*TDFY SVGGEAN
7620	21521	A	7680	365	1	PDASQ*HCTNGQSNRLNLLIKALLTTA KIWIQPKCPPVDARIKKMQ*IPRMEHPS AIKKEILPSVATWMSLEDTPVPSRISQAQ KDKYHTVSCMWNLRMLNAEPEGRPVVPR GVQGWGAARA
7621	21522	A	7681	387	3	FFFKKEFCPRKKAKK*NWGPGLGPRG* KNFPPPPPQKRKKGGPPQGGEILGFL* KKGFPMPGRGSKLWPLGFSPLNPPKRG GKKGEPPPPQRGKPGGPPPKGLFFFFF FFLRQSLTLSPRLLV
7622	21523	A	7682	107	290	ELNKRWGLGAVAHACNPST*ELNKRWG LGAVAHACNPSTLGG*GRWIT*ALEFKI NLDNKRSHLKIKKQHQQQKNSGLDA
7623	21524	A	7683	1	348	GTRERKPTWLWYHRERGMERDCSCVPGS SGISESRVWVQVGMEVYPAIIYLCLEPK YLVISEFSPAARIWFLGLSVVAHTCNPS NLGGQGGRIIT*SQEFKTNLANIVRPHLF FFLF
7624	21525	A	7684	364	77	GGPSIFPRLLALLGGGGPGGPPLPRGNFS FFNFFVKKGVFFPPGVFFPLPPGVLPFP PPFWAPG*PRPPNFFLGAPGFFPFFFLG GGFFFPVAPGGV
7625	21526	A	7685	3	24	HEETIIQVKREPVE*KKIFANPTFNKGL TSEIYKKQLNRKKPNPI*KQSSK
7626	21527	A	7686	1	125	GTRPGMPGTYSNYPDTYTA*KIISSTGS FISKTAQPGPWE
7627	21528	A	7687	459	298	LSLPSSWNHMCALPHPASFFL*RQGLAL LPRLVSKSWAQVMLLPWPSKVLGLQV
7628	21529	A	7688	374	248	FPHHNVEVIVRPLSPRYPIISHVTCTY RSRWP*ASEGSQKK
7629	21530	A	7689	284	163	GTVAHTCNLSTLRGGGWIT*GQEIDTS PAWPPKVGLQA
7630	21531	A	7690	83	255	KVDYVSIKSEFF*DRVSLYHPS*GTVAR S*LTTTPNPGIKQSTCTVPSSWDYRHV LPLPTRTIFSVPTQSLATILI*ITNLNY INLGKIHFL
7631	21532	A	7691	3	193	HERLDPADFSFNFFSVDVGLAMFPRLVL NS*HQVILLWPLTVLDYRHELLRPAWG FYLYNFT
7632	21533	A	7692	1	364	NFKSFFP*LFYLYHLLFFGFGLFLFFLI KLGSSLFINFSKSVL*FTNWIYFSVLV FTDFCFIFIISFFGFSLIYFIIAVFPLK FIGFILSFI*ITVFYQQAQWLTPIVPIIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WVAEVRGSL
7633	21534	A	7693	370	151	GKKYSVASPGKLWPPQGFKTAPPPFFFF FFLK*RCGFTMLPRLVLNPWPQGILPPQ PPKVLGLQVLRHHIWL
7634	21535	A	7694	3	373	WPGYTLNQAYAKIHFTIIFIGANLTFFP QHFLGLSGMPRRYSYDPDAYTT*NILSS AGSFISITAVILIIIFMI*EAFASKRKVL IVEEPSQSAGITGVSHCARAEYLFIDRR DGLSLCWPGWT
7635	21536	A	7695	406	394	KFF*KKFLFPPTPTFLLEACLFFFLPPI KGFLFKYIAPGIKTPPPKKEKFSSSLKV LFSPPYFFFIPPPPIFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFEG ECWRL*W*FYFYFFKESPHCIP
7636	21537	A	7696	2	334	ILINNTFLALLLLIITFWVPQLKGYIKK STPYECGFDPISPARVPFSIKFFLAIT FLLFDLEIALLLPLP*ALQTTNLPLIVM ASLLLIILALSLAYE*LQKGLD*AE
7637	21538	A	7697	2	95	LNLTIIYIILTTTAFLLLNLSSTTTLLL SRT*NKLT*LTIIYIILTTTAFLLLNLS STTTLLSRT
7638	21539	A	7698	423	326	RQCLTMLPRLVSN*SQVILLPWPLKVL GSQA
7639	21540	A	7699	400	32	FHKEYESYFFSPNQPFPPPPH*NFY VGVLKKQPPKKKFFLLFTPERFFPFEL *KKNIFFFP*YFFFPVLVIFL*PPPLFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFSSNSFPFY
7640	21541	A	7700	125	407	FINFSTFVVKPTTCNMQKHTPIARTKD LCITIFFFFLEKNFLFVQVGGQGGILG *LKILLRG*KQFSCFTLPGRWTNGGIPP PPKNFLKKFF
7641	21542	A	7701	50	225	PWNMVKMSCWLKGVAVHCNPSTLGRGR RIA*AQEFETS*VTQ*DPVSVIKKRKN FK
7642	21543	A	7702	2	146	EIALLLPLP*ALQTTNLPLIVMSSLLLI IILALSLAYE*LQKGLD*AE
7643	21544	A	7703	1	93	ILIINTLLALLLLIMTMGLPQPKGYIKK STP*ECGFDPISPARVPFSIKIFLIAIT FLLFDLETALLPLP*ALQTTNLPLIVM ASLLLIILSLSLAYE*LQKGLD*ALLL LIMTMGLPQPKGYIKKSTP
7644	21545	A	7704	2	112	GRVGKHHFGFEAAA*YHVFVDVG*LFLY VSIY**GS
7645	21546	A	7705	1	325	TAGQFLPKLSILLSYNPAITFLGIYPKI LKTIVYMKCTCTWMFIAALFIVVQTWKQQ SKLWYIQTIKYYSVLK*NELSSYENTSK KLRCILLRERSQYKKPPYFLIPTM
7646	21547	A	7706	2	169	SRSRAGTLAT*TINLPCTLMIFTLIVL TILEIAGALIQAYVFTLVVSLYLHDST
7647	21548	A	7707	263	346	MLINVPLGLLFVGVILSKESPSVDQGGV QWINLFSMQPPPTGFK*FSCLKA*ASDN LSPHEQYRLALSFLKLT
7648	21549	A	7708	343	163	PKEF**RQGFHVGQAGFKLLRSGNPPP SASQNGKITGVNPLAWQTNNIPPMAP
7649	21550	A	7709	459	144	FWPGASSHAFDPTTLGGRGGRIA*AHF KTSLGNIVRPPSDTCNPKVLGLLA
7650	21551	A	7710	2	83	NFLPLTLALLI*YVSIPTITISSIPQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7651	21552	A	7711	19	181	KVHTKACT*MFISSLFIITKNWKQPIFSSIGE*VNKT*YIHTMEYLLFRNKRK
7652	21553	A	7712	392	49	SDIFNSDIFSHY*CSVF*SYLAYNRYLSFL*LFLEFIYSYP*IDHAFHCFLHPVSSFWDFFLFIFSFLLFSYFYSFYF*FYF*FIFNFIFNLFFILFYF*FSFFSKCLKFPC
7653	21554	A	7713	334	208	FFF*EWVLTTLPRRLVLPQAPAILLPWP
7654	21555	A	7714	2	408	PKVLGFTGVSHIKI WNGMEWNGLKWNRLERYGMQWNGLEWNRTE*TRMVWNAMEWTRIELNGLEWNGMECNGMHLNGLEWNGMERNGTDPWNGTDPEWNGTDPEWNGTEWNGMEWNEVDSNGMEWNGIDSNEMGWTRMEWNGMESTRV
7655	21556	A	7715	362	223	VWFMPIIPTLWEAEVGG*LEPRSSKPAWATWQDAIFKKKFKHQHP
7656	21557	A	7716	2	335	LIVIINTLLALLLIITF*LPQLNGYIEKSTPYECGFDPISPARVFSIKIFLVAITFLFDLEIALLLPLP*ALQTTNLPLIA
7657	21558	A	7717	2	142	MSSLLLIILALSIAVE*LQKGLD*AE SITL*LPQLNGYIEKTPPYECGFEPICPARVPLSIKFFLEAITFLFDLEIALLLPLP*ALQTDDELPLIVMTSLLLIILTLSLAYE*LQKGS*AYMPRPRPFVHKILLRSYLLII
7658	21559	A	7718	6	92	FFEAAA*YWHFVNVV*LFYVSIY**GS
7659	21560	A	7719	417	164	PLEPLISGRGLPQIAPPPKKGSPPKSPRWFFFPPP*KKKNYFPPPKILPPPGFF*NPFPFFFFFFFIFFYFFKTALPL
7660	21561	A	7720	25	401	THNS*DPNWD*IPHYA*P*TSTVKKKKKKKKKKKKKKKKGGGLIKKFRGGPKYTGGGKIIFFFFMGGKKKPLGDFLKKNFFLGGGNLKGHPKKLSLQKKKNFKGRGGKKTPLCRRGKKFS
7661	21562	A	7721	388	2	APPPFFYFFFIFFFYFPLGVGFSGK*N
7662	21563	A	7722	389	71	SKVFWISNFKKILRVFICSLEKGINPFLBKCFYMFVFVAFIIRLNFSLOAKFFLLNFALLPFPEIFFFFFPFFFPQIEDFWHPYIEQVYQLSLFSL
7663	21564	A	7723	77	220	FFLPHQKQVFPPPPFFKIFFFSSRVFFFWCGWAQKPPPPKFFFLKTPPGFFLPPP*KKKFFFSRFFLPFGFFFKPPPNF
7664	21565	A	7724	16	258	FFFFFFFFFFFLLN TPRRGWAYWLMPAYPAILEA*AGGLLEPKSLRSTWPTWRNSISPKRK
7665	21566	A	7725	353	111	ISSFVFKRRSFAMFPRVLNSWPRVLP
7666	21567	A	7726	2	185	PRPPE*LGLQACTTTTFNFDFGIFLRPLKEDVTARDQREILYVFALFYGGGA
7667	21568	A	7727	346	143	IFGAGPRFVFKAGGQGANRSLSLKFPFGNKWSFPFSPSKKWEGRG*PPRPPFFFFF
7668	21569	A	7728	411	221	FFIREGVSLCCQGSQIPGLKQSS MSMGHTRLSSAWTGKPPLSVEDDFEKLIIWEISGGKLEAEIDLDPKDEDDLLLELS*MITD SQAFLYLESFLLLLLL*FLFFEMESHSVTQDRVQRHLSSLQPLPPRFQQPSRLTLPSSWEAEVGG NLRPPGSSYSPASAS*TAGIPGARHHTQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIFAFLAEILKNLAKLYLIPRKPNIIYYL PNCYINI
7669	21570	A	7729	2	303	AAASTNMLLFFLGRHLVVEWLGHMVGLI FTFKKLPNQAGRRGSHL*FQHFGRQRWE DHLRSRVQDHPEQHSKTPSSSLQKNKMSI ESNLLNIHKLFFSTGRM
7670	21571	A	7730	67	65	SICEYCFVSSVFVLKRLFSVMQAFSLEG CVSCQS*AFLQHYLFKKLYFLY*WGLTM LSRLVLNTWPQVIHLPPVKVLGL*APC GNEA
7671	21572	A	7731	354	238	QSILDDVAMVLD*QAEVFIVKMWRLLIY VHEAKKIGLVK
7672	21573	A	7732	33	186	RGALAVLSRLILTPGLKESSCLDLPGKW DYRWEPPRPGCFF*LMVLVLSF
7673	21574	A	7733	1	181	VNAGADCSSIGGVPFLQHKKCHGKDYEP RGITTLERSYVEETTEHLVSKSK*PLRA QINL
7674	21575	A	7734	336	80	HKLKEPPGVFPVFPFKNLEFGPGPPKFF FKKAFSPILSFFFGKIFKIPRFRGENFA P*NFGKNS*KPRFSPPPPKKGGFFFFF F
7675	21576	A	7735	2	163	TPVSTGTPVPTLT*VPSPFIIPVSEKWA GCLHLCLNFTCTELRLTSLLTIRS
7676	21577	A	7736	87	258	KAPSVCLFSALLMLLRMSARTSVCTVRP LSPS*AVISPTCTYTSRWPEATEDSQK
7677	21578	A	7737	1	103	LDSKGIYMTLQPSKLEPKLEANVEIREH MLENSSRF*RDLYDSAAFKARTKARSKC RDKRAHVGEFF
7678	21579	A	7738	193	300	GGLPPPPFFFFFLKKRGFPVWTRGGPN PPPLEMGPTPPKGWNYGGGPPP*FHPF GGVGPPISKGGGLGPPRVITQKPLFFKK KKKNGGGGKPPYSPFLGGVKQKGVNP KGGGSKPKFPPPPPPGGKKKKPFLKKK KKKK
7679	21580	A	7739	150	17	GRVAQVWVWLMHAIPAL*KAEAGRSLEPR SWTPDWGTWHLPISTK
7680	21581	A	7740	1	358	SPPRPPPPPPPPKKEFKKLENPPPPK NPQKQNPPTKTKKSPITTPKKKPKIGT PPQTPKKINCS*KKKNPPENKKGLNYP NKNPHPHAPPKEPKQREKPLVPTKKKKG PSPKKKK
7681	21582	A	7741	235	147	F*FFLGDEISLCCPGWSLTPGLEQASCP GLPRRWNYRCEPPHSVKITF
7682	21583	A	7742	131	12	AASTYQG*FKICGAILRLMPIVIEFIPL KILQIGPVFTL
7683	21584	A	7743	1	184	NQYPWCFCNHSMSGKESKTLNRSGMVAH TCNPSTLGGQGGRIT*A*GSKSSLGDKV RPHLY
7684	21585	A	7744	347	202	SLFVETGYHYVD*AYLELLASGSPASAS QSFGISSVSLCTQPMFQFE
7685	21586	A	7745	138	263	KKRKTYIHTKTCM*MFIAALFIRVRKWK QSKCHSADEWINKF*YIKICLSIHQLND IWIASTF
7686	21587	A	7746	358	169	AAAVAERTONTEKTEDLVGLWIKKVIY WPGVVAHVCNPITLGGRGWIT*GQEIE TSLPTRR
7687	21588	A	7747	78	346	AIQMLRNQVKIKLPKSPVEIIPFKIVPQ FOVQKIKSQNNFLLLFQESQIFFATSTG

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						SVRPLSPS*AIISPVTCITYTSRWPEVTEKSQKK
7688	21589	A	7748	222	98	KKKARHGLGAVAHACNPSTLGGQGGRIT*VQEANIVRTCLY
7689	21590	A	7749	314	52	LNNVDLQFFFLGPRKKRNLDSSSLFVSAEEVRLMYCFNKLAILHYF*FSNKFIVFV*KFHGHLLENMGSKFDNIGMNAMANKDNASK
7690	21591	A	7750	371	216	YHTHTHTHTHTHTQIPSLPLNLEGPVGYYLLSCGSLHLKNLW*KCMRKERKK
7691	21592	A	7751	3	238	FLIQTFGFHVSAQAGWELLR*GNLPALAFQSAGITGMSYLCVAESLYLLPPFLKILCSSLTLSPYDTWKVALLCSYTV
7692	21593	A	7752	2	247	NSDIFDIYIIQYIFLIYLIYIIQYIYLI*VFLIIFFKFTLK*EFIFISLSISFRLAFIVYRDVILLFLFFFS*NFVGDSIS
7693	21594	A	7753	359	2	TLKIRPLLPLPLFFFFFF*KKKIFFFFPPGGGKGV*SGFYLMGRGTFSLFFKRFFLFYPPKEGGLRGSPPPPSFFFFFFFKRGFPFLARGV*KKGPGQTPLPWLPKSLGLRG
7694	21595	A	7754	3	174	CSVTQAGGQWCGHSSSLQP*TPGINQSSYLSFPSSWDYRHATMPS*FLFFIEIKMLQ
7695	21596	A	7755	292	219	IWPLSHVHSNPETHSPSQVDQGLFTTLLPCLSGMYVQFPPLAEMPFISSLLLENACLSLCEGSEAQKPLLWEGLSYLPPPLNQLPLCL*LCVCISGGVCRCMLCILGVCMCMHVCVSVCPCTHTLAQETKGC
7696	21597	A	7756	2	195	VALMADGAIDTESNDYGAFMPLGIERGLDRIWEMPELWLRPNEFDCMTD*PCIQHAPSVSCGLA
7697	21598	A	7757	4	280	DHIVDMITPSFTRRTIAVF*DLNLYIVI RGHITSILKPNKLNKLWITYTIEYYSALKGNEILIHATIWINLENMQDEINQTKDIYCTISLI
7698	21599	A	7758	352	107	FLTRASRGHNGETIVTSWPGAVAHVCNPSLGGRRRWIT*GQEFKTSLANMVITFFISKNSNRFLSQFPISLRPTHYKVLS
7699	21600	A	7759	92	4	RPSRRRGGWT*GQEFKTSLGNMVKPCLY
7700	21601	A	7760	92	4	RPRRRRGGWT*GQEFKTSLGNMVKPCLY
7701	21602	A	7761	328	124	PLFSFLFFPFFFFFFFFFSSRRDGVLPCCPGWS*TPGLKLSSSLCLKPCWNYKHEPLHTAHHNF
7702	21603	A	7762	1	167	VDSIDKRPGAVAHNNPNSTVGSQGGQIT*GKFNPSLANTVKLFKKKKRKRKRGALF
7703	21604	A	7763	309	226	RPRRLTLSPRL*CSGATSAHCKLRLPGR
7704	21605	A	7764	349	7	QVFCFLFFVCFSSIFMTFNE*QGLKVTSGLSNVY*FLLIWILGKITQYDIGRCFSEYGSPEQHNGLGIVRNASSRLGVVAHTCNPITLGG*GGWIT*GEGFETSLANMGKPLLY
7705	21606	A	7765	43	339	FFFFLFFFFFFFIIFLLSFFF*DHFFVSLFISNFVFLPPIFIFTVQAHLFICLLFFPICMFLNLFPNFNYYFYPPPLFFYL LFFFFG*FFNHLFY
7706	21607	A	7766	352	102	HTSCLIIKSSLSKMNISCVSSSISFFF*FLIBIGSR*VVQAGLQLLGSTDPASAA

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						SQSARITGLSHHAQLSSTSLVVENVEW
7707	21608	A	7767	346	90	TPFSFFSFPFPFFSFPFRFFFSNR DRVLVCYLGS*TPCLK*SSQGLPKCW DFRCGPPCLTSTAFYISITVNFSPSNCY S
7708	21609	A	7768	278	87	AASTGVGPSEPSAGYLLVCRLLRSLEK CSIRVGVT*FSRCHLSPLSLTRKGNLSLT PCASRV
7709	21610	A	7769	5	272	AVYHPINESCVLNIGKDSCLLY*LFEKK KKKKKKKKKKKKKKKKKKKHYE*FNTFPG VARKINLFLCIQKVDAGGGLTWGGGPP IFFFL
7710	21611	A	7770	198	33	QRQPSRQCRAWLGMVAHAYNPGLTG* D RRTT*GQEFKTSLGNIVRPYLYEKM
7711	21612	A	7771	97	410	A*WLMPIPIIWEVKVRLLEPGSLRPS WATWRKP
7712	21613	A	7772	5	415	ILCVYLHFGVTHPFVHL*YMHFLPLTLA LLI*YVSIPITISSIPPY
7713	21614	A	7773	1	342	VVRVTSGHSG*AAAYAT*YILSAEGSFF PLTEELLI*FMKREAF*KR*VLIIEHP SINLD*LYGCPTPYHTFDPVYLSKRR RRDSHPKCLASRLPHVLHDFKKKKGG RR
7714	21615	A	7774	398	122	SPPPPFPSSPSFFLPPSSSFFLFFLFF FFFFFFFFFFFFFFFFFFFFCRD*VSLC CPA*SQTPGLK*YSYHGLPKFWNYWHEP PCLAYFL
7715	21616	A	7775	1	336	FNFLIIIIEMESRSVSAHCKLSLPGSS NSSASASRVAGSRGAHHHTWLF F*KKKGAPPGQGGLTLKKKNPPPRAP QRGGINGTTPRPQNGGCKFFPWGEKKKF
7716	21617	A	7776	1456	1232	FAIESHCVTQAGVQWCNLSLQPSPTBF K*FSCGLPSSWDYRCVPPHPANFYIFS RDRVSPCWGWSKTPDLK
7717	21618	A	7777	400	2	NTEFPYGPPIISLLGM*P*EMETYIPRKP CTOMFLEVLFTIAKK*KKPKRS*LING* ILVYPLMEYYSATKRFDMIHNTKNVD AI GNIILSERRQM*KTHIVYSIHRASCTAE VRIKVSYKRAATWIKSILIA
7718	21619	A	7778	360	218	PYLANF*NLL*RWHLNMLPRPDSNSWPQ VILSLWPPRVLG*QRGRVEQRGARGNW MSKCEGGDCLCWAGA
7719	21620	A	7779	1	372	FEVRSCSVAHAGVQWHDHGFELGSSD DPSVSASCISRTGASHCTQG*L*LLTK VL*VSACLSVNTLRLTSLKSDTFLGS RSKLSLGLSLQTYISPSRHFQILLCFR SLFPRFLVKHKK
7720	21621	A	7780	372	219	ATSLLSYFKKLFPQSSATTTTISQ*S STSRQDLPPAKRLELETSDDP
7721	21622	A	7781	358	145	IKNIHDSWEDVKISTLTRV*KELIPVLT DNSEGLKTS*EVTAEVVEIARELELEV EPKDVLVQFHDITIN
7722	21623	A	7782	317	146	GRVDCCKPFYRFQMLLVRLGMVAHVCNP STLGGRGGWIP*GQEFKASVSRMPRPHL Y
7723	21624	A	7783	13	186	DRVSTQTSWAHPPTSAS*VAWTGMHH HTWLNFFVFFVEMGFHHVQVQVIRLPLLS WK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7724	21625	A	7784	339	221	KWDLAMLARLVSNNSWLQSSYLSL*NCW DYGSEPLCPAL
7725	21626	A	7785	355	3	FGNSGRVDLFFFFFFLDVRVSLCCPGCSA VTNLEVHHSALQPQTPLKPPSSHLSLLS SWDYRRVPPHPS*GLF**GK*YSITQLR FLNLHLESGLRSLLPKPVASTVRIRTQS GLGLK
7726	21627	A	7786	1	201	QQFSHVFRLLFQFSFSCQEPSSHIQPG VCTRNTKVSQAW*CVVPVIANREAETGE SLEPGRRSTRP
7727	21628	A	7787	270	1	RPRRHLPVCVLMGLPKCPGLPHTLTTLTLP YTLTTPSPTRSLGPPECK*SFHLSFPSS WDYRRMPQRLANFCRGRILLCPDWSSS PGLKQS
7728	21629	A	7788	229	2	DGWVRINWAQPGTVAHAYNISNLGGRGR RIT*GQEFKTSLTNMEKPCLYSDHEVRS LRPARPTWRNP ISTKNTKM
7729	21630	A	7789	118	263	CSKSYYPDAVVHTCNPSTLGGQDGWIA *AQEFKTS LGNIARPPISVF
7730	21631	A	7790	246	359	TFIFSETRSHSVTQAGV*WHDHGS LQP* PPWAQVILSC
7731	21632	A	7791	70	102	AA*SRLTATSLSRVQAIPLPQPPEQLGG QGGRIS
7732	21633	A	7792	7	312	FLDFQLRLHSNSYCEDKGVFDEIYEIC IVLIICKK*RKFLNQKKKKKKKEKPLI* KKKKNSQKKWFDFPWLPPNPETKNSLFL PKEFLWLKTKPPFPLTLT
7733	21634	A	7793	1	341	IKPE*YLLFAYTILRSVENKLGGLALL LSILILAIIPILHISKRRSIIFRPLSR LY*LLAADLLILT*IGGPARYPFTIIG QVASVLYFTTILILIPTISLSENKVLW A
7734	21635	A	7794	1	143	YGSTFFVATGFHGLHVIIGSTFLTICFI RQLIFHFTSKHHFGFEAAA*YWHFVDVV *LFLYVSIY**GSTFFVATGFHGLHVI GSTFLTICFIRQLIFHFTSKHHFGFEAA A
7735	21636	A	7795	2	257	KWAIIEEFTKNNSLIPTIATITLLNL YFYLRLLIYSTSITLLPISNNVKIK*QFE HTKPTPFLPTLIALTTLLPISPFIIL L
7736	21637	A	7796	22	326	RDASDCSFQNLVPVPLVVEK*MVFLLT KKKKKKKKKKKKKKKKGGGPKKNSWG AKIIPGKKKI IFFLEGQKKLWGFFKK KPLFWGGKKRPNPPKKN
7737	21638	A	7797	506	281	RGAN*NRSGCGKRHEERERERERERE RERERERERERESPRPKRQRETEIQ TSLTSLVSLAPPPTCVF
7738	21639	A	7798	435	336	MRSNIHFFSHTHTHTHTHTF*ILKQH TFSK
7739	21640	A	7799	411	106	RNPPPLFFSPPLQRGFPPIYWGPPRFF PPPPL*KTTPPKLKIGAPPKKKPPPPPG EKMVSF*PPPPPPPPFFLRRPPLFSP GGGPWGHFRGPPPPPPGV
7740	21641	A	7800	2	296	FVPSTANWCFFLWSVF*TGGSNYFFVHR SYSQAGVDLIFIRLANTISNLSFI**RG GLAMLPRVLLETRAQTILHSWPPKVGL QVWATVPSFQFLKN

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7741	21642	A	7801	344	105	PGFFFFPPPGKRGFFPKPFFLGTPGFFP PPLF*NPAP*FFFWAPKKKIFSPPPGK KIFLLKGPPLEFFFFFFFFFFF
7742	21643	A	7802	68	216	VHTIAKIWKQPCPSMDD*IKNMRYLTY VE*YSVLKEREILLYWGHYAM
7743	21644	A	7803	407	3	GFIH*FPLFSGYTLDQTYAKIHFTIIFI GVNLAFPPQHFLGLSGMPRRYSYDPDAY PT*NILSSVGSFISLTAVILIIIFMI*EA FASKRKVLIVEEPSINLEWLYGCPPPYH TFEEAVYIKSRQKRKESNPPMY
7744	21645	A	7804	2	156	THRRITILSQGL*TLPLIAF**LLASL ANKKKKKKKRGPPFKKFPWGAKE
7745	21646	A	7805	2	309	THSRITILSQGLQTLPLIAF**LLASL ANKKKKKKKGGAPLKKIPGGAKIKRGME IKNFSQKGGEKKTQRGIFGKKPYLGGGQ NWEKLPKKFKGLKGGKKNF
7746	21647	A	7806	110	362	TLSDLERLLMKAVSHFLMIDLLEKC*CV LKNQSSKKKKKKKKKKKKKKKKKKKKK KKKKKGGPLLKNSWGGPNFPGGEKIFFF FRRGGF
7747	21648	A	7807	295	108	KQRGVFFFFFEMESRSVVQARVVQCNL SSL*PPPLGFKQFSLRIVYRKDSLSEFN KPRLLP
7748	21649	A	7808	2	142	GSTFFVATGFHGLHVIIGSTFLTICFIR QLIFHFTSKHHFGFEAAA*YWHFVDVV* LFLYVSIY*GSTFFVATGFHGLHVIIG STFLTICFIRQLIFHFTSKHHFGFEAAA
7749	21650	A	7809	390	2	PASLLHCG*ISDCCASNE*GSVGLGPSE PGAGYNLLVCHLLRPLEKCSIRVGTRF SRCLSPPLDRKGNLSLTPCTSQRQCL ALLQLTLGALHPVSCTHCPTISGEMNPV SQLEMQKSPICVTHAG
7750	21651	A	7810	1	157	FLHFGQAALLLTSGDPPASAS*SAGIT GVSHRAQLVCTFITIYVFLKNSSY
7751	21652	A	7811	368	44	QNFPKKRRLPPQPPLFFLVPSPKGG FFFFLGRGFFSSAQALL*FIYFIFFF FFFSFFFFLYFSISPDSKGDTHDILL GVSWWTRSLPLWIARNMHKVVGW
7752	21653	A	7812	400	80	PQNSFSPPGIGGFFPPFL*NFFFSPPKA FFFLGGFSPFFPPPKSFFFKIPGFFF SPPLKKIFFFFPPFLAPPRFFFKAPP PFFFFFFFFFFFFFFFFFYFRHI
7753	21654	A	7813	119	230	SEEFETSLRCIVIPSL*KKKKKKKKKKK KKKKKKKKKKKKK
7754	21655	A	7814	3	412	HEQEH*LLLP**PLAII*VISTLAETN RTPFDLAEGETELDSGFNIEYAAGPFAL LFIGEYTDIIIRNTLTITIFLGTTYDAL SPELYTTYFVTKLLTSLFL*MRTGYF RFRYDQLIHL*KNFLPLSLALLI
7755	21656	A	7815	1	183	LRRLERLSEFSTRRERERERERERERERD TRIDIYIVSQKRKKYIV*IRRNFVYHA EFSKR
7756	21657	A	7816	484	97	QPRTPDLK*FACGLPKCWDYRHKPPCL ASDGNHS*SSPGLLVLSASVSPSGHMS PSQQTSPWVSEESLLGRVPGFLYFPV DAPGPGAWLAHVQAVLKLGGSSDPPVL PSQSAGFAGLSNCAWPW
7757	21658	A	7817	2	219	ADRLRNS*EA*EREREREREREREPY



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						PPSHIYTDNRH*MRHEERTLFLWGSGE VRDAAPWVSHIPNTAL
7758	21659	A	7818	190	292	NSHLIFPWTKVFFMS*CTYNLVLPGSEK KFYSHA
7759	21660	A	7819	498	139	RRAATPAPAAAEPPPPPLQRP*PPSEPPD TQRDARGRRRGEDPGNSPFHPNPDRQPS RALCSTPRMHLRWIGPAFFLMTSLSVSG AVIPRNGGPGGVSSGPELLQLLCGQAGS STIRKIPS
7760	21661	A	7820	489	330	ELGFLHVPQAGLELLS*SNPPASASLPT SWDYRHDHRTGHHPGIYDSKMCIF
7761	21662	A	7821	490	260	FFLXXNXFXFFFXFXFXFXFXFXFXFXFX FFXXXFFFXFFFXFFFXFFFXFFFXFFFX FFFXFFFXFFFXFFFXFFFXFFFXFFFX
7762	21663	A	7822	493	482	VGQAGLKRLTSGDLPASASQSAVITGVS HRARPIMYFRYVQ*AKGSHV*RWY
7763	21664	A	7823	456	121	ASFFPIQYKGLGGATPPQEGGCG*GIPI KWGYKRRPGGPHGGSKRPPTQ*KKSYFI NVLVLFYLRDKGLAIPTLVSNNSWAQVIL PEWPPKVLGLQTRVTVPQONILKENMFF
7764	21665	A	7824	294	457	LCIGFVILISYFNIMENWYCRPGTVAHT CNPSTLGG*GRQITRSRDRDHPGQHG
7765	21666	A	7825	26	235	SVWWSQTGNKVKFTISW*IDKQMRCTH LMEYYSIAKRNEVLINATTTWINLNTIK LSKRSQTLKSNL
7766	21667	A	7826	30	303	SYVSVEFPSSGPTLPSFWHQTPTTYL NSVASAINLTQCPH*PEKKKKKKKKKKK KKKKKKKKKKKKKKGGAFKKKGP*KTPK KTPGGF
7767	21668	A	7827	464	21	REPPHPAPADILILHFWPELEL*ELISVV LNTRCVVICDDTPRKLTCQMPRLLLQT EPL*VLFSNLGSGFSLSKS*MGLVNFFC KGTDSRSFSLFVAVFCLFL*RWGLAMLH RLVLNCWPQVILPPPPPKLLGLQVEATT HEFHGTE
7768	21669	A	7828	372	205	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFIKKPI
7769	21670	A	7829	463	313	DIYPERNSKIMSFAATWMKLEATILK* LKNRKPNIVCTHL
7770	21671	A	7830	449	266	VVQMRFLHVQAGL*LLPSGDPRASQVQ SAWITGVSHHAQRSIFFKRNNDCDRPD NTECT
7771	21672	A	7831	480	148	TELRLSHGAAEFHRPREWYGIFKVLKER DFYPRIIYPAKIIILRHEGEMKTFDPKQT LRHFINTRPVLQEMLLKVHQSEIKGC** ATNNHLKVKKKNSLW
7772	21673	A	7832	23	131	QRGNSKGYHLKMIQEEIRKLEEEKNQL EGEIIHFYKMAASEALQTLSTDTKKD KHGKKQ*FL
7773	21674	A	7833	16	339	NTDTLGSMAFCRDGLAMLPRFLNTGL KRSSCPDLPNCWDYRHGPPYLASFVLLK *TLSILLPYHKMHTCFMVLCTNFCG GVCPGMELLCLKVYGYLSLKHTFH
7774	21675	A	7834	355	70	KKTPRGFSGVFLGPFYKGLPFFFFFFF FFFFFFFFFFFFFFFFFLQFFILCQQFL S*STEKTVHSKYILSFPFHCLIFCPFIL LCSTFCNGAHY
7775	21676	A	7835	494	282	PENGMIQGGACSEPR**HCTPAWAKER

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						DSVSNAKTIQNKKNLGN*HSISTAKAKN IIIS*YKSELRKKM
7776	21677	A	7836	305	185	LVIETCLTVRPLSPS*AIISPVTCTYTF RWPEVTEESQKK
7777	21678	A	7837	179	191	LGCRKYLFLYLNGLKCLYIKVCVCVCICI YIGVYIGMCVYICITYILMAS*NQVTSF LSFYVFLNLYR*IPVKVITVLFNLRLMTG LP
7778	21679	A	7838	466	343	LGRRLQENHLPPEGRGCSEPRSRPCTPA WETEEDAVSKINK*INK
7779	21680	A	7839	451	89	LIRDTR*SGVICLPKQAWAMVGAPPPASL PPCSLIISDCCASNQRDSVGVGPSQPGGG YNLLVRRFLSLSEKRSIRGVNRFSRCH LSPLSLTRKGNLSLTPCASVRVQCLALLR LAHGARTH
7780	21681	A	7840	442	164	AHTNQFSQCIKKSVPDLMEEYKKAHA AI*ENPVYEKRPKKEVKKNRWNCPKMSL AQKKHQA*KKASSLRAQEQAAS
7781	21682	A	7841	494	359	ICMLPRLVLNS*PQVILLPWPVKVLGLQ A
7782	21683	A	7842	577	224	IFFFFNKIFLFRPGLNLMGDIWVPSTPP LQG*TNFPPQPSQEVGLQAPPPGLIL VFLSRQGFPLGRVGFHFPPGDPFPRP FKKIWSHPGGGKSPPKKKKKKEIAEVLG AFRLR
7783	21684	A	7843	404	56	HTLSTNVCSSYLNLDFFSLRGRGLIMLP RLALNSWAQEBILLPQPE*LQLLRRLRQ ENLLSPGVQQPGQHNETPTS
7784	21685	A	7844	1	323	INTLLALLLIITF*LPQIGYINNSTP YEGGFDPIDSTARVPFCIKFFLEAITFLL FDLEIALLLPLP*ALQTNLPLIAMASL LLIITILALSLAYE*LQGLD*AE
7785	21686	A	7845	419	159	FLFFFFFXXYVLSCGIY*YWCNLFSS* QYFFFYVMAFRIFLFTFLHFYNNMF* CTYFYLSC*FEYICSHIIHYFIYFLHL ENF
7786	21687	A	7846	475	124	FFFFFQPPQKEGGPPPPKNNFFFFTRI FFFGVFFFFFPQKNFFF*KTGVEFFF PFF*KIFFFFPGVFFFPVFFFLSPPP SSSFFFFFFF FFLKRQAS
7787	21688	A	7847	6	189	LIDTVSPSVALAGVQWCNHSSPQP*PPS LKRSSRLALPRFWDYRCAPLCKAHSENS NHEK
7788	21689	A	7848	20	249	KINFIVVELTCSNTVHTFYVYGFDKCIL PTTQLFFFL*ETGFHSHVARLECSGVIMA HCSLDILGSSWRPANFLNFL
7789	21690	A	7849	101	398	LFQKKKKKKKKKKKKGGPLKKKPGGGK NKGGEKKKIFFLKGGKKNPRGNFKKKT FFGGKKKGEKPPKKKKSPEEKKKF*RGK GGKKS LICWVEKNLG
7790	21691	A	7850	87	226	GSLSPIMLVLPFLIHL*KNFLPLTLAL LI*YVSIPITISSIPPQT
7791	21692	A	7851	2	440	GAIIIRLLH*FPLFSGYTLHQTYAKRHF TIIFIGVNLTFPLQHFGLSGMPRRYS YDAYTT*NILSSVGSFISLTAAVLTTL MS*EAFASKRKVLLVEEPSIDLERLYGC PPPYHTFEPPVYIISRPRKESNPAKL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSQPHG
7792	21693	A	7852	1	80	SSLLLLIIILALSLAYE*LQKGLD*AE
7793	21694	A	7853	5	135	ATFLYFS*K*SLSMLPRLVLNSWTQAIL PPWTLKVGLCFFDPL
7794	21695	A	7854	38	419	FVMMPLHSSLGEGVRPYLKKKKKKPPWE GGSPPKNFKNQIFA*NQKPPFFFIIPN KKWGSPPGGGASPL*SHPSGGPGGPNNK VKISKPPCPPGGTPVFTKIPTFT*PWGP IPEKEGRKTVCPRTH
7795	21696	A	7855	398	61	FFSPRPRGGGFPPPPKNEFFSPPTIFF GGGVWNFFPPPKMVFFLKISPVVFFPPL IRKKIFNLSPGSFWSPOGFFF*GPPPKF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFF
7796	21697	A	7856	1	121	LDASGRLPSPKPIKIKNYNRP*EPK*T KICSLHSLPPQS
7797	21698	A	7857	1	332	TPPIARPAENSARGAEGRRR*IIALQVC NKKWPPTKLHCICKKKKKKKKKKKKKK KKKKKKKKKKLWGGGGGKNFFKKGGKK KLGGCFKKRGRKKKK
7798	21699	A	7858	3	191	SPRHLTRAAGIRHEGTGLKLLTSGNLP ASAS*SAGITGMSHRIGPRMLDLTLVS WKQHGL
7799	21700	A	7859	503	62	FFFFLNCCLSLRHLIKLFEPQFLHL*N GGMVLSIILSIKSPLSLSYSWL**P REKIKWGGQVRWFMPINPRTLGGGGGQ IA*SQEFKSSLDNMVRPYLSEPP
7800	21701	A	7860	355	86	YIKG*QMVGNRGASQAGMTGYGMPRLIL
7801	21702	A	7861	336	225	PQLAGPVKTVRKVKKEKARVPEEKKN FKAFASFRKGRANGRVFGIRAKKAKEAA KQDV*KKPPIPLAGGSPTREPPSQAHLF PQNPPRGNNP
7802	21703	A	7862	465	170	GGPPPKTHPFGGERGGKYHRGKKKPPGH QRVNPPSPKKKKKNWGRGKNPFTPLIGG GQAKKPPQPRGEC*KKVPPNNSVLGK KNFFFPKKKKKKKK
7803	21704	A	7863	495	275	RSFFFFFFFFFFFFFFFFFLVARK*YVFL ATKKKKKKKKKKKKKKKK
7804	21705	A	7864	493	70	PLTASISLPVNWRYIAPHRVVVIK*KSV Y*KYLA*CLAQSKCPKSVCSHLSSP*LH FVPPPNPAEAMWTARQC*CIRGLGGKGT LCVAHTYNPSCSGG*GRRIV*AQEFKAS LGNSEPLILKKERKKESQAWWLIPPIPA F
7805	21706	A	7865	67	385	VARTTGMQHHAWLIFFIFIIFVETGSHY VAQTSLEFLASSDPFTSVQSTWITGVS YSWS*PGIAHTCNPSALGDRGERIT*GQ EFKRS LGNI VRPCLYKNNKNKKN
7806	21707	A	7866	454	0	LSFFFFPLGDRVTLCCPG*SAVARSQLT VALNSWAQAILLPQLHKHVPPCLANF*N FF*RQRYTMLHRLVLNSWAQVILQPWPT CPTAAQA
7807	21708	A	7867	1619	698	PATSSSSSSSSSSSSAAAVAAAAATAASL PPCRPPLRPPQPLAPHEVATLAPWRG*K PSFTSSGKRWLTSEPQTSGSCASCL*SM RASSPSSG*SKKKPPLPAEAAASVAACA VCWRVRAPPYVAATTAYTMVMGWMFAFP WEVIWTRWRMMSQAIRPLQTWTNSVTAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						S
7808	21709	A	7868	52	187	LDFN*RRCLTKLPRLVLNSWAQVILPPW PBKLLGLQV
7809	21710	A	7869	33	373	AGVQWRDLGLLQPPPPGFKRFSCSLPS GWDYRHAPPHLANFVVLVEMGFHHVGOA GLKLPT*GDPPTLAYQSAGITGMSHRAR PGISVFHLKLHSFDPFKIIFRPGAETMP S
7810	21711	A	7870	100	119	VFVEIVFPEGLLFSPCSFHLGCFRIHLK AEF*FFVETGSMLPRLVSNNSWAQVILPP WPPVVL*LQA
7811	21712	A	7871	471	446	LLMLPRLVLNSWAQVILPPQPPKVLGL* AYI
7812	21713	A	7872	449	33	FSFFFFFFLGGKDLFFSPRGGGGGANSA FFPPPNFGKKSAPPPPLKSV*NPAAP TGVFFFCCGGA
7813	21714	A	7873	334	41	PCPSLFFFFFFLRQSLTLWRLECSGVIS AHCNLCPLSSWDYK*HCPYLATGAPGLL SQSELSYVTL*LQESRPLCIPVDFMTFL PSLCFQSPNSTTL
7814	21715	A	7874	342	716	STGIFLFVCF*DGVSTLAQAGVQWPDLG SLQSPPPRLK*FSCLSLASSWDCRHVFP LLANYLYF**REGFTVLAMMVFS*PCD PPTSASQSAGITGVSHCAHPGMFFLNWP LKSCPSESGAAV
7815	21716	A	7875	454	215	PPPARCH*PP*TLVHAVEFKSHHYSLI SSTQGHKHCGRPQGGLPRKTRDLCSLVY LLTFPSLLSYDPAKSLSARNTQE
7816	21717	A	7876	492	176	PCGGRGAGGNWGWPPWHLRASASSRWAW ALQPHTRSSQAPGPTGPRQ*GAQHLGQQ LLCSISHQALAAPPQGRAQDLQPAMPEP SPRPPLPWAAQ
7817	21718	A	7877	281	439	TWSIDL*HMAYFLFFSFLFFAFLSFSLL SFSLLFFAFLFL*VPSFSLFQQRSL
7818	21719	A	7878	507	338	LLRRLK*EGHLSPGGRGCSKPRLLHCIP HWATE*EPFSKTINK*N*S*MKMKMKIN
7819	21720	A	7879	55	298	PPCLANFLKFFL*RQSLPMLSRPFSNSW PQAVPLPRPPKRNQLYLYFGCCSQLCNP QHLCSKQHTFKILFDIEKHFRLEH
7820	21721	A	7880	145	292	YFGGQIYFIFCRDRISLC*PVLLTSLV SNSWPEAILPSQPPKVLGLQA
7821	21722	A	7881	3	203	LSLLPRLECSGTFTAH*SFKLLGSRDSP TSAS*IAKTGMRHHAQLRFFFFVPGGV CVCVCGCVYV
7822	21723	A	7882	324	211	AWWLMPIPTL*EAKMGGSLEARSRLRPV WAHNETPFLF
7823	21724	A	7883	2	124	QHFGRLRQVDHLRLGVHYQRGQHGETPS LLK*INVYIYMT
7824	21725	A	7884	367	141	KCWDYRREPRLAQGLEFLFNFCFEIVT EPPCPALAYF*NFL*RWSLATLRLVLN SWPQAILPRWPPKALGLQE
7825	21726	A	7885	471	215	RGMCVSHIFLCVGARYNISSARESLLKE FTECTERKHTHTRAHTHARATHHTHT HTHTHTRV*NSRSQPYCRVHACSPAYLG G
7826	21727	A	7886	462	204	RHSS*LGLPKCWDYRHEPPLACISSF* RKSDISLSDELGTCKCHKWWPQVVKSRAG SVGRDPCSGHFILAGFGQLGA

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7827	21728	A	7887	409	152	PVFLALERNPQQDFLRPGVLDQPP*QNNKISFFFFFKKKKKYIYICMVVHAYNPSYSGG*GGRIT*AQKFKTSLNNTVRPHLYK K
7828	21729	A	7888	1	152	GVHVCCDCKCICVCLCVGVGHECLCVCVSK*VHMCHREGTIFGNISWEGD
7829	21730	A	7889	101	399	EIINIVFFVFYFLLPLFFFWGGRPKQLNPEFLTNSWKKNHKTIGGKNPMGG*KKAITNPQKKGRKRSFSF*NKAQPTQKGNGQNSQGSKAVGALTAH
7830	21731	A	7890	478	142	KPSKKKKRGVLFNFYKKKAFFSKPPKPVFKKKLLKNPFFKAKKQFFKTPTPLRPFREKFFPGPPKKKKRPPGLFKNN*KGPPWPREKKRVKKKKKKVKSHYNNHMPISVH
7831	21732	A	7891	497	320	PPWKFEFEFWFSP*LHKYPPYVCVCVCVCVCVCVDFRFFKPAPSPQSHFGINLSFLL
7832	21733	A	7892	217	23	IPPFKKFF*EMGSHAVT*ARVVQWHNHA SLQPETCGLKGFSHLTLNPSWDCRSVPS SSARRQSH
7833	21734	A	7893	652	470	SSSSSSSSSSSSSSSSSSSSSSSSSQFERKTRSA PQVEGKGNFCSLEAPPPGLSLFSCLNF*RSWDPGPPP*PHATPKTRAGDGLCATHHRARHCTPGLRFLFLAL
7834	21735	A	7894	25	178	GILFFWRDGLVILHRLVSNFPVSSDSPISASQSWDYRCDPPCPACPLIFW*LLKHSF*FFWRDGLVILHRLVSNFPVSSDSPISASQSWDYRCDPPCPACPLIFW
7835	21736	A	7895	104	451	ILSFMTTWMEADIMLSISQTQTDTRYCMILLVESKNVNLPRGMMAHAYNPSTLGG*GERIS*GQEFETSLVNIARHYFYKRNFKIKSKFKKIVRKSQKKNVRRWLLEARNKGRYG
7836	21737	A	7896	510	335	SCIVSLHRSWDLWHVPPFLANF*IFRKG GVLPCCPGWQIYTFQLQIPFLSITPVAFSG
7837	21738	A	7897	37	260	AGNSQNQGGGACSEPRWRHCTPA*ATERESVSKNKQTKFLCSVPYFESTHFTCTNEATGAWGVEKVALGHAASW
7838	21739	A	7898	35	466	THTCGGIRKCLTNKRENQK*SQQKPSAPKEPEVKNKQKTKKNPKKKKKTPQIQPTKKPFRNPNLRVFTFFVTQNKTPTRGRKTFQKVLFPPNPCLGNKPQTLLPRGGLQKKKKKIPFFYSHPPPLAQKKKATPWQNGLGFT
7839	21740	A	7899	494	149	PARLLSLHSYEVKSVLPKEEGLLNPFVQSVTAHPTSCIGLEEI*LLD
7840	21741	A	7900	494	114	GAEGGPLSKKKKNLLPDYHTGPMLSLYLWPFSLNGLTLTLMCAHTHTHTHTHN*LSRVGLPVLKPGQYQANGNRWSP*YNIKE*PRKTRVMPVTPQLRNDGPMLTFWCSSRNSFAMHVLGKL
7841	21742	A	7901	19	454	VVCNSSVSIHTHTHTHTHTHTHTHSWVGWHMPTVLSTQAEAGRLLGSGSLRIQRAMIVPLHSSLGNAARPCV*HTGSCCVSQAGVQWHNHSSLYPQTPGPKQSSSLSLLSR*DYRHVPPHPASCVCVRVCVCVCVCVCVYVYDRGITPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7842	21743	A	7902	3	393	DAWDPLNPLVNLVSPKRNSSLDTRKKP CRESKKFNTHSRPKSSHQLRKRSSSTPT T*KIPNI*LNSSTPSRAKKRKKKKPKK KK*KNSQKKKKPMRKTKKKKGGGLKKI LGGAKFFGGRKEKIFFF
7843	21744	A	7903	424	139	LFFFFFFF*G*GFVIFCVGVGL*LL TSGDLHISASQSAEIRGVSHAPPLSLI VVFISQCVGILNHTVHLQYIQCSFVHHF LINQEKIDIK
7844	21745	A	7904	1	181	SQ*LY*LLAANLFILT*IGGQPGSYPT IIGQASGLYLTITLILIPTICLIESKI LKWA
7845	21746	A	7905	3	281	HAYAHASATFFVSTCFHGLHDIMGSAFL TMCFIRQLIFHFTSKHHFGFQAAA*YWH FVDV*LFYVSIY**GAVLKEPWGGQS
7846	21747	A	7906	1	84	PTRPLTMLPRLVSTPGLKQSSQLSLPKC *DYRCEPACTAYSF*LTMPLRLVSTPGL KQSSQLSLPKC
7847	21748	A	7907	3	392	DPDNYTLANPLITLPHIKPE*YFLFAYT ILRSVPNKLGGRLALLLSILILAIIPIL HISKQSIIFRPLSQSLY*LLAADLLFL T*IGGPRSYPFILIGQVAFVLYFTTIL ILIPTISLIGDRILKWA
7848	21749	A	7908	2	231	GCVEKGTLSHC*WECKLVQPLWKTWVGF LKLKIDLPDPAIPLGIYPEENKFTL GPLHSVGRSSRKLPGYSRV
7849	21750	A	7909	529	297	KIFIGAPVFCPPPHFFFLIPPF*GVEKI FFSFFVLLPPGFFFLFLGLFFFFFKLFF FFFFFFFFKIPFFFSKKVGVGK
7850	21751	A	7910	410	61	FNNQAMQVFPFPPLKIFFFP*RV*FLE GGWSNLSPPK*GPSPKFPTRVL*GPP* GKN*NFGFPG*NWAPHRFF*RAAPFFFF C*DRVLLPRLVSNS*AQVIHPPWPKVL GLQA
7851	21752	A	7911	512	314	ANFC*LFIETGFPHIGQAGLELLTSNPN PALASQIAGTTGVNLRPGQDFSSYSEN PLVYGSLYIA
7852	21753	A	7912	1	264	SSTTTLLSRT*NKLT*LTPLIPSTLLS LRGLPPLTGFLPKWAKKKKKKKKKKKK KRGGGWKKKPKKGGGETSSKKDTFFK KGGP
7853	21754	A	7913	416	129	FFFFFFFFAPPKIKTPPFFFKREVYIY* ALSVFQSVCKALYIHFRIISSQYPC*LG FFFFFFFFFFFFFLKGSLLDLSAYCVPG SVQCALHTLSH
7854	21755	A	7914	397	34	IFSNLFFPPQKKMFFPPPLKYFFFSFT ALFFFLVFPFPFPKIFFFNPPKFF FYPS*KKKFFFIPIVYFLAPPEFFF*AP PPPPPPPPPPPPPPPPPPPPPPPPPPPP FSVSKQPLFCLKI
7855	21756	A	7915	396	86	IFLSPRK*GFFSPPPP*KFFFSPPKPLIF FGGFFPKFPKPPKNFFQNPFGVFFYPP FKKKKFFFPPLNFGPPRVFF*RPFPFF FFFFFFFFFFFFFYLWVC
7856	21757	A	7916	351	112	SFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFF*KYVFIYISLSLIPCKFLK GRECDIHFCDIQHSYSKYLGHFKCSTND RQMNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7857	21758	A	7917	445	2	FFFFFFFFFFFFFFFFFLSYF*LIHYAEGIG ASPCYIMLGYNFSSFPCTISIAPEGNF YRLYFISHASADAWVDPFLDRYRRGIN
7858	21759	A	7918	2	407	PPPPQVYFNIWRTIFFGEGLLHIFPQK RFCFYKTYTNYIKTLFIKKNI FSLAHI KMVPPRSIY*TPPPLFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFL
7859	21760	A	7919	107	11	KMWYIYTLECYALKKKKEILLFDTTLI NLKDIMLSKISQHRKHT*FKT
7860	21761	A	7920	1	70	FFFF*AAESCSRIKCSGTIIAQCNPELP GLSDPPTSAT*VAGTKGVCHHTQLRFIF IV*LSGRILLQDQVQWHNHSV
7861	21762	A	7921	123	260	GIQARKEPGAVAHAYKLSTLGG*GGWIT *GQELETSLVNMVKPCL
7862	21763	A	7922	184	399	LHLLMRVLKKKKKMGGLYRSPRGAKVN PALQRDLSLLIGSRILSNLIGFKAPHS WGG*AFFAATGLHGLHVIIGSTFLTIGF IRQLIFHFTSKHHFGFKADD*YWHFVDV A*LFLYDSIY**GSRILSNLGI FGKAPH SWGGTKWDNPPPDMSKSS
7863	21764	A	7923	2	407	GRVGM*EAFASKRKVLIVEEPSINLE* LYGCPPLHTSNKKPPHTKKKQKKKKK KKKKKKKKKKKKKKGGGLLKKLWGGPK NTGGKKKNFFFFWGGKKKNLGDFLKKNL FWGGGKIGTPPPQKNPLGEKKF
7864	21765	A	7924	1	398	PTRPPTPTSSRSRAPPPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFVSAALFFGKKKNFFFFFF*F *GFYFFPPLYFFICGGGGVFFFFFAGW NIFFIPKKNGIFKTLRGKG
7865	21766	A	7925	2	335	NLTFFPQHFLGLSGMPRRYSYDPDAYTT *NILSSVGSFISLTAGILIIIFI*EAF SKRKVLIVEEPSINLE*LYGCPPIYHTF EEPSIKKKKKKKKKKKKKKKKKKKK
7866	21767	A	7926	1	328	RTRGRTRGESNPSLRITQNSPCHLSHPIL KKKKKKKKKKKKKKKKKKGGPLKKNPG GAKI*PGPKKNLFPKGGLKKTPLGNFE KKPFFGGGKKRKKPPQKKKTLEKKKF
7867	21768	A	7927	27	226	LSR*KM*NKSHIYSFEKKKKKKKKKKK KKKKKKKKKKKKKKQKKENRPKNGDSEN GHPKSKIFWL
7868	21769	A	7928	398	2	GGGGGPGGRGP**NPHKKEGRDPPHPK KKFFPRRRKNRGGGGRKSPQKKKAPQ KKPGRGFKRAPQKKKTPPPPRKGGPPP KNFKKGAPPPPPPPPPPPPPPPPPPP FFLGILARTTTTNDMKNHR
7869	21770	A	7929	3	156	HASAHASAPV*SVLMTAVLLLLSLPV LAAGVTILLADRILNTFFDPA
7870	21771	A	7930	405	249	ASAHASAPLV*SVLITAVLLVLSLPVL AAGITILLTDRNLNTFFDPA
7871	21772	A	7931	921	699	DHPGQHSEILSLQKMTMSQCGGAHL*S QVLRRLRREDCLSPGSQSCSEL*SHHCT LACETE*DLVFQKKKF
7872	21773	A	7932	423	259	HDLGSLQPLPPGFR*SSYLCLPSSWDYR CEPLRPAQRRGILMAATSRILTRSKGW
7873	21774	A	7933	395	35	PRVKRFSCFWLPSKWGPRPAPWPGYFC FFC*NGGSPFLPGGSWTLPNYSPPAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QNGLVQALRPPGPPTFPFLIFPTKAPWS WPFPGGKKKKLSPKGHSERHLHHKYIR LLSQHGGM
7874	21775	A	7934	1	118	NF*IFCRDWGLALSPRQLSNSWPQVILP POPPKVLGLQA
7875	21776	A	7935	322	383	KKKTGLIKITSLCFVKNFTFKTKWQAPE RKKKVPIFLSYKRPVFKIYKKLFPFCRK KIKKKIPPPGFTSFSCSLPSSWDYRHP PPCPVNFFCIYNKNGVSPG*PG
7876	21777	A	7936	3	131	GFHRVGQVGL*LLTLGDPPASASQSAGI AGLSHRSQPLTWSL
7877	21778	A	7937	334	146	HPQGLNI*NMVSSSGAKHSRSLSPKW WDCRQEPPCPVIMFLKRGINHALYSPSR KLLHFL
7878	21779	A	7938	2	371	SEPGAGYNLLVGRF*SPSEKCSIGVGV RFSRCCLSPSLTGTGKNSLTPCASRVRO CLALLWLQGVVHPLSCTHCLALPSEM N PVPQMEMQKSPICFIADAGSCRPELFLF GHLGSSPQSKL
7879	21780	A	7939	2	95	RLNLGGGGCCEP*SCHCTPAWVTKRNSI SKK
7880	21781	A	7940	1	191	PTRPSQTPGLK*FSLSLPKSWDYRCEP PCLAVILSIPQNSSMPNIFAASYSS*F GLYSSRW
7881	21782	A	7941	127	383	SKDCVRIVLLRAQAKAGSYRTVNWCRPG AVAHTCNHSTLGSRRGRIA*GHEFKTSL GNIVILPLYKKNKKKKRGARLKEPNLT P
7882	21783	A	7942	235	3	KNILPGYFCFFLREKPPPPGLESLFSKK KKKKKLARHGVAPILGRMR*EDRLRPGV QGCNELWWCHCTPAWATEQNP
7883	21784	A	7943	3	225	EHGSLYPPTPGLKQSSYLSLSL*DYR* AAPCPANFFIFNFI*REDLTMLRLVSN SWTQAVLLPPKVLGLLV
7884	21785	A	7944	2	232	TLPLDNLSTIYPNKKKKKKKKKKKKK KRGGPFKKKKF*TRGGGKKNFFFRAPKI FFGGRVLKGGGKKPGEPTN
7885	21786	A	7945	394	41	WCRWLETWGAGGSGAVPPPPPPHSSS WDLALQGGSGASSPFGAVAHACNPSTL GGQGGWIT*VQEFETSLANMMKPHLFSK KGPVTAVAHPAKHAHRAWCTPTMHMTQH VLHVL
7886	21787	A	7946	405	100	FFFSPRFSSSLFLLSSFFFFFFFFFFFF FFFFFFFFSTGLFVYWSPTH*SLPVPRIFFF SYLWQTEVETMLGTE
7887	21788	A	7947	391	212	KEMQIMPAMR*HLTPVRMVTIKSKAKC WQGCEBKGTLAHSWWKCKGTAETGKLAG F
7888	21789	A	7948	106	301	LQLPITQLVWHSIYFMKKIRYRLGVVAH TYPNSTLGGQGGRIA*QGVFKTSLSNTA RQKKKKKKG
7889	21790	A	7949	342	208	GLGAGHTYPNPSTLDN*GGWITSGQEF D TSLANMVKHHVVQTGQF
7890	21791	A	7950	391	21	RQGFPMPLRLISNS*PKGSAHLSLPKCW EYRSEPPSLATWYVTLRHFCSLTLGQ GRSKFHMKWESRLEGLLAKVSSLRSSYC SSLRILGLEILLSPLLFLETGSGSVSQ AGVQPLCPGLK



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7891	21792	A	7951	146	355	ENIRQTQNEDEVVVKSSNETVFCNKNIITSLGVVAHACNPSP*GQGRIT*AMEF*TSLDNIRPCLYQK
7892	21793	A	7952	289	327	KGIPPLPRLKDKGPPFFFLKRESLFLP*FWKNGCRGPPLFFFLRDSVSLPRLVNSWP*VILLPQPPKVLRLQA
7893	21794	A	7953	861	586	DRVRSVAQARLQWHDLSLQPPPPGF*QFSCLSLLSSWDYRRMHTWPFVF*WRWGFTCVAQAGLDLLSSDNPPALASQSARIIGESCCVLLK
7894	21795	A	7954	402	52	PRKVSIS*PHDLPASASQNAIGITGVSHRTRPSFNFSYIETAITETRSLQSPGMN*SLPSGMVGFKPHSFHISANFCEALAVQQTILGEVPGHAPLSPPRQBRVCPKVKCLKTALK
7895	21796	A	7955	259	3	YNTKVLSPFILL*TFLKHLWLGAVARAFNPSTLGGGGGRIA*GQEFKTSLGNIERCRLYKNLKLFLSGLFLMAWRGAKRVTRTG
7896	21797	A	7956	171	386	LPIRLFSLVFTTIEKSRPGMVAHTCNLS TLEG*SGWIT*AQEFETSLGNMAKLSLPKIQESASLITRSQNK
7897	21798	A	7957	397	283	PQPLPPGLKQFSCLSLPC*DYRRDSARPAKKNPTFNK
7898	21799	A	7958	169	324	GTHRVEMCQWLGVVAHACDPSPLGGQVRKIT*AQEFETSLGNIGRPCLYIK
7899	21800	A	7959	290	397	DCSSCCSPLKGR*RG*AQWLTPVIPALWEAEAGGS
7900	21801	A	7960	496	298	LSKTGSLYVAQSVVYWLFTGTIMVHDSLKLLCSSSPVVSAS*VAGTTGAHRCCVLTTFQPDVYRL
7901	21802	A	7961	404	174	PGPQKGSFF*KKKKKKKEIDHILSHKANLNKC*RIKII*TMUSDQNEIKLEIIIKRQLLKETLFLEMKKYTIRKLS
7902	21803	A	7962	25	99	PGLFLSS*HQVILLPWPVKVLGLQL
7903	21804	A	7963	436	106	GGGKSPPPGNWAPPNGPGLFF*KKKKKNPGGGGGRFFPPPPGGRKKKGVPGGGGFYLTNFP PPPPWGKKKNFFFKKKKKKKKKGRIAICYIILFITSINFKKAIFI
7904	21805	A	7964	212	395	ERERKERDRGEREREREEREGRKKHGR*GGREGERHRPRGAEDPDGRATDKRTGAL
7905	21806	A	7965	344	345	FSDCYKRSSCASWTWYTRLAHQPPARP GAAPSPRKRWVDFAVNRNFPSSRRHPCATPRPAPGATGRPSRVPKSTAFTQMLTQPRDPHLPLPIPLSQPPSP*PAPLVMR
7906	21807	A	7966	397	298	RGFTMLPRLVLNSRTQVI*LPWPPTVLGSLSIF
7907	21808	A	7967	92	268	IKMSLCPNFFFFFFKKQNVGPRAGAYPCNPTILGGQGRKIT*GQDLKTTLVNMGKPHY
7908	21809	A	7968	257	107	RTHTHTHTHTHTHTHTHTHTHTCENSKTKNIANNCS*LESQRNNGKCTYAKF
7909	21810	A	7969	413	12	PPPPPLTPWPCFFPQIL*PVGHSAPPLFK*LKIPRPFFPPPPKGIGAPPPKIFFPPGFSLPPFVKLPPGEKILFPPPKKKYPPPPQS*SF*PPPPPPFFFFFSTSAKSKKNFLFIFSPFFNPKYYNT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7910	21811	A	7970	399	212	TGVQWSNHSSLSQSTPGLKRLFLLLLS IWDYGCMPYPYLSFKN*FCTKGGSCYVAE ADVNIL
7911	21812	A	7971	584	424	RPRRENRLNPGGGGCSEPRSRCTPAWV TE*NSVSNRNKTNQNPIFFSCKQFD
7912	21813	A	7972	105	1	PSMPQLSHL*NGILGRVRWLTPVIPALW EAETGRS
7913	21814	A	7973	363	28	SSSLGGHPQLWFHTLKLRPVTVSYA*NK LCDKIEKKLFPTIALHNKFLRKKLTRDV KILFNKK*IKKEGPNF*NILCLWIERI NINKVPYPYPSKVMYRSNTLPLEVAVFKSQ
7914	21815	A	7974	404	250	FFFFW*R*GFTMLPRLVLSNWTQAIHP ALASQSAGITGMSHHAQPLSIIF
7915	21816	A	7975	2	60	FSCGLGLPFCWDYRHAPPHLANFCRDGVL NY*PQVIHLPLPKVLGL*ACTTTTPG
7916	21817	A	7976	325	81	KTIHSLFLFGQFFLLQPLLSPPIPHAAPP TPHLIFLLLLFCF*FFK*RQKQGLTTL PKLISNSYSQVTLPLQPKVLGFQA
7917	21818	A	7977	406	282	QWRDLGSLQPPTPWFK*FSSLSLPNSWE TKAGRSREPGGD
7918	21819	A	7978	382	221	DCIISASYLQKNFFFFLGDVKLLCHPGW SAVA*S*LTVTSKRHFYSSEISLY
7919	21820	A	7979	423	29	FLW*RRGFTSLPRLVSNFWAQGICLPWL PKVLGLQA
7920	21821	A	7980	3	238	SLAFFVETGSHFVA*AGLELLSSSNSPA LASQSAEITGVSHHTQPE*GYSHM*PQY PYQLRFNSDTIILSNVLFVPNF
7921	21822	A	7981	324	128	WLSVSPYTFELSLLVGYEFVIHDVI*TL IFVVVVVSLFCFLWFFLVCMFVVFVFC CCFLSVFCT
7922	21823	A	7982	1	86	NLTMLPRLVSNWSAQAICLSWPPKVLGL *AQAICLSWPPKVLGL
7923	21824	A	7983	1	137	RPAFNCIFFVETEFCHVAQAGLELLGSG DPPTSASQAGATTGMSH*D*PANFCIFF VETEFCHVAQAGLELLGSGDPPTSASQ AGTTGMSH
7924	21825	A	7984	2	277	PRVRSVQRVIYQYV*NLQIHVPFDSTNL GIYLTDLPHVWNDNMVYVFAAVSFVIA KY*NPCLTRRQCCKLWPIHAMEYVVTIK KNEDGRA
7925	21826	A	7985	211	42	GPQKWPRGPGENLGGFFFFFRCRDDGL TMLPRLALNS*VHAILPPQPRKVPGLWV
7926	21827	A	7986	409	183	LLRLK*SSHLSLPKWWDYRCEPPCPAIF FKRKQILKESFPGENTCCHLNFNSLEVLK NKRRTCYNFENTLAVLKNM
7927	21828	A	7987	2	194	RFFETQSRLQLPPPPQLK*SSHLSLQSS WYRHPVPPCLANFFLFWYFLQGQGFAL LKLKFLFK
7928	21829	A	7988	483	209	SSPSLGNFCIPSSGGVSPCWPGWFQTPD LVIWPPGPPSLVFFFFFFFRDEGLSMLLR LTLNF*AQVILLPLPB*LGLQADRQVP LYPAEVF
7929	21830	A	7989	164	29	KFWFWLGTVAHACNPISILGSQGRRIA*A QELEPSLGNENRCPCLYK
7930	21831	A	7990	3	474	PTRAPLRAPFETIVQEEFSSKHHPGFEA AA*YWHFVDVV*LFLYVSIY**GSPPPP PKILIKNGAETKKFFF
7931	21832	A	7991	469	323	VETGLHHVAQDGLLEPTSGDSPASASQN

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						IGITGVSHHA*PDFTFLEQF
7932	21833	A	7992	469	13	KGDTVSSSDSSPSCGGLFPVGAS*LLCL FTQALAMVGARRPFSMLPCSLISDCCAS NERGSGVMGPKSPKPGVGYSLVCRWLRPL EKRTIKVGVTRFSRCRLSQLPLARKGNS LTPCVFWVRHCFGSHSVGCTHCPAPAVR QAPVK
7933	21834	A	7993	15	439	IASGRPFSTKFFLVAITFLLFDLEIALL LPLP*ALQTTNPLIVMSLLLIILAL SLAYE*LQKGLD*TEPNKKKNKKKQKQ KKKKKKKTKTKGGGLLKKILGGAPILW GGKNMFFFFWGGEKKTGGLFGENLFLG GGK
7934	21835	A	7994	392	186	YFYIINNFFFKKIFI**IFFFLKKFL *YSPKKVFFLFF*IFFFFPSSSLFLFF SSSSPFFFFFFFFFFFFFFFFFLRG
7935	21836	A	7995	11	386	TWEVEVAVS*DHAIALQPGQE*NAISK KKMTGRMFIEVSFIASSWKQLKCS*TG E*MKSLWYIHIIEYYLTIKENKVLHEHV SRLTLIDTGRERSKTKEYTLYNPIYTNL RIAKLSGCGGSHL
7936	21837	A	7996	3	186	DSFCF*RQSCSITQAGVQWGDGRSL*PQ SPGLKRSSCFSLPKHWDHRDEPLHPAGV AVLN
7937	21838	A	7997	316	649	RDHSFFEMESRSVAQAGVQWHDLSLQ ALSSGFMPFSCSLSPSSWDYRHPPPCPA NFLYFLVEMGFQHVQNGLDLLTS*STR LGLPKWLGITGVSHWHPAQDGGFHHVG
7938	21839	A	7998	468	336	RRGFTMLARMVIS*PSDMPASASQSAG TTGVNHHIRIHRSL
7939	21840	A	7999	464	283	TLCCGIRPTNIMKGNLLYSKISGLNVSL LPKNPRRNINNV*PNTWALQPSHVDI
7940	21841	A	8000	46	487	RQRLSLQKFLLPFVQLCPAHRGGVYRG RQASLSCGGLHPVRVSPQLCLPT*VSAM AAAPHPASLLPCSLISDCCASSEQSSVG VGPSKPGAGYNLLVCHLLRLLEKRSIRV GVSQFSRCHLSWLP LARKGNSRTPCTFR VRRCLAL
7941	21842	A	8001	295	1	TQPWGTRKRLPLKKKKKNSGDREWRWLC NSVTILNATMYTSEWLRPGTVTHCNP KTSGG*GGEIA*QEFKASLG NIA*SWL YKKILKISPLWWQT
7942	21843	A	8002	144	317	ELFYLKEMV*RPGPVAYACFPSTLGDGRG GRIT*AQEFRTDLGNIRPCVYLRKKKK RG
7943	21844	A	8003	69	291	HCVWTMIFIVIKYFYLNPNQNSMRYYS HFMDKETDVQSD*MTC*RLGAVAHACNP STLGGRIA*QGEFKTSL
7944	21845	A	8004	3	176	IVAHSSLTPLGLKQFSCSLPSS*VYRNM LPRLANY*FFGTNRVSLSCQGS*TLAS LLGSSSSPASACQVAKSTGTCTYHAWLI IDFLVQTGSRCLAKAGHELCSCL
7945	21846	A	8005	419	178	NPPPKKFLSSSSSSPLHLNWGTPGFF PPPPF*NPPPEFNFGAPKKKKLSPRA EKLVPFKGPPPPPPPPPP
7946	21847	A	8006	429	225	QPLPPRFK*FFCLSLPRR*GHRHRPPHP FNFFFF*YFLRWSFVLVAQAGVQCMDLS IYLNEFWLLDF

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7947	21848	A	8007	756	224	PERHQPOHVFPPLLHFSTPSPAPPKSHA AAPNSNPQAHAPPAPPAPRAHSPSPPP RGATPPFPFPFSSFLAAVGRAPIFPREP LLPSSSSPPPPP*IGPEPPGFSPPPLKKT RPPK*N*GPPKKKNFFPPRPKNWFL*K GPPPPFFFFFPPFLRQSFTLVAQAGVHKT RLHLKKKSN
7948	21849	A	8008	170	559	SSHLSPOSSWDYRSGMVAHTCNPSMLGG QDGRIT*AQKFQTSGLNIVRCHFVFKKY FKNKIFFYSPFINTNPKKKKKGGAVLK NQSLRPRAGKVLVFLWGHLIQFRGPRFK NGGTGKPGGLEPNLLAPR
7949	21850	A	8009	1	662	RTRRTSRWWYMPVLPPLSHYGEAGESLGP *KWMVD*APIAPLHSTLGDKMTLPDIKK KNGETVANTSPLSTTAKPAKLFLKAKKD QLMRDLFLPKTPKKPQMTGLDARSKRW LKIIWRRHGIWPLKNIGPTEDVQASAHG GVEENMTSDIEIPEAKHDHRPTEDVQVS AHGGVEENITSDIEISEAKHDHHLVEDL SESLSVCLEDFMTIGSQWKPICLS
7950	21851	A	8010	377	2	NFFFFFFPPFWGFFFLGPGFFKVF*IF PFFFPNPPFF*FFLGVLFFKK*IFFF PFSIRFCFPKFFFLILFFFF*PFFF FFFVYVDFFSFILIYIFFVYFSLPFT VLIISLIYHFAPA
7951	21852	A	8011	1	363	PTRPLF**RGCFMTLPRILNSWPQVIC PRPPKVGLQT
7952	21853	A	8012	278	39	FXXXFFLSPPXFLIFFFFFFFFFFNFFF FFFFFFF FH*DQ*FSNFDFTPFTTLISNII
7953	21854	A	8013	79	412	MNECILGKGKDGFFEQCENLGLC*FL KVP*DSDIWLGAHAHAYNPSTLEGQGER ST*AQEFKTRLGNMTRPCLYQKHTHKKK TKKKPHPGLGWANGPTYLGVGTKIT
7954	21855	A	8014	277	19	FGNIHNFFLIGSRSVTQAGGQWCNHS *PQTPVLKQSSHLSLPSSWEIEAASVQV RITALQGRQSKTLPGNSGPVLRADARR SI
7955	21856	A	8015	1	130	ARIVSIS*PCDLPASASQSAGITGISHH TQLAHNTLKASPTLF
7956	21857	A	8016	4	417	RLMPPHLANFLFF*RHGFTYVAQVGLKL LGSNDPSASTSQSTGTTDVSHCTQPHLL KSSHSTFPLKTLDSMATNCSDWKVHYLP TACRALLPCPLPSACFPSSLQVPSVFTC CVPATLTITLLPLLRAFEHVTLCPLE
7957	21858	A	8017	388	158	CVTWASNCINWICFPLS*INSHLCNEIT VLI*GEIYNVCISIYLCIYMCVCIIYISV CVCVCIIYH*TPYLIHKCLI
7958	21859	A	8018	154	382	GIKRPGAVAHNCNPSTLGG*GKWIG*AQ EFKTSFGNMVVKPQIYLLKKKKKKGAVLK DPSLRPRAGKVIIVFWGLPI
7959	21860	A	8019	396	237	FFFFFFW*G*GFTMLPRLVSNWAQVIH LPWPPKALGLQVRTMVPGRLRANF
7960	21861	A	8020	412	168	GNLLGSPLPGNVCKNKPFI*KKK*SL AVLPKLVSNFWP*MILPPWPKI*GVQA RAPPPSQILKKKKSSHPYNSHVNSL
7961	21862	A	8021	1	124	TRFLHVSQAGL*LLTSGDLPASASQSAD YIFIISPAKIIFL

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7962	21863	A	8022	3	200	HLSPYFYFFKDRVALCHPGWSAVVQ*PI VTSIFWSSC*KLTSVVRWRPSWLTR*N PVSTKNTKN
7963	21864	A	8023	3	132	FLFFFQF*FMRLGLAMLPLGMNSWA*V ILLPQPPEWLGQA
7964	21865	A	8024	3	187	VGQAGLEPPTSGDLPASASQSAEITRMS HRAQTK*DFIGSFSEEF
7965	21866	A	8025	405	231	SDKWIKKMRYIHTTEYY*ALKRKEILTH ATTWLNLENILLSEISQSPKHRYVVIPL T
7966	21867	A	8026	175	382	GKRIFPPYPPEGGKTGPPQTPGLFFFF LKKK*PGGLGGARFSPILGGVGRKNSFT LKGGA INLKGPPSLPPGGKRWAPPQKK KKKGQAWWLMPIPALWEAEAGRS
7967	21868	A	8027	83	374	GDQVWMLMHACNPSTLGGQCGRITWDRE FETSLANIFFPISTKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKASSGGGVSK KNFSPRAGKEIFF
7968	21869	A	8028	382	148	SPHCSLDLVGLKQSSHLSPST*DHRCV PPRLAIFSFAPLFFWEATTTTKATMLP RLVLNS*AQAILLPQPLVLRL
7969	21870	A	8029	88	208	SGSV*ENNPLSWAWWLQSIIPATQEA EV GRLLPRSSRSA
7970	21871	A	8030	1	283	NKSRIKKA IKMTEKMKKEIEMMKLMNQL PNGEHHAMIQMMMKIEMKGRMKIKE*DK ESDKDDRKDEREDRDEDEPTPERRTS RDDSDDDEDRDEGKNEDKRKDDSKDDDE ADEDTDQDDYDPMDAHKA ADEDDDEDED EVAEQMTKKKKKKKKKKKKKK*KKDRK DEREDRDEDEPTPERRTSRDDSDDDE DRDEGKNEDKRKDDSKDDDEADEDTDQD DYDPMDAHKA ADEDDDEDEDEVAE
7971	21872	A	8031	2	139	LQTLPLIAP*LLASLANLALPPTINL LGELSAQFAVIGMYILY
7972	21873	A	8032	80	324	YLHFFYFVR*KLMGLDTVAHTYNPSTLG DPERRIA*A*EFKTSLGNMVKPCIYKKK KKKKKKKKKKKKKKKKKKKKKKKKKK
7973	21874	A	8033	299	158	GNQPGASAHTCNPSTLVGQGGRII*AQE FKASLGNMVKHYLYQKHKN
7974	21875	A	8034	416	60	AQWLTSIIPPL*EA EVGGFFEPRLSPA WATE
7975	21876	A	8035	398	271	FYFL*DEVSLPRLVSNWTPAILPPWP PKVPGLRHEPRPA
7976	21877	A	8036	385	151	FLYFL*RLGLTLLPQLVSNISSDPPT* ASESAGITGVSNHAHLRICILTRLPGNS SH*NVRAGLGDTQSSALIPPG
7977	21878	A	8037	3	406	PASAS*VAGITGTHHHAQLIFVFLVETG FLFFFFWAVLFFKTKNGPPGGQLFFFA APPALGGDFGGQGATFSPKGLGVLGET RGGAPAPKKLGAKKEPSHLLGGGAQNLP KPRGQKGFYFYFLARDFFLG
7978	21879	A	8038	428	20	LANQ*WKPPSNPWETKISPKKKKGPPGQ GPPPLTPPLWEAPKARKLGSPWLPR*NP LFPQKPKKFFGFGGPPYSPLPQLSPK NGVTPEVGPSHKPKFPSPPLGQK*TP FPQKKKPKRLKRCMFLHGSTFQSL
7979	21880	A	8039	3	194	QNKISQVWWYTPVILATWEAEGGESVBP GRQLW*AKTAPLHYSQDEKYLKASVDS

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						YCLISCH
7980	21881	A	8040	415	96	LEPL*KYFPILDAIKNICDSWEEVKIST LTGV*KKLIPMLMDNFPAFKTSMEKVTA DVVEIGELELEVEPADVTELLQSCAKLE GMRSCFLWMSKESGFLRWIYSW
7981	21882	A	8041	413	254	PGFKQFSCLGFPKR*DYRHKPPCPASKY FKINYLRNITYRSLILKN
7982	21883	A	8042	409	102	GFFPFGPFFF*PPPPGVFP PPPPPNFWF *GFGPPPPPLF*FFFRGCPKKIWFPPFF LWPPPLFFFFFPFWPKKTPPKKARSLKIF FPLGPKKIPNPPPPPPFF
7983	21884	A	8043	414	153	GRGWATNFYFFLIILK*FFFIFKKFFFF HLFFFFFFFFFFFFFFFFFFFFFYKIF LFTLVLTCPQTS CREAEFPD HKVC SVLK ML
7984	21885	A	8044	401	292	NYLPPQ*KKKYYPQGPFRKPIKKSPPPC FFFFFFFFPSFPFPLNIPPPQKGFPPK KYFFNPPLFPPLFFLKPPPLFFF*GPKK KNLIFHPPSKKICPFKRGPP*FFFFFFFF F
7985	21886	A	8045	370	14	TPPPTKTPFFFLYPPPWREKREGFF*KA NMSPPVWKKIPPLPPYIYL*KGGSRYL AKLSLNLKGSYLSFCFPPLPPSLPLSL FERWGLTILPKLVLSWAQMILLPWLPK VLGLKV
7986	21887	A	8046	395	268	PFFFF*ETGSCSIVQGVQWLFTGTILV LISVGVLTCISIDL
7987	21888	A	8047	379	98	GPAHNSPPLGCESETPLGYPGKPRFF*K NKKINPARGPGPVVPPPPQG*AGKRPLP PRRGFQLTQNGPPPPPPGKKKPPFQKK KKKREPAIC
7988	21889	A	8048	369	177	RNTRGGPTFFFFFFFFFK*NLARLSRLEC HGTISAHCNFRLLGSSDSLPLTSDNDIGQ INKSLFA
7989	21890	A	8049	1	128	ALGLVAHAYNPSTLGSQRGKIA*GREFG TSLGHRARPCLYKK
7990	21891	A	8050	166	163	PVHQGEQT*QDKCLR*STHLGLPKC*DY RREPPCQASKLVPTGILADSKHSCQTM DSCFSNQLYKQR
7991	21892	A	8051	402	245	YFKSVCQAQWLNTYNPSTLGG*DGWITC GQEFRLPWPSGITGASHHAQPHFF
7992	21893	A	8052	404	268	QQLWRLRQRDCLNLGCGGCSEPRSCYCT PA*ATEPDPVSNKQINK
7993	21894	A	8053	1	154	GFLRVGQAGLELLTLRLDPTSASHSAGI AGVIYRAWPGEAYLFSG*WLRFT
7994	21895	A	8054	406	150	PKKKKNPCPPPEVKFDSLKRAPLFFFFL EESCFVTQAGLECSGAILAHCNLCLVGS SDSPLSL*RWVGNSHFIFTSLLSVSPRS N
7995	21896	A	8055	1	125	TAVILIFMI*EAFASKRKVLIVEEPSI NLE*LYGCPPPTH
7996	21897	A	8056	400	260	HMSPHLAFFFSFLFL*RLDMLPRLVSNS WPOAFLQQLLPQVLGLQV
7997	21898	A	8057	396	263	FLQPGTVAHACNPSTFRGGLIT*AQEFK TSLGNKVRPCLYKKQY
7998	21899	A	8058	402	211	FSCWCTKPKAAG*FPAPWGPPFLNPP GAGTNFPGPSPSGGFGSPPPWPGRPRP CPNGIFFC

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7999	21900	A	8059	1	279	VLLYHPGWSAVVQSWLMQ*TPSNADIWR IARGFKRSSHFSLLSSWDHRHVTPCLAN FFLIL*IWGLAMLSRLPLRLRKPVLLD *APSPCGLI
8000	21901	A	8060	408	315	SLTMLPRIVFNS*AQAILLPWPPKVLGL QV
8001	21902	A	8061	198	2	RIQHVESNCHLEVEGGWAQWLTPSTLGG RGRMIS*AQEFETRLGNTPRCFYKNLK SQPGMVVRI
8002	21903	A	8062	3	294	GLSPTAHPITAFTSQPLPSGLSVCRLFL WAMCEQCPLPIRPCCPRIIGPECALYT TSCLLHQLKKREGF*KKKKKKKKKKKK KKKIF*WGGGKK
8003	21904	A	8063	197	184	IHDFFLFFF*GRVSLCCPGWSAAQSRILT AL*PGELKETFYI*IRSWDHKHAPPLP APF*LFWVTLIITPSTHEVSSAVCSLLY VKSEQKCQ
8004	21905	A	8064	3	373	TSGSLAKRPADCLSAQPTFPSSLCGCSP VRVCITVPRCTHARAHTHTHTHTHTHTH SNHG*APGALYIQELQRGKVSHVPEKEK SDPETA*TKGG*HVTNPHGRQRSGBQEE HRI CVGRCCSG
8005	21906	A	8065	532	106	ENKPIHNLSINKYIGKILRDKALLYCPG WRAVMQS*LPVASNSWAPAILLCPGFLS TWDYKRVPPQLVKIFSKKKKNKPTNILR PKCHTRNQDIYKRGKVGLCSYCPALL LLLSLLLLLLLLLFSFSTRDSASGACSS LP
8006	21907	A	8066	411	130	PHAQLIFLRR*SLTVFPRVVSNSWPQAI LPPWPPKVLGPQARAMVPSPKLVLESIL RIPTSVIFFPLNLCNKLAEIKEGCSA AFLFNQRFAN
8007	21908	A	8067	3	32	DAWADAWGSLTDEWVEKIWIYHAMQYYS SFEKREIL*YVRTCMNLEDTMVSEIRQS QRDDYCMIPHI*GRTRGVH
8008	21909	A	8068	410	116	STFNITQWPGTVAHTYNPNTLEGQAGRI T*GQELETSLGNITRPNFLFCQACPGQ GLSTVRMCGSLHYFVLPLRPLKCLDNR KSPFFYHPVILPCYE
8009	21910	A	8069	158	289	DLCSLRNIVRPQLYKK*KISQVRKKKK KKKKKKKKKKKKKKKKKKKK
8010	21911	A	8070	388	1	AETPPCFLFKPFVLGGPFFGKAFFQKFP GGGFFPSPISGPKPPPPRNPISLKGKRV PSPQSPIMVFPGAF*RPPFFPLMVG*KI KIFLPPPPPPKTPPALSPPFFFEAEFRS CWPGWNAVMRSRLSATS
8011	21912	A	8071	15	336	KLDKRYDRGTGSPGTTASGYLIEPLVAE ASYELILSLAFFFFFERRGLALLPRLEGS GVIVAHCTLKLLGSGGPPASAS*VAGTA GMNHHEGHEPGLFEKQNSGFIF
8012	21913	A	8072	396	274	PHLHTWESSL*RQGLAMLSRLVSNWPQ VILSPWPVKVVL
8013	21914	A	8073	189	54	NKPLGPGMVVQACNPTPLGGQGQWIP*A PEFKISLGNLAKPCFY
8014	21915	A	8074	3	257	HAFVLLFETRSLSLRLLESSGAMIAYCR LELLGSGDPLTSASQVAGTKGM*DDAWL RQVSNWPQVILRLSHPHMFLFQFSLET
8015	21916	A	8075	1	119	TLPATWEAGAGGLLEPKSLRV*CVFTAT

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						VNSSRTPAWAA
8016	21917	A	8076	232	266	LPYCSGQWCLGLPIIQGVQWHDHGSGLQP RLPGLNQSSCLSLPKCWDYGREP*YLA* YQARYHGSLARQNVFNIRPGIMVHARSP STLGG
8017	21918	A	8077	390	143	LGGFLVFCPPAKKGFFPNPINLGTPRFF PPPPF*KPAPEINFGGPKKKKIPSPPPG VKFDPLKRPPPPPPPPPPFIRLLV
8018	21919	A	8078	424	144	LKNYIFFTFL*NRDRVSLCCPRLVLNFW AQEILLPWPPKVLGLQA
8019	21920	A	8079	182	45	VHKAGMVAHAYNPSTLRGRGGWIT*GQE FETSLASLDNMVKPRLC
8020	21921	A	8080	405	163	YFLEEMGFHHDQAGLELLTIGDPPGGM SHCTWLNVLNLIQKHPHRIQNNV*PH ISGPVKLTHEGNHNNHWMSTQKHSP
8021	21922	A	8081	39	240	QSKTVSKKKRKIIFCRYRVS*SPGFKQS SHLGLPKGWNVRREPPHPASTFSQSPFV KDHFCSGVSS
8022	21923	A	8082	2	263	DCCVSSE*GSVGVLSEPGAGYNLLVFR LLRPLEKRSIRVGGSRFSRYLSWLPLA RKGNSPTPCTSQVRQCPTELLGLHPLCD KPQ
8023	21924	A	8083	1	248	SVGVGPSEPGA*YNLLVCCLLRPLEQHS IRGGVSQFSKYRQSWLPLARKGNSPTP* ASCGMRGPALLWLTLGLHPLSNKPQ
8024	21925	A	8084	3	255	HLSLPSSWDYKRMPPHLANFFFFFLGKK GVLP*GQTGLEL*N*KNPPA*PPKGAGV KGVTHRPKP*NGGKGRFEKDTGGGFL
8025	21926	A	8085	409	145	LRGPYKKNFSQAPGRKIGSFKKAPPPF FFFFF*GQSLCCPVGLSTGVIIAHCSLE LLTSSDPASSASRVAGTTGACHCS*VLQ TFTF
8026	21927	A	8086	199	26	GFP PPPNKTEIF*RPPDFLNFFFLVEMN LTSLSRLVSNPWAQAVLLPWPPKALGPQ A
8027	21928	A	8087	222	3	SVGITGVSHHVLWYFTLKGFLGRGAHSC NNSALGRRGGWIT*AQEFETSLGSVARH HLYKKYKNYPVAVVRL
8028	21929	A	8088	415	197	TILCFYHQNSVFSSNPFSL*IFIF*D RVSFCHPGWSAVVQSWLTVFPILCATVK YFTCQQYIIMIFALNS
8029	21930	A	8089	297	71	FIFPENKNRPEVVAHACNTLRGRGGRIT *GQEFKSLSNIRPHLYKTKTQNILSK YIQYLGFLTLQIDLANIY
8030	21931	A	8090	185	415	PFGLKQSPHLTLSS*DYKHTPPCRVNF FFFLGGFGFFPKAGFNLG*RNFLASPS KRAGMAGINNLAGPIFRFFKK
8031	21932	A	8091	2	125	RKQASKKERKE*KK*RKKERKKERKKER KKERKEKERKEEP
8032	21933	A	8092	8	412	KGPQGTTLTCIFDLSYSSSLSHWSQSLC VAFPLPECIFPHKPLCPACHFFQSWG LALLPKREYRGKIGVNGNLELLG*NNPP SGTSKIAEPAELFHHTHARPFNWIKTD FPYIAQTGF*LRPSRNPSTLEV
8033	21934	A	8093	249	143	NIFAATWMRLTIIILSEVTQG*KTKHQM FSLICGS
8034	21935	A	8094	3	280	PERWDYRHEPPGPASFT*LLLFVFNL*R KGLYVGQRGRQLLASSSLPAPASLSAGI



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						IRMSHCTPAWVTVRPCY*INK*INGKDT IRQNLKKM
8035	21936	A	8095	404	16	QMGFCLFFFLPSSKEVFFFPPIFFFYRESF FLFHFFLDPRQY*LYFIIKKNIPLPSPF IFFFLIRVSPYIFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFWGSMEL LSKAHQCISSHGSG
8036	21937	A	8096	358	200	KSYFIFSLIIIFSHYFFLLFLKHLLATYY CFLIDCTLFFSFYCPFCCLFVLLSGRFP RSCl*TFH*RLYFSFPIFNVQKLF*LSD ICFCCLYLFYLFYFETVFCSCCLGWS MMA*FNGMFKDRI
8037	21938	A	8097	2	132	KEEKKERKE*KKRKKERKKREKKRKR EGGRKEGKEGKNSST
8038	21939	A	8098	48	331	PGTWHACLGGEDILKQWTKGRGRRAGSH RTSWIEPLETVFLELEAGGRLESPGKNY SRLGAVAHICIASTLGGRGRQIT*GQEF DTSLADFCST
8039	21940	A	8099	7	373	NGRLRRGFAMLARLVLN*PRDPPT*AS QSAGITGMSHARP TIESFIHYCWECKM E*PLCKLILYFHLFIFKRQKLG VHWCHH SLLQPPTPGLQRSFRLTPPSGWDYRRGP PCPANI*LII
8040	21941	A	8100	116	432	YLRNLFYQRFASPAILNLMCSAL*ESH TVAQAGVQVHNLGSLQLPDRFKRFSCL SLPSSNIFAPLSYFFRNSFTNISPSSEI GPQITDPLFIKKKIKVSVMVE
8041	21942	A	8101	361	138	FNLLGRKKKNFGGLKEGESRRPPNPGPQ FFFFFFLFFFFFFSG*RWGLTMLPRLVLNS WAQVILLPWPKSLGLEV
8042	21943	A	8102	1	199	PTRPFVFLMEMEFYHIGQTALELLTSGN LPASASQSAGITGVSDR*LA*YLFFPHE LFCYFALLLI
8043	21944	A	8103	412	46	KGGSPPPPPPPKIGRKGPNNPGDPFFFF SPFFRGF*GSPFPKK*KVLLVGFLKPK PPFPLGWNPPPPVGGFSPPQSLQFFF FKKVGWVFFFLPFFFFFFFFSPFFLFFS ETESHIAQA
8044	21945	A	8104	192	2	EETLSFFIIKYLYLPRNQVCKRL*RRL GPVAHACTPSPGGQREWITRSGVQDQP GQGETP
8045	21946	A	8105	373	183	GGPF*FQYILILFDNFFFSLSFPFSQD FFFLSSFFFFFFFFFIINYFYFF
8046	21947	A	8106	373	281	SPKTAPPPFFFFFW*RLSLTMLPRMVS N SWAQVLLPQPPKVLRL*ATQRKKHFRQ EQI
8047	21948	A	8107	3	114	FLIFVHIGPNYVAQAGLELLSSDDPPAL ASQCAGITGMNHARPYYLL*TLNIPLP YDPEIFLLGIYPR*MKTYVHTKACT*FF ITPLFVIAKTWQPK*PSVLGLQA
8048	21949	A	8108	416	243	PGVFPFPPF*NEPPEIIFWAPKKKKYFP PPPLNFVFFKGPPPPFFFFFFFFFFFFF L
8049	21950	A	8109	2	211	SVTQAGVQVHVSLLQPRLPGLEQSSCLG L**CWDGCGHEPWHALVTTSKHTESCSL LCIPTATFLGLVT
8050	21951	A	8110	172	28	HVVCFTSFFGFYFL*ROGLTKSPRLVP

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						NSWV*VILLWPWKVLGLQA
8051	21952	A	8111	2	225	QKSAKNFYHLSIYLSIYLSIYPSTIYHLS IYLSIIYLSSTYE*VILEQKWNSTKKG CL*CTIQTNCL*QLKE*VIRLIPKL*YK IKLPTCWSVHLNWFNLCNISWYLYLAM **RKLVCFA*FVVYNSNKLITIKRIGH
8052	21953	A	8112	392	221	PFPKRESPPDKVNPPPPDIFGGGKTKKK TLANN*FPPKEKEFFVFFFKKEDFF*NI VGNFKTPSKI*AVCF*NPVFKKKKGAPK KKSSFKNF
8053	21954	A	8113	369	112	IFFSTIYYFXHPFFFFPPPLFTPPPLFF FFLKKKKFFFFFXXFFFFFXXF FFFFFFFFFFFFFFFFFLAF*HVV SF
8054	21955	A	8114	418	248	KYYLPTPGY*NLILLNGPPFFFFF*D RVSPCCPRLP*TPRLTQSSCLSLPRSWD HRCMPLRLVTF*FTFKLSHQSLRTLTY TLAGTTLG
8055	21956	A	8115	229	78	SFKGAAPFFFF**RQNLTMSPKLVSNS RPQAVLPWPWKVLGLHRGGWIT
8056	21957	A	8116	356	66	PLFPPFYIKNFKKKFFFFFYFFFPFP PKHYSHKDIFFFFIKFFPSSSFSPFPF FALSSFFFFFFFFFFFFFHA*FPVF FLYKIPMLYPQL
8057	21958	A	8117	212	81	ERLSHCSNLNLPSSNPASAS*VAGTSG THQLVMVHAGSPRF
8058	21959	A	8118	367	2	GVFFFFFFSPAKGVFFHPFFFLGPRFFP PPPPFFPPLWFYFWGP*KKY*FPHPRGY EFFFF*GGPPHFFFFFFFFFFFFFFFF FFFYAEGIGVSPCYIMLGYNFSSFCGT ISPRVRPRV
8059	21960	A	8119	38	215	FFKSAPHHTRLIFNFFFLEKTGSHYVA QAGVELLG*SSPTSAFEIGGITGLFLS FKN
8060	21961	A	8120	266	2	PQIFLFIFETRSHSITQVGQWCDHSSL QPONPGLKQSSLSS*DYRHTLTAPG*FC FL*RCGLAMFPMVLSSWPQAVLKIHP CGMC
8061	21962	A	8121	3	332	DAWADAWGHVPPCPANFVLV*TGFLHI GQAGLELPTLSDPPASASQSVFIYFLET ESHSPAWEATERDSVSQKKKRGRFKGS NFTSAGLQRFIFFMGPPKLISRAGV
8062	21963	A	8122	378	66	LFIFLPIREEVFCIPG*NWAPPVLYN GRPFFFFLLETVFLHAGQAGLELLGSSD LPVSASQSVGITGMSHRVQPKLRIFVNI SFPFEIFCEIMLLVPLAQP
8063	21964	A	8123	2	316	ISMLLALLLRITITRFLPQLNGYVEEFTP YECGFNPISPRAPLFIEHFLVDITFLL FDVQIALLLPLP*ALQTGNLPLIVMPSL LLIIILALRLDYERLQNGSD
8064	21965	A	8124	331	14	ITSILIIITF*LPQLNGYI*KSTPYEC GFDPIPARVPFSIKFFLVAITFLLFDL EIALLLPLP*ALQTTNPLIGMSSLLLI IILALSLAYE*LQGLD*AE
8065	21966	A	8125	2	228	IIITF*LPQLNGYIEKSTPYECGFDPI PARVPFSIKFFLVAITFLLFDLEIALLL PLP*ALQTTNPLIVMSSL
8066	21967	A	8126	451	200	KA*WNRFAILNVTKYTCESQEBVKIPTF

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						AGVWKKLIPARTDDFVHFKTSVQEVATD VAKIASLLELEVESEDVTE*LQSQDKT
8067	21968	A	8127	2	396	LIVINTLLALLLIITF*LPQLSGYIE KSTPYECGDFDISPARVFFSIKFFLVAI TFLLSDLEIALLLPLP*ALQTTNLPLIG MSSLLLIILALSLAYE*LQKGLD*TES GWEKLVKKEKADKLKGRP
8068	21969	A	8128	1	350	GTRGLQTLLEPLIAF**LLASLANLALPP TINLLGELSVLVTTF*SNITLLLTGLN ILVTALYSLYIFTTQ*GSLTHHNNIK PSFTRENTLMFIHLSPIILLSLNPDIT GFSS
8069	21970	A	8129	375	1	LTCFSEHRPPPRANFFFSRKTRAPFFLP GGFQIPGNFFAPPIFPNGGPIPGLDPO PGPLNFF*KSFFPDPKFFFLFFPPPI*N SGVFLPRNPVFPKTPNLEFFSPFFPGD GVLLCHPGRLPRA
8070	21971	A	8130	32	211	GIRHGFAMLPRLVLNSWPQAILLPWPPK LLG*QAGVELLASSNPALASQTAGMTG VSTRPPVLLPTLGTHLCDACLGSSL
8071	21972	A	8131	396	5	KYRDGPPPPGKFFFFFF*DGFSLCCPGW SQTSCP*KSSCLPEG*DYRHEPPHMTLS SSY*CSQMCKCINKNCLGSCVVAHACNL SPLGGRITWGKKFETSLDNIVKNRLKK KKKKIYQGGGDHPCIFTN
8072	21973	A	8132	347	34	KAGFVIRPGPQEFFFFFPQDGIILCFP GWRAVAKS*VTATSNWAQAITGMLPPC PANF*KIS*RQSISMFPRLVPNSWPQVI LPPQPPK*LGLHVCLVPSLA
8073	21974	A	8133	102	270	DYRRTPPHLANFFYFL*RQILTVLPMLV SNSWVQAILLLQDFFSVQLKMGFLSVP
8074	21975	A	8134	338	47	FLSTQKESSPLHTHTHTHTHSHLLTH HHGRGQERGRGR*GG*WRTGTHSPHGP HCVRLRSRPSGELGAAGGCSLIQPKI EDPGQSGGPREV
8075	21976	A	8135	68	467	SLNLRIPFCLCLNSFDCVFLGLLFEAG FCSVAQAGVWYEHGSLQP*PRGLK*SF HLSLPKFWDYRNEPPHPPFSCFKALNFK DYCDSGTVPCPFMKELSMFIHALTESF VLFIVMSKLITTKHLTIISNV
8076	21977	A	8136	500	355	FHHVGQAGIQLLTSGDPPA*ASQSAKIT GVSHRARPQTSFLNKLPSLR
8077	21978	A	8137	58	222	IYGYEGRGSVAGSLSSL*SATDSDLDY DYLQNWGPRFKKLADLYGSKDTFDDDS
8078	21979	A	8138	345	196	KGDQAQWLRPGMVAHICNLSTLEGQGG IT*AQKFETSLSNTLRPPISFK
8079	21980	A	8139	500	355	FHHVGQAGIQLLTSGDPPA*ASQSAKIT GVSHRARPQTSFLNKLPSLR
8080	21981	A	8140	3	231	HASADAWGRNEWPCAVAHANPTTSGG* GGWIA*AQEFEFETSLCKIVKPHLSKKK KKKKNFSPGWGSPPCPLF
8081	21982	A	8141	416	26	ARIFPNNSFWPGQGPPFPRLPLEGPGG VIP*CQGVQARPAPPGPRLFPKPKIV GGGGEPLFPPPERAGPKCRPFGEAGF N*PKPRPCPPGWGAQGGFVSKKKKKRNE DSKIPLIGKYPVGIRNMA
8082	21983	A	8142	413	35	RGAGGGGSPPGPRYPSQOHLRLARTPTP FARSRGSPGVRGSGWRGGLGG*SRERP

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						LPSLPALPRSGASSGPLDGGACQGPGR RERWAFLLGGIRADARGCRAVTSPEPYRL PCAGAARARR
8083	21984	A	8143	166	368	ENILWAAMVVLDCHPSTLGG*GGRIT*G QEFKTNLANIERPHLFFFFFFFKRDSLFA PRAEGGGPILF
8084	21985	A	8144	1700	621	DLRDHSLVQQGPACLTTRCGEPILSHSEG SKIGSERESGEHSRHPPEAPPSPVEVGRS RS*QQDS*GFGPGNGQDTRGPLSHAAPN WTPDPAAAVAAGGTSLLPRGGGGI*RG SHTARSGARVGSANAHARGGSGFSRHSG SHGCLRNQSPRLGKAGALCGSAWVSGL* GSGLTSPRGRERLRMPGVAKGRPR*GN PRRGRGKQHGIPASGLPGRCWLGIKMT LQPRTRAPEELFVPQESSGSTPEKMLVS FHGSSLRNEATPRYSQQEEAGNRWQQS LSLERWPPWTSHPLGTPPLMPVAVARCC ILPGLWPLLSPPSGSASPVSQGGPCLSL WPNAFKKDDFPVRQGDTSWRSVS
8085	21986	A	8145	390	38	NTTTFNIYFFYFFFFSLFIYFFFFFFFFFF FFFFFFFFFIFILFIYSLLVFGVWVLGL GLALALLAKLFLVNSLCRRYRG*SLLY AWL*FFIFPLRYIYICARQFLSPILYL GKWF
8086	21987	A	8146	20	187	KLTTSTGRNPGRPTRPNF*VF*RDGLI MLERLVSNSWPLVNLFWPPKILGLQM
8087	21988	A	8147	417	64	VRPRVRPRVRPRIRKKKKKKKKKKKKKK KKKKKKWGGF*DFWGGEGKPPPLQKND LLFWGFFLKSSFFFCGGLFFWGGPFFFP PPPNFLGVGCKKKTFRLLCGPFSAFFGG EKN
8088	21989	A	8148	351	187	RLGTFYLSNLRFLYLSITHGPPIYIGRL TSQNLPLLLDLT*LEKLLPKKSQTYN
8089	21990	A	8149	465	60	PPHFVGNPKKNSQFFWAKKKKKIFLGP *KMAKKGVVFWGRKKGFQRGKKG*KG GQLFYPLVLSQVLGGGQNHGPPGKAGFGE NFFFGQGLGWAISRWLRTPLFLAGGGE DPKKNFKPPPKIKTLGAGVKKK
8090	21991	A	8150	1	175	WDYRHVPYPYLANVFFVIFRGDKVSLCCP V*GPTTELKRSSCLGFP*GWDYRREPPH LA
8091	21992	A	8151	59	35	RWNSRPRRPLKFLTSGDLPASASGSAV ITDVSHHAWPETFFR*RA
8092	21993	A	8152	269	159	ARVEVSKYIYIHTHTHTHTHTHTHTHT HTYTTKKLPS*LFQVCKMEKFGRLVVQ
8093	21994	A	8153	1	256	PGPPPRFFFFFFFFFFFFFFFFFFFF*TLKI RFIWRKQKTHNPKDGIHQDISQVLSLQ ITNHFHRRYFCTNFTCIQERDINQSLFL F
8094	21995	A	8154	252	41	LIIPVLICIVFIVLQKRFISVISLNKGL FRNHFFIF*RWGLTMLPRLVSNKAQV ILPPWPPKVLGLQV
8095	21996	A	8155	21	443	HELSLI*FISTLAETNRTFPDLVDGESE LVSGFSIEYAAGPFALFFIGEYTNIIII NTLTITIFLGTTYDALSPELYTTYFVTK TLLLTCLVL*IRTAYPRFRYDQLIHL* KNFLPLTLALLI*YVSIPTITISSIPPQT
8096	21997	A	8156	2	205	LLHLMKHFNLEIQKAQ*TRINLKRISIR

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						HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8097	21998	A	8157	2	205	LLHLMKHFNLSTIQKAQ*TRINLKRSISR HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8098	21999	A	8158	2	222	VYTWGTGKARVFPGEF*LPVWIPTRHLK FYNEPIRDANESASAETENPQSSIIHPQ DEQNGDIRRTDKVTIHQ
8099	22000	A	8159	1	297	GFHHVQGSGLELLTSGDPLASTS*SAGI TGMSHHAWPLNCSYGDSESWLKCPELTV ACWEEGWKRKLLMENEQGREAHQKLESV INFYIKDSMTKRYK
8100	22001	A	8160	138	437	NEYDHFSTIKERRDFIVCVFFFFFSKKS LTVGTQGGPSYLEPPFLGNKEFSCFL GSWDNNGGATTRLG*FFVFFRKKGVSPCG PGWS*TPDLRKTPPSA
8101	22002	A	8161	330	148	QQSKTFFFFFCKKKKIYICMVVHAY NPSYSGG*GGRIT*AQKFKTSLNNTVRP HLYKK
8102	22003	A	8162	391	255	RPAPADF*FFFFYRLGLAVLPRLVWNSW PQATLLPQPLRVLGLQI
8103	22004	A	8163	131	3	HKVSLCYPG*SALMQS*LTVASNSWAQA ILOP*PPE*LGLQA
8104	22005	A	8164	97	440	NKGSCLCPPGGRPGALSHETARSRGSPGP TPQKTGNNGPGPPTPVNLEFFEKRGFT VGQGGGLKLR*RSPPPSAPQKAGITGGS RRPGPIQKKFLKTLGGETKWMALIKTY LK
8105	22006	A	8165	541	295	FSQKKKIFISTNLSHQESKIYICKEME SHSVIRLLEGGSAIMNHCSLKLPSSTD PASVS*SAGIIGVSQHLANYTFKKIF
8106	22007	A	8166	440	259	PPQKFFFFFFFVKTFGRHV*AGFRLD SSDPPLAFQSVEITGMSPSARPMFGVF HSLR
8107	22008	A	8167	23	405	FRICHLRLVHLLVYFIPSFTDNHLLSTS AMFLYSNDVIAQNVSGPFLGIIFRTEF FFFLKGEFFAPQVGQGGNGL*LNPPP PGLKGFSGLTPPGGGNSGGGPPNKNFW IFKKGGGSTLWPRII
8108	22009	A	8168	23	388	PYFSCALPRHHPPTNLGPHLGMGAPWG QPSVAHHTLLFFFFFLKRDFCFVPRVEK LWLEESSLNPLLGLKEFSCLTWRTGN NGGPPPPVIFCF*KKGGVYPWPGGGE TPALKETPGL
8109	22010	A	8169	612	498	NIHFSLSFSHTHRHMTHTHTHAHTYI RTP*DNVPQ
8110	22011	A	8170	2	288	VNLITFFPQHFLGLSGMPRRYSYDPDAYT T*NILSSVGSFISLTAVILIIIFI*EAF ASKRKVLIVEEPSINLE*LYIKKKKKK KKKKKKKKKK
8111	22012	A	8171	381	101	QKSLQQPSNIATILEEVQVIFLGSFYHL QRWEMRLTKWLRGLGAVAHACNPSTLGG MGGWIA*AQELTSGDPPSSNRQLFTG EHNNDNKLI
8112	22013	A	8172	136	360	TKKHFGLLK*TKKHFGLLKKKKKKKKK KKKKKKKKKKGGGAFKKKKFFPRGGGK IFFFGAPKNKFGGGVLKTGGGKKPGVT KK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8113	22014	A	8173	358	58	EKVSVFLLMKCSGIILLPCRLTLPGST DSPASVCRMPAIAAGPRRHA*LVLVETGF RCVGRAGLQPLTASDPPTSASPGAAIAD GVSFTQCSMVPRIRVQ
8114	22015	A	8174	254	370	GLTVLPGLVSNWAQVILLSWPPE*LRP QAYATGAGFLL
8115	22016	A	8175	48	269	FYVILCLRDRVLLCCLGWS*TLGLKLSS YLSLLSSWDLQHVPVPHSASCLTF*VKAC FLLKYLKRLKIYAKIM
8116	22017	A	8176	1	338	PTRPINTLLALLLIITTF*LPQLNGYIE KSTPYECGFDPISPARVFFSIKFFLVAI TFLLFDLEIALLLPLP*ALQTTNLLPIA MSSLLLIILALGLAYE*LQKID*AEF
8117	22018	A	8177	426	130	QSLDPPGNMVTLSLQN*KNPPP*GGAVF PPFGRLLGGENPPGGSKEQKRPAPOGG* PRQPPSPKKKNADSEFSIFNLQPALCK QYCIVLHALENKILF
8118	22019	A	8178	396	244	KIHLLYICMIYIYVISRHYILR*HHTA HTYTHTHTHTHTHTPKNTKYTLW
8119	22020	A	8179	2	119	TRPGNWPGVVAHFYDPSTLGA*GELIT* GQEFETSSSLY
8120	22021	A	8180	2	80	FLPLTLALLI*HVSIPITISSTIPPQT
8121	22022	A	8181	438	333	SPLGRLRHYNCLNWGGKGCN*PKSCPCP PAWGK
8122	22023	A	8182	393	19	IEFFFFPPPSPAKFFFIKKKRFPLWG GVF*SPPPGFQKTPPPQKVGFSRVFPP PKKFFFGGKGYFFFKPPPPPPIL*K GGAKISPPPPGKKKNPFLLKGGKKKT PFIFFFPPKKIKN
8123	22024	A	8183	24	269	GSQQVLGFCDRDRVLLCHPGWSAVM*S* LTVASTSWA*RILHCSLLGSWEYRHTPP CL*NRNPQLTVKWRVKDHNKKSHR
8124	22025	A	8184	154	361	WHNHDPLQPQTHGLKRSSHLLGLPSIWHY RHVPPRLANFLNLSFRQGLAMLPTPSVC HLLVFLS*HIYWTFGYLS*SVCSHLLNF L**WHNHDPLQPQTHGLKRSSHLLGLPSI WHYRHVPPRLANFLNLSFRQGLAMLPTP SVCHLLVFLSETLGFK
8125	22026	A	8185	228	337	RPGMVAHACIPGILGGRGGWIT*GEKFE TSLANMVK
8126	22027	A	8186	314	127	DIQPKNEGEGEEQELWLGMTAHAYTPS TLGD*GGRIA*VQEFETCLGSLARPPSL QKNFKN
8127	22028	A	8187	10	420	TQEAENVNWDHATALQPGRQSETPSPE KKKKKRGPPRWGENFFPTPGGF*KDGGN KKTGFPPFKRDGPPPKNWTWPVQKRG APPEPPPLGGALGREPLGGFFGKGGVET PPPIFKKNNPPEKKPHRGFNFFAF
8128	22029	A	8188	398	1	LKKKRBPQTFSPKIQF*KFFPPFFPKKS FPKNNLLKKRAPGGPIFFFFFFYPLFK NPSPL*MGSPPPPLFNPNK*KKPPLKK GPGF*WPFQKKKPPFFFFFFFWRQGFTV LPRHTPSCLVNFCIFCRDGI
8129	22030	A	8189	30	153	AWYVRREDHVSLLGG*GCGKPWLCHGTPA WVTEENPKGKIK
8130	22031	A	8190	206	45	HPSQNSLSKN*ERVSVCCPGWSAVAGSQ LTAASTSQAQVILLPQPPE*LGLQA
8131	22032	A	8191	3	228	TCVCLCVYICDVCVGCVCVYIDEYIQ

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						IYRYIHTYIDIYTHI*YIYHTYIDTHMW VCVYIYIYIYRCMGVRET
8132	22033	A	8192	41	416	ICRVKETASRPLLETHSLSLVELS*FCL TAQ*RNDFLALKHLTAVLYNLILHSSGF WSSLKSHFIFLAL*YYL**FI*SN*RRD LAVLPRLVSNWPQVILPPQPPKVLEIR YEPPSLALILFFN
8133	22034	A	8193	2	183	KRLSIWQKKVEGEGFQGMVGPVSVAHA CVSSSLEGGQGGKIA*GQEFETILSNIVR PHLY
8134	22035	A	8194	2	465	AGVQWHDLGSLQSPPPGFK*FSSLSLPS SWDYRSAPPCPADFCIFRRDWAGWGVGC GFHRVARAGLELLTSGDPPASAPGAGI AGMSHRTQRGQDNFASWRRGGPQMSPS PSCFLQNTFSLKPSWVAPYPHASALGG GEYGGPPSPQPHLE
8135	22036	A	8195	397	149	LICLTDLPIRFLSLLALVFTVFNTKVKV KDLIKLGVVAHTCNLNLGG*GGRIA*A HEFETSLGNIVRAVIPCCFSVILSR
8136	22037	A	8196	355	95	KKIMPTLCLKIPS*YRCEEIIQLSLQSS CDHRHMPHPPTNPF*RHLSMLRSLVLN SRPQAVLPHGPPKVLGLQAPATAPGILS LF
8137	22038	A	8197	382	112	KTDFGKKGSPSSPPPPFFFFKKSFAPSPR GEKKAPLKSQRGLCPPKPKDPPPPGSG* TQDKGPPPPGQPIFFFFLKKGVCLFSRG GSKTFI
8138	22039	A	8198	32	361	ASRIGFILQEFPLPVRVWTTNPSAGADGY NFLEKQKGTEKTSQSVQAQAQWCHRNL L*P*TSELKQSSCLSLSSWDYRMVFL LGKQVTLIGKRALSVPYPRDVVSLC
8139	22040	A	8199	1	314	INTLLALLLIITF*LPQLSGYIEKSTP YECGFDPIPARVPFSIKFFLAATFLL FDLKNALLPLP*ALQTTNLPLIGMPSL LLIIILALSLAYE*LQGLY
8140	22041	A	8200	3	109	FTSKHHFGFEAAA*YWHFVDVV*LFLYV SIY**GS
8141	22042	A	8201	3	216	DAWAAVGHHTRLIF*IFVEIGSLCVSQ AGLEILDSSDPSSASQSAGIRGMSHGA GQEHLPFRPIGKIK
8142	22043	A	8202	1	267	RIHTGEKPYKCEECGTGFGKGPSTLTTHK FFVYCREVAVLLKNCYSHLYPH*IIVNG SEADKREMCLLCIFFHPLAEEQENVENK RKYNP
8143	22044	A	8203	422	92	PLVFALPPKIGFAPTPSSSPPPPLFF FGPPVFPPPPFFNPPPPFFFPKPKKF PSPPPRGKIFPF*TPPPPPFFPPPPFF FFFFFLLFLYLLFILC
8144	22045	A	8204	445	260	VCSPPLFIWVAPGFSPPPLFKNPPPNFF FGAPKKKNFFPPPA*NFFFLKGPPLFF FFFFF
8145	22046	A	8205	103	248	GPGVVAHACNPSSLGG*GQWIA*AHEFK TSLSNVVRPISAKKKGGPF
8146	22047	A	8206	407	197	QLIFKFL*EQASHYVAQAGLELLGSGNP PASTSQSVKVTGMSHGAWLLAPTLRSTS LNYNSLSVLLLP
8147	22048	A	8207	1	142	SCSVAQARV*FRDLGSLQPPPPRFTPF CTPAWETVRLHLRKKKKKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8148	22049	A	8208	2	370	PEVFDYPN*FKNL*LHKTCTQ*L*AALF VITKTWNQGCPLTGEWINKLEYIHTMDY LAIKINELANHKMM*RTLKCILLSESR* SRKATYYMISIRHPRKGKTITIEVQNSS CQGLGERQKGL
8149	22050	A	8209	363	108	KKPRVEACLSPGVGRERAKRER*KRERE RERERERERENEL*KLSLADLCIKNG*R EFFKEKRYVKRYAKILRVSGRKQKYGNV
8150	22051	A	8210	386	254	LNPGGGVCSEPRLCPTPAWVIR*DSVS EKGGKKRKGPENSLTATNF*ALSCNLDY LRCSMLKMQRQRKRKERTEVRFWQLHHN LTLGFV*LIVYQRE*RRTGWFVAKYMLY TFS*PGSFPRLRKCVHEHVFGEYEPACSP FPLIHNQLHKAAC
8151	22052	A	8211	3	131	AHLFIAWFTEYFKPTVITYCSKKKIPFK MLLLIDSAPSYPRALMBYKGMNVVFMH DNLTFILWPMQ*VIFTS*SYLRN*FC TIAAIDSDSDSGSQSNLKIF*KGFTTL DAIKNICDS*EL
8152	22053	A	8212	86	286	WSIWECTVISVQLFHKPKTSFKNTSYWS GVMAVTNNLSTLGSQDPQIT*GQEFETS LANMVKSCLY
8153	22054	A	8213	393	344	SFFPSLPSKWGFKNLVPSPGYFLFFLNK GFRYFGQGGFKILNSNYPPLASQKGGI SGISPPWRALVFF*WRNLGPN*RTIVSP NYGLK
8154	22055	A	8214	3	313	QGLVLWHSGLLQ*PPGLRRSSCFSLP CSWEHRCPTPHLANFLILCVVCVCVET GSHFVAQAGLELLGSSDPPLSISQKSWD YKV*AIIPRAKQNYLMLFY
8155	22056	A	8215	165	348	RPCPLFPEDLLTFSREGPGTMAHACNLS TLGGQGGGIA*GQEFETTLGNIVRPHLY FYLLK
8156	22057	A	8216	379	218	VFLVETGFLHVGQAGLKLPTSGDPPASA SVSAGITGVSQKCRF*YNVFIFQKSSLL NALPICSLTMLLGNLFMFMTPKFPTCS
8157	22058	A	8217	32	276	RYLPITIAALFTIAKI*KQPKSSLLDKWI KKLWCIYTMYYSAKLVILTVVTTWMNL VGFIPGDINHIOKAKYCMISLICGI
8158	22059	A	8218	171	2	KGVFGLGRLEFFFLDRVWLCLPEWSTVVQ SRLSATSAS*IQAILPPQPPEELGPLCP
8159	22060	A	8219	530	73	TKPTVGSNSRSYINQTYFPSTLTFGGL MRLTIYHFFFLVYYNPRVMVTPAYM*L LILFYSSSIRDLLIAKQCLPNEGFS PHAC*TNATLLFPYSI*YGLPLSFHLIFPV CFSFYFL*R*GLTMPMLVLSSWPQVIL PPQPPKVLGLQA
8160	22061	A	8220	350	135	FFFFSQTGVAQNRVQ*RDHNSLQ*PPG LRQSSCLTLKPCWDYRCKPLCLASWYF KDKVYTSTPVHTQEY
8161	22062	A	8221	185	331	PGMVAHAYNPNTLGG*GGKLT*AQEFET SLGNINSVPKKRRKRREMM
8162	22063	A	8222	73	232	YCSFKFITLTCLSWLGTVAHTCNPSTVE GGGRIT*GWEFTTSLGNIVRSCLY
8163	22064	A	8223	418	211	AMPSLLTYLLTFIFCRKKKIFFYWGFT MLS*LVLNSWTQVILPPWPAKVLVLRPL ALFYSLLVLPSPF
8164	22065	A	8224	227	33	ESHSTTQAGVQWHDHGSGLQPPPGMSLY



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						CH*CLRFWSWRPAEKGWCSLRFMELE SWSGASDAF
8165	22066	A	8225	244	287	TDSPTSAFRSAGITSISHHTLPKSTF*I FCRAGGLAMLRLVLNSWPQVILPSQPP KALGSQA
8166	22067	A	8226	53	235	NNKWQGVVAHTCNPTTLGG*GEWIT*GQ EFETSPANMAKIPPLVMFAFCFEETDNK SHTK
8167	22068	A	8227	275	25	GVLMFNFKFCI*QNSPFMLPGVVLNSWI PAILPPQRPKVLGLQAWTILYKWWYGKE MWHKEICEGTHDVL SKLLTTRFRKRL
8168	22069	A	8228	386	211	QLKLPLPKGNKLRPP**KFFFFFFFQ GLTILPRLVSSSWHQMIFFPPQPEVLGL QA
8169	22070	A	8229	1	117	VFILFYF*DGLAMLRLATNSWAQAAILL PSAPKVQGLQA
8170	22071	A	8230	356	26	WHVHGSQQP*PPGLKQSFCSLPSWDE RCAPPHPINYFQICRDRVYKRWANMVIS PNPLVLISQSAGITSKIPCPGSEISTIF IFSHQLLLVRGVYPDMLVLQLGKTICI
8171	22072	A	8231	3	188	FPSLRPA*IFFYIYFFFLKNKVFLCHPG WTQLLDPNWTQAAGLKQSSHLSSLSSLN FRGSA
8172	22073	A	8232	2	253	KLDYINCGTNLAQKCLFCLFGSLFFQR* GLTLLRLFLMNSWPQAAILLP*PLTVLGL QATMLGSQVPVFDLGITLCRCRFGKLE
8173	22074	A	8233	373	65	PEKAGSCLELAFGLQMQHPPWASTLPAA LTDPLATVFNHVSQFLKSHTHTHTHTH THTHTCTRLLVLFL*EALTTTPLLRSI CKHRESACSLSLTWPLCC
8174	22075	A	8234	390	46	RVFKPG*NPPLVKAPAPPLFFGGV*GRS PKKNPQGGGGGGPPGFHPPFLTPFFP IFLRREPPPPFFFRGGLGPPPPFKTPFF FFFVWKGKFLPQKKKKFFQSISTRVS IHK
8175	22076	A	8235	387	216	QKLGVLVPPGRVIFFFFFFFCC*GGGL TMLPRLVSNWPLAAILLPQPPKVLGLQV
8176	22077	A	8236	1	201	REFFFTIPPQCFPQFILSF*RRGLAVLBR LVLNPWPQAAILPPQPELLGLQAHPTTL GPVFYSYCVRA
8177	22078	A	8237	399	229	SVGGGGLTMLPSWSQTPGLK*SSHLSLI KCWDYRPEPPHLAHSLLNLQLYCHTKL S
8178	22079	A	8238	192	335	SHTLPHSSNFSYFW*RQGFAMLPRLVLN SWARAVCLPQSPKVLGLHA
8179	22080	A	8239	442	254	GRDRVLLFCPGWSQTLGLKRSSCLGLPK HWDYRHEPPHAPENIKFCVWPTLYFYWP ALVQINLP*QLQGTCEVACMC
8180	22081	A	8240	381	180	VLKLFFCSHRGPTMLPRLVNSGLK*SS HLGLPNCWD*RCEPWHPASLCLLTSTFW PPTLICNIHK
8181	22082	A	8241	388	260	NAIPFYITKCCNPSTLGG*GG*IT*GQE FENCLANMVKPCLY
8182	22083	A	8242	1	145	GFTILVRLVLNS*PLDPPALASQGAGIT GVSHCAQLIYVFQRLQLLW
8183	22084	A	8243	1	173	GLTVSQAGVQWCDHSSL*QTLGLKQSS SLSLPSSWDYKCKPQHQAADFFLMEFFQ M

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8184	22085	A	8244	202	327	TLFITFIFF*R*GLAVLPRLVLNSWPQV ILLWPPRVLGLHV
8185	22086	A	8245	42	289	KEKRSTIILFIFFCRDGVLLWLPRLDLNS WPKTIFPPWPPK*LALQAHTTIPRGGS IILICIRDVKRERKQYAKSKNPEGET
8186	22087	A	8246	592	485	NIVSQAGVQWHNLGSLQPLPLGLKWFSC LSLLSS*DYRHVPPCPANFCISVETRFC HVGQAGLELLASNNPPAPASQSTGTTGV SPCTRPRVYVFLWLILANGPS*RAETLV NLATNQEDADSSILAPGLSGHCF
8187	22088	A	8247	307	12	MCSPVFSPPKQKNPLFLNFFKKEFLFFFP GGRQGGHFGFLAPPLPGLNKFVLDPFG NGDTGKPPARGNFFFFFGIFSRDFV SPC*PGWSLIPDPR
8188	22089	A	8248	392	237	HYQASLAPLTSGDLPASAPQSAEVTGV SHRAWPTVLI*SFS*KFNWV
8189	22090	A	8249	153	386	FFPPGWPKPSLLEPPPWLGKFPPTLL GGGD*KRPPPPGNFCFFKKNVSPLWE GWF*TSNLGNPLPSPPKRVGIT
8190	22091	A	8250	387	166	IETILDAIKNIHDSWEEVKISTLTRVWK N*IPTPMDNFEFGFKTSLEEVTDVGMIA RELEVEPEHVIELLHDIS
8191	22092	A	8251	405	266	LFAIVKR*NHPKCLLIYARINKMWHISI GWNIIISLISKGMKFSYMLTWMNLEVIM LSEISHSQKVT*YMVPLA*GHLEKLNCL PIKQQTPIPSSSSP
8192	22093	A	8252	379	201	PGANYACNPSTLGGRSWGIA*AQELET LSNMTPKQPCSTPQCFLVNQLLLQNL LYP
8193	22094	A	8253	78	311	LTLYFHTRRKKGLK*IFYFI*SILSQKD LKVGTGPGAGAHTYNPRTWGGWGLQAG KRIT*AQEFETSLDNTVKTC
8194	22095	A	8254	303	81	TPCAENFKLRKRFFHHIISLQRKMNYLIS FLYF**SHSLTILPRLVSNWPQAILLP LPPKVPGLQVSATLPLGL
8195	22096	A	8255	2	376	MGYNLVCHLLRPLEKRSIRVGVTFSG CPPSPPLPARKGYSLTPCASQVRQCLAL LWLTGLGLHPLSCPHCPTSPVMNPVPQ LEMQKSPVFCVSHAGSCRLFLFGLH LG TQSSLDSPFKKVI
8196	22097	A	8256	70	356	LITAYNLTYDLWKMFVYLRKIYTLH WVECSIYTCWV*FVYSMVSWNRIDSPGK KKTNIYDQLIFNKGAKSTKLKNSLFNK WGQDKISTYKK
8197	22098	A	8257	403	85	PFCPPWFPPVFIPPLRKSGTPPGPGEF PGPGFSNGGNPRPLKKSPPKSPGWGRGP LFPSPRGV*AGNFLGPRWRGPWAKFVP LPSCLGHKARFFFPKKRRKIK
8198	22099	A	8258	249	2	YCEGDLGSYRPGVSKCMFESPRDIRIM PWPGAVCYAYNLSTLGGRDGIA*A*EF GTSLAYIVKPHLYTHTHTHTHTHMY
8199	22100	A	8259	2	189	IQCVCTKSHFCHPGWSAVAQSWLTAAS TS*A*VDFSHLSLLNSWD*RRVTPRLVN LILFPS
8200	22101	A	8260	453	128	FFFFFFLIETVSHDVP*AGLELLSSSH LASAFQSAEITGVSHHAQPSVSWLIHS S
8201	22102	A	8261	420	79	KNPTFFFFFFLIETVSHDVP*AGLELL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSSHPLASAFQSAEITGVSHHAQPSSVS WLIHSS
8202	22103	A	8262	1	262	NSRTERLGSWQSHFCHKEMEAHFVVQSG VQWCDLGLSLRPLPPGFK*FSCPIILSGW DYSQCRPCRTCSLI FMHSRSPSPSEKK WTC
8203	22104	A	8263	321	100	SATKNYLLSRQSFIGNGLGAVAHAY NSSTSRGLGGQIA*A*EFETS*GNMMRP HCYRKYKNLARHSTYSPR
8204	22105	A	8264	145	275	KPRDYSFFF*WKRDLMPLRLASNSWTH AILPPWPPKVLRLQG
8205	22106	A	8265	73	351	SLCYRSFARCDRPPKKGQHFSSYLQDAQ WARTLLSTIAQNNSAEHLKTTDW*GAV AHACNPSTPQGRGGRIA*VQEIETSQGN TGRPHLYKK
8206	22107	A	8266	382	232	LVETGFCHVGQAGLKLTLTSGDPPASASQ SAGITGVSHCAWL*T*YS*DFQ
8207	22108	A	8267	397	130	IGQAGLKLTLTSGDLPTSASQTAGITGMS HRAWPTFSLIAR*NASFQVGHFSPKYQV GTLAKSLKCHQVRSDTLEFILCCRIIYE TLGKF
8208	22109	A	8268	309	97	DTWYRTRRKDHCTITETRIQSVRPLSPR *AITSRVTCYTTSR*PEANEEPQKITFR HCDLFLPTLTDQLTL
8209	22110	A	8269	2	224	DSSGIPGSPTRPPTRPKKQKLPCDPTVS LLGICIDYDQRQ*SVFQRDICHSHMFITA LFTIVNIWKQT*HPLMDE
8210	22111	A	8270	374	2	TSWESARKPPPIHSHTLKGGFFFLFMFF FF*NKICKDGLTMLPRVVLNSWAEGIL LPRSPKVVGIELATQRRASILLCNPTY ACGIFQHVNVNVLKLMKQCPFCPAAPT TKTQNFPPRV
8211	22112	A	8271	1	379	PTSASQVAGTTGTHHHIVLFFFIFGIFEK KGVFFPSPGGF*TPKPKPPPGFGPKRGG KKGPPPPARGMGSGVFYPPPPQKPFV LIGGQILFKGRITLDFKKRAPPPPPSLF LPKHTPSFWIKWDP
8212	22113	A	8272	80	401	AWGMRFCLLLYSCQYLISDIAHFSAFF FWKREPPAPQVKGGPNLS*WNPWLQG *RGFSGLTPKGGNGYPPPPPLIFFFL RKNGFFPGWPGWSKTPDLRKPPC
8213	22114	A	8273	405	95	PPKRFWGSCKGFPQREKKLGSPTFPKKK KDFIYSYLSKSLKKE*INRPSAAHTCN PSTLGGQGRIT*GQRFKISLSNIGRPH LYEKIKNVKKLKI KPNKL
8214	22115	A	8274	167	52	DREQRPGAMAHTCNPSTLGG*GGWITRF LANMVKLRLY
8215	22116	A	8275	276	23	KYVSSRPGTVAHSCKPSPLDGQGEWIA* VRKFKTILGNMMKPHLLFYKKLTFKNVK CIFKKYCATESRYVTKEKQKDRKKGTKE
8216	22117	A	8276	1	114	FTMLARMVWIS*PRDPPASASQSAGTTG VSHHARPLS
8217	22118	A	8277	2	87	TMLLRLFLNS*AQAVILPWPPAVLGLQG
8218	22119	A	8278	357	347	SEGLALYQLEAFTVCDLRERGFRCRGRSL WPLITWAWRGGVFLLVQFQEVCCRLALG SLSPDPVLLPESGGPTSASQSAGIIGVR DRAQPNVCVEIGSYSVTQAGVQ*HNHGS L*P*P

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8219	22120	A	8279	371	125	FFPKKNEPPG*PPPKK*RKPGKFILAPS PPFFGGGEFYKLKRGVLKQKPGPPGVPK ILKTPPRLGKNKPISPPPGQKKQNFF
8220	22121	A	8280	377	63	PPVFPWPWGQGGGFF*ARGLRTPWPTR ENPVFF*NPKN*PGGGGPF*IPPPWPG* ALKFPLPPRGVPLTKNIPPPPRFSHR RVFFPKNLKKKNPCLIESL
8221	22122	A	8281	2	284	LPK*VKNFVHAKICT*MFVAALFVITSS WKQPRYYSIEKWINKLWHISAMEYSS LKR*ELSSHEKT*KNFKCGLSEKSSQE KDTWCLIPVI
8222	22123	A	8282	318	40	APRLSLVVFVFIKRLDSSPGSRITWT NCFENHLCVCVCDRFLLCQAREQWRVLG SPQSPSPKFKRFSCLSLPSSWDSRCKTP *PANFCGLC
8223	22124	A	8283	30	343	CYQKASHATEKSFM*RVNPCSILCCCY KILPQQPQSAVITLISQNKKKKKKKK KKKKKKKKKKKKDGGGALKKKKIFSPR GGRIFFFFWAKNNLGGGL
8224	22125	A	8284	163	392	FVVLNFSVIYSISDFCWYEQCLKSVF SFLSS*SLLEPNPNPNSQAQALVQE NKREYEKRVSAIVEQSWNDS
8225	22126	A	8285	406	63	KKKLILAKPGVNLDSLKRAPPFFFFFF RHGVPLCCPGWSKTPEPK*SSCLSLWSS WDYRREPLCLAYSPVLNITHLSSPNVKL CRDSQESYDPIIMMVIIITEGGMICGV IM
8226	22127	A	8286	1	322	TNTLLALLFIITF*LPQLNGYVEKSTP YECGLDPIPARVPFSIKFFLGAITFL FDLEIALLLPLP*ALQTNLPLIGMSAL LLIIILALRLAYE*LLKGLD*AE
8227	22128	A	8287	395	181	HGSLHPGTPGLQQFSRLSLPSSWGVRHV PPCLANF*IFCRGGVSLCCLGSVEGLEC QARLPVLVRAELGLD
8228	22129	A	8288	3	246	SSTLSFSPG*DYRHVPCCPANFFFFWIL EKTFFCFVPQGGFNLWA*TSPLNPPWA SKGAKITGGTPGMGLINLANGRP
8229	22130	A	8289	138	421	LLSSVFFFERDFCFVQAGGQWGNLG* WNPWFRGLKNFPGLTPPRSWNNGGPP PLIFCFFLKKRVSPRGRANFLDLGT PPPGPPKERE
8230	22131	A	8290	141	375	RTFFFFFKTEGYFVAQAKQGQGDHGLQ PQSPGLKGSLLRRWDYGSMPPCPSIFF F*IF*KNGASLCGPNNSTGG
8231	22132	A	8291	407	209	IGGPPGFSPPVFKNRPNLIFGPPKKK KNFPPPGGKNWFF*KGPPPPPPPPPP FFFFFFYTL
8232	22133	A	8292	86	433	PPXPKNLIEGGAF*KRHHFPPPRGRVR FFFFGPPQKTIAPGQNPGGGKPGWSP FSPGEKNXPPTHXGGPVLGAPPPPGI VLI*KKTGLPLFVGRAGTNPNLGGPPAP PPKG
8233	22134	A	8293	147	342	LVKFEYTVLPKNRYRLGVVAHAYNSSSL GGQGGRI*TA*EFKTSIGNILRSHLYK KRKEKKLN
8234	22135	A	8294	6	152	CCGHAPHPANFYSL*RRSLAMLPRIVS NSWTQAILLP*PLKVLALQV
8235	22136	A	8295	18	205	IPTRPPTRPPIGRNLNHTFTATRPVYY

<b>SEQ ID NO: of nucleotide sequence</b>	<b>SEQ ID NO: of peptide sequence</b>	<b>Meth od</b>	<b>SEQ ID NO: in USSN 09/515,126</b>	<b>Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence</b>	<b>Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence</b>	<b>Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)</b>
						GQCSET*GANHSFMPITVLELIPLKIFETGPVFTL
8236	22137	A	8296	1	199	YLYIYLSTILLSTIYLSYLSYSTYLASYLAT *LAI*KBIYYEYVLVMTEAEIFHILPS PSWRPRKVMV
8237	22138	A	8297	1	318	PTRPTRILLSRPIKIQTALHKFSLCPEY LQ*ADYLF*SLWIRPDVAVPHACNLSIL GG*GGRIA*AQEFEISLGNIVRPCLYCI IKNKIKKKKPLQIIAFLCFKD
8238	22139	A	8298	416	304	GFLHVGOAGLKLLISGHLPA*ASQNVTGTGMSSHARL
8239	22140	A	8299	352	31	EMILKAAREKK*IIPYNEPLICTVDFLV ETLQARREWDIFKVLKKKNKTKNPFYT KIEYLVKLSEFKYEKVTKTLLDP*Q*LTD FINTRHANRTSNRRKRPIIKKH
8240	22141	A	8300	382	266	RWDFVMLPKLVSNS*AQAILHVGLPKCW DYRREPPLHA
8241	22142	A	8301	2	273	PLTRGPSSASDALSSGGPYHPSECCTFY TTYKIPQRIMDYYETNSQCSKPGIV*V VHTHTTGGRGSQQGLEGSREWNNWNGDP QRTSQV
8242	22143	A	8302	77	430	GMGLSMHRTHFQYLAHIHPCVHVHHTHT HTHTHTHTHTLCM*HTEIHKSVRYGTE HAQDPFSIFSPTYPMCACTHTHTHTHT HTHTHTSVYVTHKVCETCLSFFYPESG TISHAQEILKRCLENKTHLGVCWFTSLL SVANIVFFSYKRQVAARGLFFSLSQA E
8243	22144	A	8303	137	396	SSVKTMNYLKPVVHMVADRC*LFQCPLP KKKKKKKKKKKKKGGLPKKKKILTTRGG GGIFFFFGAPKKISPGRV*KKKKKKKKK KKKKGGLPKKKNFNPGGGNFFFFWGPP KKNIAGARLKKPGGGKNPRSP
8244	22145	A	8304	329	144	NGPPFFFFFF*DGVSLCCPGWTAVARSRL LTFAVFFTLNCSVVGIIHSELQHWFQDYL KLKTF
8245	22146	A	8305	404	157	RTYNPSTLRGRSGQIT*GQDFDTSLGDR VGPHLRKRKNRYSLVECFYRIKEKYPE SHKKAMKMLFQLKPDFLHFQHIATN
8246	22147	A	8306	394	294	SLCFLTTPRPDNFGALIKNFYSPTPGWV SCVLSKGPPFFFFFFFKDGVLLSCPH*S QNPVVFALWSGTPELK*SSHPGLPKAW DYTYEPHQAVELLRY*RSFPVLLLDG ICIEHSPFFSPRGSLIP
8247	22148	A	8307	280	2	VVDSHTVFFTSVITVMLFSIQYVKQLEN IKSWPGIVARACNP SALGGRDG*AQEFD SSPGNTAKPCLPQKNKTKQKTKNKGVT LETBSRWRL
8248	22149	A	8308	136	330	MSYQRSVNVKYSNNACEVTTWARHSG SCLRLYNPSTLVSGGKIP*TQEFETSL SNIARPPLY
8249	22150	A	8309	3	118	IFVVVLVQMGFHHVQGASLEL*PQVIHPP QP PKVLGLPA
8250	22151	A	8310	2	366	TRVDPVRVRSSTRNLCLPGSSHAS TSA S*VAGTTSACHHARLIFSFSFFFLGFSE KTGENFFAQGGFEPLGEREPPPFGPPGF WGGGGGGTFRPRRWKFQKDIIPPLVSN RGDOPEPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8251	22152	A	8311	253	446	SKTFQARGGVTEMGFRHVQGTGLEILTS GDPPASACQAAGITGVSHHARLRI*YFI RIFILMTC
8252	22153	A	8312	430	88	GVGRIQISWSPWLPKPKNSPGSPPPQ*VG APGGPPPPPGPYFFFFFQKGFPLFSGRV *GSGSKNFFVFPKKNWGTSPPPPEGR GFFFFFFFLSRDGASCCPPRPPKVLGL QV
8253	22154	A	8313	400	323	HRLMPHPIDFFLFFVETGSCYVAQGAC ELLGSGNLPGSAS*NARITDVNHHAQP* KSSSGPGTQQC
8254	22155	A	8314	4	421	GGRIARTQEAQVAVSQQCTTALQPGRHS KTPSQKTKKKKSPGGPPGPPPPGRFFFF KT*KKGPFLKPPQRGDPRGKKKRGGG LWKKPGGKLGPTKKKTRGGGANPPPLW GKGGGPKGAPRAFP*TKKKPPPSGRNQ
8255	22156	A	8315	213	32	RCPGTVGHGCHPSPLGGQGRIP*GQEF ETSLANMVKPYFFLNSKKTKNHPKKN SQAW
8256	22157	A	8316	422	153	AATLYTHKTPHCYFFLDRNLLCCPGWS QTPGLK*APCLSLPSSWDYRHKPPRPVT SPIFRIKSYDVIPPPYLE*NPMMLYLP S YCHHI
8257	22158	A	8317	1	284	BRQDWESRLAMECAFHLEKSVNQSLLE LHQLAMEKGPQLCDFLESHFLNQQVKA IKKLG DYLSNLCKT*APEAGLA EYLFDK LTLGGSEEDT
8258	22159	A	8318	187	37	TRDFFWPGVVAHA*NCSTLGGQGRRIA* AQKFESNLGNRVSHCLYKKFKN
8259	22160	A	8319	2	250	KYEQSLQEVWDCVKRPNLRIIGVP EEEE KSKSLENIFGGII EENFPGLARDLDIQI REAQRTPEKSIKRSSSRHIVIRLSK*E VWDCVKRPNLRIIGVP EEEKSKSLENI FGGII EENFPGLARDLDIQIREAQRTPE KSIKRSSSRHIVIRLSK
8260	22161	A	8320	371	196	NNFSILFFFFETRSH*VAQAGLVLLGSS NPPCSASRVAGVTGVHORYQQDDFKNFR HN
8261	22162	A	8321	3	235	FISVSFKYSKHIPNNMHLKFLVFLNFF FRDGFWLRSG*SVVAILRCGHSSLQPLT GLKQSSHLSFQGSWDYRRAPH
8262	22163	A	8322	1	395	LEVPLINTSILLASGVST*AHRLTIES NRNQIIQALLITILLGLYFTLLQASEYF ESPFTISDGIYGSTFFVATGFHGLHGII GSTFLTICFIRQLIFHFTSKHHFGFEAA A*YWHFVDED*LFLYVSIY
8263	22164	A	8323	322	83	MHQSFVLVAKVKGKGRWRFYSCLMIKSA PVLSTVHTNLLCWPAGVHVACNPSTLGG QGRWMA*AQEFETSLDNVGKPHP
8264	22165	A	8324	12	249	GFFLPPPPGRGEKRGPPPPPLFFWFFFK KGEFPLGGGNFLTLEPRLAPPKGGK*G GDPPPPGFFFLKKKPKPLKLG
8265	22166	A	8325	139	335	ENILWAATVVLDCHPSTLGG*GGRT*G QEFKTNLANIERPHLFFFFFFLKRNFFFA PRVEGRGPV
8266	22167	A	8326	1	246	FRRGLAVAPRVLLCYPGWRAMVQS*LTA ASNSWAQAIHLSLPKCWNKYHTPPYPTC *NSACWDESSFPLLVSAMEVCGQPHS

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8267	22168	A	8327	422	107	TYVVRQQRKKRGLFFFFRFLPPGGGQ WGHFWFLQPPPRGV*RFFFLNLPRNRPW DFKGLPPPPAYFAFFLKKGVFPFGQGF *ILAPKGPPTSTSQKGWGFKD
8268	22169	A	8328	1	161	FRGTRWVCHVLFYLSFFLRQGLAVLPR LILNSWAQATLLPQLPE*LGLQTSS
8269	22170	A	8329	422	103	PPYSPFFGGPGGGVPKVRESGPPGPPQG NFFFFKKPKNPPGGGGGLIPSSGG*A KGMGLSPRRLPLS*NWPPPPPPGGQNK LEFPKKKKKRRKKKFNFEHRG
8270	22171	A	8330	46	422	STFFPLASQSAGITGVSHRARRSSSFQC TQIPLFPELPLNLGFGSRHGRGFSSQVL PAQSSSFDLDSLVLGY*MLSHISLGN RALGFIPPHLSKWENGSTLRSIVLSQIE GLSSTLSFPHPV
8271	22172	A	8331	429	112	FSHLGSSPRQGFTMLARLVNS*PCDPP TSASQSAGITGVSHHAQPHAVFYIRLPD SQVLCHQMPYWPYTAHYPHRWIFSLVLQK NLSVPPPLWPIQSQPKASILLN
8272	22173	A	8332	291	19	KTFPPPKI*KFPNFKFTPGCGGPPPP FLKKFVSPGNPPPKIFFFFPPPPPPFF FFFFFLRRGSLISIAQDGIQWHYHGS LQQLPGLR
8273	22174	A	8333	307	123	KYFRGGGGGR*FPPLGGVKQKKRGNPG GGGSKPKLGPSPPTRGKKKNFSPKKK KKKKK
8274	22175	A	8334	3	169	HASADMCHQAQLLLLLLVETGLCHDGRA GFGS*SQEIHPRPKVLGLQHFLIY
8275	22176	A	8335	1	208	LCVCVCVCVCVCVLF*WRKGLALSP RGECSGTNMAHCSLNFSGSSNPSVSPSH VAETTGVRPLG
8276	22177	A	8336	1	352	ILFYFIFYFSCFEMGSRVSQAGVQC PDLSSLQPLPRFKRFFCLTFPSSRDYR CVPPHLAKFCIIRRR*AAIGQAGIELLT LSDPPASAS*SARNTGVSHCSGSPFINF LNWQI
8277	22178	A	8337	420	272	KAPCQFSGEKTVPKHCWNSVWPKKKQ QQKNLCPCLVLYTSINSQ*TMGLNIKA RTVNIS*KYKEDP*TGKK*INKSCPWTG KKKKFLARTQKTAIWDTLINWTSPLK MSTKQRHHLKMN*PKWLLFFVS
8278	22179	A	8338	427	202	LIIYFCHQSVQKKGVLPLQEREGWABA SLKISNISLSHTHTHACAHHTHTHT HTSS*NGIKTVVITIKSFA
8279	22180	A	8339	2	164	TPGHGISLCRPGWSAVAPSRLTATSASW VQTILLPWPE*LGLQESRLLRDHL
8280	22181	A	8340	422	1	PEGPPGKTKRAPPPSFKGNPPLKKGK GPGAKPPPKNGVFFPPKVKGPQKNFG GTQISQPNKRGAK*FTFFFL*KPPQKKK GPPPGKIFKGPKF*KFPSPGFFFFFLK QGLTSPRLERSGANTAHCSLKLSSSD
8281	22182	A	8341	1	456	RTRGAVSQGHAIALQPGQSETPSQKKK KKNPAPGGKGKIGGTAKKGRNFDANI LGNPSRPGGAFFGG*TAPPGKKRGSPPG IFGGGKGPKKILSF*KAGGGAFFPS PVGTPFFRGF*KGKILKKKKFSKPGGG NPENLSPTNFFF
8282	22183	A	8342	407	2	RQFILGAPGVFPPPGF*KPPPKIIFWGP

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						KKKNFFPPPRGEKFFSFKGAPPLFFFFF FFFFFFSPFFFGALFFFFFFTILFKTKFG VFSCCKGIPPKFFKRSRPPNGAGRLPLL VGPLPGVPQGGGAERKISQGSFQ
8283	22184	A	8343	441	1	PPPYILGGPRVFSPPFFKTPPQIFFLG PQKKNSPPPPGKKIFFF*RAPPPFFFF FFFFFFFPFFFGALFFFFFFTILFKTKF VVISWKGIQPKLFKRSRPPNGGRLPLL GGCPPPGVPRGGEAERKFSRGSFQRTGG SAPEFRA
8284	22185	A	8344	466	323	FGVAGTQNPGRNPRVFSFRGGPPPGVPQ GRNPPPPWFPLNPPKHFLTP*VFPPLE PPIEWVGPGRP*PSYGFSSPVARK
8285	22186	A	8345	657	347	LEFWFFLRQSFTLVAQAGVQ*CDLGLSQ PPPPGFK*FSRLNLPSLLDDRCAPCPA NEVLLVETGFHHVQAGLELLTSGDPPA SASQSAGITGVSISAQPAQ
8286	22187	A	8346	3	212	DCSRGPPPHLANFGLLEKTGSNHVDQAG LKPLSLRDPPASAS*SPGITGGSHRAQF *FIFKRGMAPKGF
8287	22188	A	8347	9	255	IPGPTHPSDFFLYEIDLFPKN*KGFPFP PRGGGKNPPPPPPFFFS*PPWKKKITF QTPLTGVFGAPKNFNFWGGFKKIGF
8288	22189	A	8348	79	312	NAAGFEVGISKA*ALETQLIITREHGSN KERYAVTFESHMGTVLHLVEQEHTVGY ITASCALKC*IESGGFLNDYI
8289	22190	A	8349	1	369	FFFFLKRDRVSPLSRVYKWHDYSSLQ LQTPGLQ*SSCLRFLSSQDYRHIPPCPT NF*KCFVEMGSCCVTQGSQTPGAQAVL PPWASQRHWGLQGVRLCSLLLSNCPHS RLVWSWLFSGC
8290	22191	A	8350	434	324	LPILSPVWVHMPVVPVGTREAEA*EQ*SL EPGRRLQ
8291	22192	A	8351	3	253	YMCSKFFFLCSCGAISACHLELPSSD PPPT*NF*VIGTTGTCHHEWLLFELFG KMKPHYIAQVGFKLLERNFLTKTKVFP
8292	22193	A	8352	3	1431	SPRGGIPSLKQVYSSLTNSRPSQHLF* EEALQRAREEEKREKETSHTFQSTLTDI QGQIEQQSERNMKLCQENTELAEKLKSI IDQYELREEHLDKIFKHRELQKLVDK LEQAQEMMKEAEERHKREKEYLLNQAAE WKLQAKVLKEQETVLOAQLTLYSGRFEE FQSTLTKSNEVFATFKQEMDKTTKKMKK LEKDTATWKARFENCNKALLDMIIEKAL RAKEYECFVMKIGRLNLCRALQEERNE LHKKIRDAEISEKDDQSQHNSDEEPESN VSVDQEIDAEEVNSVQTAVKNLATAFMI IHHPESTPHQSKETQPEIGSSQESADAA LKEPEQPLIPSRDSESLPPLTPQAEA EGGSDAEPSPKASNSPAGLGAETQCEGL PVGAQADQASWKPEAEASGQAPQAPTEA SLQKMEADVPAACAAEEHVAAMVPACE PSRQPPRAAAEELPVGASAGPQPRNVA
8293	22194	A	8353	376	65	IHCGDHVQEVPKLKVCAHLMSSWACSQI PKAGDKILTFDQLTDLTKGCGTILLSG PHKGQEVYWHFSKALGTQHSHTKPCVHS RDQKFKHIRG*WASQGYKN
8294	22195	A	8354	459	85	*LEEVESELRVLEKKMIESEELKSKQTRF



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						LEETIKNQDKLNKSLKEEAMLQKQSCHEEL KSDLNTKNELLKQKTIELTRACQKQYEL E*ELAFYKIDAKFEPLNYPSEYAEIDK APDESPYIGKSR
8295	22196	A	8355	231	158	PFFIFLYQSNDIARGLERGLEPEKVG ATDSCGDLMLMKW*ESVAPMTFSGSRP LSKPRAISLLWYK
8296	22197	A	8356	2	164	THRGVENQMAEQGWKDVSVYVWGA HACNPNTLGGQGRWIT*GOEFETNLP
8297	22198	A	8357	23	291	CTHTRAQAHATHHLYFYFLYIFNFEE TGSH*IVQACLELPASSDPPASFSQSAG ITGMSHHAWPTSCILKVKMALCSINCSA ACFLY
8298	22199	A	8358	1	307	FFFFEIESCSFAQDGVQWCDLGLSQPPP PGFKQFSCSLSSWDYRHVPRLANFC IFSRDGFHHVQAGLQLLTSNDPPT*AS QSAGITGVSPRAQPCPAF
8299	22200	A	8359	75	266	FVKTRNLFITVLEAGKSNIKARAG*VSG EEHGLCLQDGLLPLEGRNAVSSHPRGQ NMMRAKC
8300	22201	A	8360	1	295	NTWVFCFVLLFRDRVSLCCSVRSTVASS *LIVNMNLSFPSS*AYRHVSSHLDFFFF FKIQRIILRLISNFWPQEIILLWLEQG LGLQPRPQVLVGN
8301	22202	A	8361	376	293	MGFHHVSAQGLKLLTSGDLPASASQSAR ITGAGHHAQPDF*HSGDSWQAPPEPRDQ G
8302	22203	A	8362	375	142	PQEEFLRFATDVGEYRAVTELERPVSES WNTQKDLL*QKRGVSTYCRHTYGVGES FSVQRRGEHVGGRLGPCELEI
8303	22204	A	8363	36	363	QLSFNPLIGKKVKLRVTFIGKQFLFLG GGVREAGAHSGAQATVRWHNLSHAKRP SCLSLPSCDHRHLLPHANFCIFWTD*I PPCRSGWVQTPELKQFTHLGLPKR
8304	22205	A	8364	455	235	GAQARAPPRGIIFFFFW*RKGFCLPRP VSKFWG*VVPLPWPPKRVGLDSWAPPPR DFIFFSFFVKKRVCILW
8305	22206	A	8365	432	175	STDQVSVAMGPS*PGAGYNLLVCRWLRP LKKCSIRMGVS*FSRYCLSWLPLDKKGN SLTPCASRVRRCTVMLRLMLRGLHPLSD KP
8306	22207	A	8366	383	83	RRLIVFICYFSKK*GLPLLRLVSNFWP QVILVPWPPKVLGL*ALKKLWLDVMVTHA YNPSTLGGQGRIT
8307	22208	A	8367	27	304	FFGFILTLKKSSN*CTLRFCFLSIGKVR IHTLGNILSRRGYGERCSLPHCLWESIC LPVQSN*ALHKKVQMHI*PFQDAIPSRGI LPDTGTGHK
8308	22209	A	8368	165	204	QNIPIAVSFFFFFLKRVSFCCPG*RAGG QSLFIGALTFQV*GILIPYPPGNWELRG PPNLTNFF*FLNLRFLGLPINLHYVHD KTSPLLYLFFFFF
8309	22210	A	8369	400	201	KERPLPFLIGSPFQGTWPRFFSKGEVK NSNFSKY*PPPFINPAPRVCFEGIEVIT KFFQVRPFFP
8310	22211	A	8370	21	408	LIPLSTYVCVRVCEVCVCVCVNI*GYA CNTLLIACNILQDVPTSPTKDKIFSGD FLTTLVGKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8311	22212	A	8371	1	94	NTLGHEN*LNSGFGGCSEPRSCHCTPTWATE
8312	22213	A	8372	546	972	PIHSLYGR*PSFCLGLALFKTLQVMHFLKDSVRNLKSSNLKVGLNFRSPQIQATIS.PPLQPKTKTYEEDPKSKPKKEEKNMEVN.MKEWILRYAEQQNEEEKNENSKSLEEEEE.KFDPNERYLHLAAKLDDAKEQAATFKLEKK
8313	22214	A	8373	502	178	QHFWRRLRQKDSFALGG*KQPGQKGENPF.FQKKAKNILG*WDQPVVPTTQKGGGGESL*PGRTKSPCTSGWGKKQNPVLKKKKNPQKTNCIPLCIYHIFLINRKTNTV
8314	22215	A	8374	362	112	YRMSVNPQVRAKRVSQRTNTPPNFFF*D.RVLLCRPG*STVVQSQTLVASISWAKAILLPPQPRQAKYFLRLVKCSSEKGERIE
8315	22216	A	8375	411	21	VLGIYPTLVSPSPGLKMTRVKLPSPGSKK.VISSNRNPVFGVVAAGG*FDKPIKAGRASSTKYKAKRNCWPRVRGVAMNPVEHPFGGILQRIKPSAIRIYAPAGRKVGLIAVRRSGRLRGANTVQEKEN
8316	22217	A	8376	450	108	AEGGRGPRK**LRSCRVDGSAGQSPGPLRTESLETPGCSPQGVVQLEPPRRPQWWPGPPGHRDRRQHRPGRARSROQGPESH*QSGESRPPAVPRPCLPWKKGVLE
8317	22218	A	8377	25	306	EQQPPPVAVHQSGPPGAPPEASPSHPGSSEKPPQVPPPPRAPLVPPQPKP*LSPPHHPAAGLLAVHALAGGPGTVQRGLPGRAARAVSVRVPAARC
8318	22219	A	8378	376	149	PAHCSLLIPGFRGSSCLSLPCNWYPGRA.PPRVGNFFFF*EMESCYVAMLPISLVLT.SWALAILPVLPPKLPGLQA
8319	22220	A	8379	98	374	SVPPPVGTVEGDAAPTGGGGLPALGR*GAAGGHVQGHGPHRGHAAPKPSAQGGPGHSRECLEPSGGAAGGEREP PRAGGGQSWMRAPSMT
8320	22221	A	8380	2	807	RPQCCVRAPRAGAVSGVPKLWSVP*SGRSAPHPTRS*VRSWSRWLRTQSWQTSRTRRSESKVRVSYQAWTASPPPAASASARP.A*RTSSRSYSSSSTCCSWLWPSSWSTGPSQTFVRNSSTLSCLCLTRKWIAMMPQVLPCTPVRPSCSAVSTITRSFLL*QALASRVLT*IAPPRGSTTRTPSPIRL*NLP*LSRGP GK*KSGSWSSSSSA*TRVVRTSAPLITSSSLLSRSSCKAQTG*ASCRPVVPPIPAGSSLGASAPGSRCHW
8321	22222	A	8381	104	327	CIAPPEMLGIKYEVGKCPGSLKSLKILK.NTHTHTHTHTHTHTHTHTHTHLYLIREGRKK*CVCMRKTDSTCVS
8322	22223	A	8382	400	270	KPKLEVRAAGQVQWLSPTIPALEEAKAGG*LEPRSLRHFMVCN
8323	22224	A	8383	178	588	ADLLSGAPGPPGGSQDNANSSEHSRACA.PAAPGP*WLQPWLC*WTQSPLEARGS*NPQVSHSSRIPGIPGAAGTSRPSGALPP.QPAGHGGSSGELHVARGCACGRPLWSHR.PCCGQLLRVTAADSHRCASRGAAPM
8324	22225	A	8384	423	78	QQQELAEALTGVTVESPEEPQRLLV*GGTVPCLACSLHRTL*TVGHGSASSFLAQG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DMEPLGDRGLQGTEQLH*GGDRASLQDI CFLLPVLSLLCPRSLDLHRHRVGVGTGFT ED
8325	22226	A	8385	434	176	FADDSRFDFLLLV*CAMLMLIREQLLEG HFTVNMRLMQDYPITDVCQILQAKELQ DSK*PGGKRPMFGREASRPCAVAPGTHR NL
8326	22227	A	8386	2	305	RLWEDPPGRNTPPGAR*PGPCGEGGHTI REEQACGWPRGHSGPWRHPQAGPLQLGQ WRKGAGQGARRSPQGSLSRPPPTLSAA PPAIHICSVGGVRLHCY
8327	22228	A	8387	331	91	EMRSHSVTQAGVQWRDYGSLQTRPPGLS FNVNWDWVGL*GDPSSPMLLPSS*ARP GGGWGPGGEGHVSKEAAGRLQGPP
8328	22229	A	8388	2	250	IHVRLWSQLFRRLRWEDLLSTGGGSCSE P*SCHCTVTWAFPLESCLCAHVYVYVTL LTALLGSLPCANPRQTAVSLPQAQLV
8329	22230	A	8389	388	176	YWDSQ*CMPSFAVPVESACICAIGHNFS KSVNSVIAVCVDGSSHKYVFTHDGRCHR EAFDVYRDICDDDA
8330	22231	A	8390	445	330	PPRFTPFSCLSLRSSWDYR*PPRPDNE LSLYSVLHET
8331	22232	A	8391	559	142	LRTLPVTLGKSLALSVPSPFYVGGNWIT NREPSAKGRGSGPNRGPCHAASCPARTH SLRHSPAGGVMLTQPRPILILPETQHPS ESAVARTDISKARRWLHSRSPWPH*DET SAGAERPGRICYIGHPAT
8332	22233	A	8392	104	400	YYEIFKKEMYSYHILHFFFFFFFSSFFFE TKPNSVNGPEGKGPILG*LKPWLLG*KH FCLTLPSGGNYRHVLPFPVNGFFFFFFF KKKKVFPFVAPRGV
8333	22234	A	8393	408	169	DQVWIKDWNIGSLRPR*KGPQTIIILTP TAVKIEGIPAWIQHSQVKAAPETWEVR PSLDNPKVTLKKMTSPAPVTLRS
8334	22235	A	8394	1	269	YCCPLFSSKALTQENSPYSSFRLLVNPPG LSLHPEGEGKWINERGRELGPSAGPLL LFLHFAEAGRRQPPDWADSEADLQQRH KLGP
8335	22236	A	8395	2	204	KDCKVNKEVERVLREFHQAGKPIGCDAS TSLPAPAPWWSNAALCCPGLSCVWCWQ GESRTCVEHQ
8336	22237	A	8396	3	285	KVTVKYDRKELRKRLNLBEWILEQLTRL YDCQEEIPELEIDVDELDMESDDARA ARVKELLVDCYKPTAEAFISGLLDKIRGM QKLSTPQKK
8337	22238	A	8397	1	192	BTGFHHAGQDGLELLTSGDCPSLASQSA RITGVSHCTRAQLLTEQYFKNQNLPS APFYKRAF
8338	22239	A	8398	8	241	LNPFLYAFLDPRFRQACTSMLCCGQSRS SGTSHSIRGEKSASYSSGHSQGPGPNMG KGGEQMLEKSIPIYSQETLVVD
8339	22240	A	8399	2	240	SCLNPFLYAFLEPRFRQACTSMLCCGQS RSAGTLHSSRGEKSASYSSGHSQGPGPN MGKGGEQMHEKSIPIYSQETLVVD
8340	22241	A	8400	10	272	CNWQNAYLTVVRCAQDCEDYFAERLYRS MKGAGTDEETLIRIIVTRAEDLLGIKP KFHQKYQKSLSDMVRSDTCGDFRKLIVA LLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8341	22242	A	8401	47	248	TRGIFFFFLNTRSHSVAQAKGLGHDHSS LKPQPPRLKQSFNLSLLSTWNYGGLLPH SALWKAEAAKS
8342	22243	A	8403	497	303	TVEASVSYYLYVAMVMQLPWGKSPASGA ESHRQCGGSGWPGGGMEGRGAERGGGC LLPQALLY
8343	22244	A	8404	3	235	LTLLAHCRMMAAAHMGPPMPMPMPGENT PGMMPVGPAPGMRPPLGGHMPMPGYP MRSPARLMMVPSQPRMTRPDR
8344	22245	A	8405	3	246	LVFSVDVGLLAHTRQRLKRSSGMSLL GKIGAKKQKMSLEKSKLDWESFKBEEG IGEEIAIHNRGKEGWIKGAQPLGQ
8345	22246	A	8406	1739	804	WEPDVSGSAAWLASAAGMATFSGPAGP ILSLNPQEDVEFQKEVAQVRKRITQRKK QEQLTPGVVYVRHLNLLDETQIFSYFS QFGTVTRFLRSRKRTGNSKGYAFVEFE SEDAKIVAETMNNYLFGERLLECHFMP PEKVHKELFKDWNI PFKQPSYPSVKRYN RNRTLQKLMEERFKKKERLLRKLAK KGIDYDFPSLILQKTESISKTNRTSTK GQVLRKKKKKVSGTLDTFEKTVDSSQGP PVCTPTFLERRKSQVAELNDDDKDEIV FKQPISCVKEEIQETQTPTHSRKKRRRS SNQ
8346	22247	A	8407	2	241	CLRFPSPPAMGLLRSGTKLIFRRRPKQK EAGLSQSHDDLSENATATPSVRMKAGSFS RRLIKRFYFKSKPKANGNPSQQL
8347	22248	A	8408	285	186	KOGLTSLPRLVSNWSAQAFLLWPPKVL RLQA
8348	22249	A	8409	1	246	RHENREELQVIADLCIKYDTLCISDEEF MNGVEYIWKGPCFCLTFTLYLKGDIFP RPPSGCLNLWIVLNPMPVIHLITSC
8349	22250	A	8410	1	102	AGSYTLHIKGGDGTGRVGTGRFTTLHR IOTSEE
8350	22251	A	8411	877	647	FFFETESHVSQTQAGVKGWDLGSLQSLAP GPKKFSCNLNLPSSRDYRSPPPPLANFCT FSKNGVSPCWPGRSSTPDRR
8351	22252	A	8412	1	130	RMLNDKTLRTDIGGNFPKNGWAAIATHS FEFAQFDNFLEEATR
8352	22253	A	8413	97	401	CNPENGLTASALGRMCLATCKAPRTL DSGDTASCRFPAPVPRPHSRSSSGSHL PGRPRCPALPGLEWSNPPGPPTSGYLF TFSTPAASHQKTLGLI
8353	22254	A	8414	348	516	VSAYGFTTEGHERFSDHYDTSWKRLIF YINHDFKLEREVWKRLEDEGIIRLYQRL
8354	22255	A	8415	714	410	LGVFRSALHGSLWLLRSFPQKSPNPLA LLLFLQCNATAYQCLLIADQHCRTKYFL CLASGIPCVS HVVHDSCHANQLQNYRN YLLPAGYSLEEQRILDW
8355	22256	A	8416	2	102	GHDPQDRLLAQDSEHNHSDRNWQRNPW PKDSY
8356	22257	A	8417	1	309	FYFENALSKSNKPIHTIILNPHVHLVGD DAACIAYIRLTQYMDGSGMPKTMQSEET RVWHRRDGKQNVHFRSGSPVTPVPIKPP CIPNGKENFSGGTSWQNI
8357	22258	A	8418	3	242	ARALTNAASHVDDMPNALSALNDLHAHK LRLDPVNLKLLSHCLVTLVDHLDPDEFT PVEHACLDNVLASVSTVLTFFKYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8358	22259	A	8419	711	296	NVANS DGLTASLWKEYGKADARWVYFDP TIVSVEILTVALDGS LALFLIYAIVKEK YYRHFLQITLCVCELYGCWMTFLPEWLT RSPNLNTSNWLYCWLYLEFFNGVWVLIP GLLLWQSWLELKKMHQKETSSVKKFQ
8359	22260	A	8420	3	97	FVVSSLCNGLIAAQLLFYWNAPPHKQK KAQ
8360	22261	A	8421	1	279	GCGIADLMSAIFNFQSLTDLILLICT CAYIPSLAPNLLDRNKTGLLGIFWKAT IVERKSPYVAVCCILMAFSILLIQKLVK MPQCICHNI
8361	22262	A	8422	1	228	RHEVFIELNHIKKCNTVRGVFVLEEFVP EIKEVVS HKYKTPMAHEICYSVLCFSY VAAVHSSEDLRTPPRPVSS
8362	22263	A	8423	3	182	SEDTGEEQVVTAEFINRGEYEIDIAGYR FQAKAKLYPVASLFTQKRRKDDMELSDL HGK
8363	22264	A	8424	1	70	VQFVFDVAVTDVVIKNNLKDCLGF
8364	22265	A	8425	2	151	ETTASSCTPASLESRRCCAPCRMPRTGF FGSSPLWRP SGSRSLKPGFQQ
8365	22266	A	8426	1	187	RGRVGP GGERLVPGVPGAEAAQQPAGDGV RAGPLQARPPAPVGVSQGRCAAGAAAG PPRPDG
8366	22267	A	8427	520	423	GKYQLQSQENFEAFMKATGECWTERQSC GSHQ
8367	22268	A	8428	1	627	GTSGTRGVTFYFTFTLYLETPKPSISS NLNPREAMETVILTCDPETPDTSYQWWM NGQSLPMTHRFQLSETNRTLFLFGVTKY TAGPYECEIRNSGSASRSDPVTNLNLHG PDLPRIHPSYTNYSRGNLYLSCFANSN PPAQYSWTINGKFQSQGNLFIPQITTK HSGLYVCSVRNSATGESSTSLTVKVSA STRIGLLPLNPT
8368	22269	A	8429	3	390	ILGCNILRVEYSLVICVSVPGSKKVILD LPLVIGSRSGLSRTSSMASRTSSEMSW VDLNIPTPEAPPCYMDVIPEDHRLSP TTPLLDDMDGSQDSPIFMYAPEFKFMP PTYTEVDPCILNNNVQ
8369	22270	A	8430	3	208	NGTHVII LCLKTCGTVVNVANDMIVAS NLGTGVPNQTPVSSGDLIRSNGLLIPG TCEITRLYTISE
8370	22271	A	8431	3	563	LPTSRVDPRVRLDRMKKDQEEEDQGGP CPRLSRELPEVVEPEDLQDSLDRWYSTP FSYPELPDSCQPYGSCFYSL EEEHVGS LDVDEIEKYQEGEEDQKPPCPRLNEVLM EAEPEVLQDSLDRCYSTTSTYFQLHAS FQQYRS AFYSFEEQDVSLALDVNRRFFT LTVIRHHLAFQMGVIFPH
8371	22272	A	8432	2	119	DGDNILVTTFIYIKSVTELNGDIITNAS WRCSEVAPSA
8372	22273	A	8433	192	1285	AGVLSTIEETDSEGLQTKVVENQTYDER LEINDSEEVASIYTPTRHQGLPRSAHL PNKAMADNSSDECEENNKEKKTSQLT PQRGFSENEDDDDDDSDSDSDSDSD DEEHGAPLEGAYDPADYEHLPVSAEIKE LFQVNQLRCVPTDVLHKLKPFIPDFIP AVGDIDAF LKVPRPDGKPDNLGLLVLDE PSTKQSDPTVLSLWLTENSKQHNITQHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KVKSLEDAEKNPKAIDTWIESISELHRS KPPATVHYTRPMPDIDITLMQEWSPFEFEE LLGKVSPLTAEDICSLAEYIDMICALD IPVYKSRISLHLLFSLYSEFKNSQHF ALAEGKKAFTPSNSTSQAGDMETLTFS
8373	22274	A	8434	3	251	TLQADHFNTRLSCGDAAQTLWARTGYLG FVRRTeltaatGERHDALYVVGALDETL ELRGLRYHPIDIETSVSRHRSIAEW
8374	22275	A	8435	1	225	QTFNLEGSQIYEDSIVLQSVFKSARQKI AIEEESDESNEDDEDEEYHEWKRYD RLGENMCLNCIWNNGGGYIV
8375	22276	A	8436	95	340	CGCGIAGLAMSALFNFSLLTVILLIC TCAYIRSLAPSLDRNKTGLLGIFWKCA RIGERKSPYAVCCIVMAFSILFIQ
8376	22277	A	8437	1	317	GPKPLVRTSREPDKDVTSGYSSVSTAC PTSSVDGGLGALPQPTSVLSLSDSHTQ PCHHQARKSCLQWRPPSPPESTVSQQQV KRINLCIHSEEDMNLGLVRL
8377	22278	A	8438	80	213	PHLSFNAGTTIKVNIKNANSLGGGFHC WTCDAARRRGTLSYLD
8378	22279	A	8439	3	767	HEDNIKQLKEMKFTYLINYIQDEINTIF NDYIPYVFKLLKENLCLNLHKFNEFIQN ELQEASQELQOIHQYIMALREYFDFSI VGWTVKYYELEEKIVSLIKNLLVALKDF HSEYIVSASNFTSQLSSQVEQFLHRNIQ EYLSILTDPDGKGNEKIAELSATAQEII KSQAIAATKKIISDYHQQFRYKLQDFSDQ LSDYIEKFIAESKRLIDLSIQNYHTFLI YITELLKKLQSTTMNPNMKLAPGELTI IL
8379	22280	A	8440	103	354	NGCECDFLFLFLFYFFETESRSVAQAGV QWHCLGSPQPSSPRFKRFSCLSTLGGRG GWIMMSGVQDQPGQHGETPFLMQAGLKT
8380	22281	A	8441	3	160	KLYPLKIVFGMNGRVWVKGTQVQTLIL ANVLEACELMTLDQRILMFIAS
8381	22282	A	8442	459	3	CGGLHPVRASWLLCLPKQAWAMAGAPP AWLPCLSLISDCCASNQDQSVGVGPSEP GAGYNLLVRRFLSLSEKRSIRVRVTRFS RCHLSPLSLTRKGNSTPCTSRVRQCLA LLRLAHGALHPLSCAHCLALPSEMTVPV QMENAEITRLL
8382	22283	A	8443	2	318	RQGNMTAALQATLLNPPINTKSQAVNDR ARGIVLNLISFKANDIEKAVQSLDKNG VDLLMNYMYKGFESPSDNSNALLQWHE KALAAEGVTSIVRVSTALIPA
8383	22284	A	8444	2	109	VTPFPMSCDLQGDACARNPQAQEHSRKD LRGYSHG
8384	22285	A	8445	1	69	LVLNSWPQVIRRPWPPKVVGLOV
8385	22286	A	8446	1	163	PSEKHNIWGVGTQFSRCRLSPLSLTRKG NSLIPCASRVQRCLTLRLVHGACTH
8386	22287	A	8447	1	147	GQAGLELLMSGDRPTSASQSAGITGVSH RARPPSSISFILELRGSVRKKF
8387	22288	A	8448	914	729	GLTMDTQKDVQPPKQPMIYICGECHTE NEIKSRDPIRCRECYRIMYKKRTKRLV VFDAR
8388	22289	A	8449	134	392	TCPPFPPEPPSPLTCAVLVPQTRWRGLG SLFRRACCVALLPLQLLLFLLLFLLP IREEDRSCTLANNFARSFTLMLRYNGPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PT
8389	22290	A	8450	37	248	AKITPLLQPGRQEQDSISNKKILRCCLT MLPRLASDSSGFKRSSHFSLPTSWDYRH SPPPLASVPFLLMC
8390	22291	A	8451	367	165	NFFVFLVETGFCCHAGQARLQLLASCDLP VLALQSAGITGVSHCARPISTLKDITKT SHFVPLKISGK
8391	22292	A	8452	2	282	GKRMAGGPENMQLRLDGNRLYITTSMF AWDKHLYPDLIREGSAMLHVDVDTALCG LKLNPYFLVDFWKEPLGPSLAHELRYPG GDCSSDIWI
8392	22293	A	8453	4	163	HHDFHAQSLLANIERIAILLVFAACEAAA VLSLLVSISNTYGLDYLHNLKLLQC
8393	22294	A	8454	374	197	TPEPKQSSHLGLSKCWDYRHEPPHQARN STFDSNHSSIAAEDKLLGYFGLSQWQPG YQP
8394	22295	A	8455	343	161	MGMGPSVPGTGYNLLVCRLRPLEKCSI RVGVSQFSKYHLSRLPLPRKGNSTPCA FWVR
8395	22296	A	8456	1	193	MGFLHVGQAGLKLPTSGDPPTSASQSAG ITGMSHRVQPYVLSICQTLHSHVCICLL IILLTTVL
8396	22297	A	8457	342	263	WLRPVVPALWEAEAGSLELRSSRPA
8397	22298	A	8458	101	303	KAAKYLQRLHFCFLNLKKNMMLLFNHR MENFKELFGPGTVAHTCNPSTLGGRGW ITRSADRDPHG
8398	22299	A	8459	3	140	YLKHLKMYVCKYLRQGLMLPRLVLNSW AQRILLPWLPKVLGLQV
8399	22300	A	8460	327	248	FPRLVLNSWPKAILMPWLCKVLGLQA
8400	22301	A	8461	327	79	SIPFILAFFIYLSFFFKETGSQSVTHAG VPGIIIAQCGLQLLGGDPDSASLVVG TTGTYPTPLSVFPNMPSEFILLCMLF
8401	22302	A	8462	365	273	MGFQHVGVGLRWPQVICLPWLPKVLGL QA
8402	22303	A	8463	375	217	QAGLKLTSDDL PASASQSAGITGVSHH AQPRHHFFKTRFIYIFSSPSSVLS
8403	22304	A	8464	238	354	RGKCFVQAFLYKECSGGQARWLTPVIPE LWEAEVGRWIT
8404	22305	A	8465	367	248	FQMRIHKWLIDLHSPSEIKQITSISIEP GVEVEVTIADI
8405	22306	A	8466	341	153	NMILGWAQWVTPVIPATGEAHWGGLLYP RSSKPAWATQONLLFTKKKKNIYIYIYI YIYERY
8406	22307	A	8467	368	101	VEMGFRHVGQAGLELLTSSDPPASVSQS AGSSTSLPTADLLTPGWVGYGLVDKNP VTLIAMQRLPAVLEKKSARKNSSENKIV LKRQ
8407	22308	A	8468	362	248	HVGQAGLALLASGDPPTSASQSARIAGV SHRARPEAPL
8408	22309	A	8469	384	196	SARLGLPKFWDYRREPPCPADDMLILMV GILETFSLIFTATMESRNYCVYFKMRNK HIISKTS
8409	22310	A	8470	386	300	LAMLPRLPNSWSQVVLSPPLPNMLGLQ V
8410	22311	A	8471	380	178	PKKNKFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFYIYIF AIVYQTLACNNKFLQMERVTRKLRQC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8411	22312	A	8472	3	154	FLVDMGIHVSQAGLKLITSGDLPASASQSPIFFFLFFFEEKQILAQAGG
8412	22313	A	8473	3	162	GLYHVGQAGLKLITSGDPLASASQSVRI TGVSHRTRPKIIFKLIFLFFLVA
8413	22314	A	8474	266	107	LCLFLIEMRFPYVVQAGVKLLSSSHLPS SASQSDRITGVSHCFWPEVFKRGIF
8414	22315	A	8475	361	169	RLPGPSNPPISASLAAGITGARHHAQLI FVFLVEMGLCQAGKHNFKEYSRVLIYSP IVSFTHFI
8415	22316	A	8476	1	154	KKLIPTLMDHGAGFKSSVKEITTAVVEM AREVELEVEPEDGNELLOSARGKT
8416	22317	A	8477	3	193	SHYQSLISSNHGKHCGRPGGPLPRKTI DLCSLDYQLTFPPLLTHDPVKSPSVRNT QELSLIP
8417	22318	A	8478	408	103	TGSRLTLSSRVECSGVITAHCNLELPGS SDPLASASQVAETTGMHHVWLIFLGIF LVKMASHYVAQDDLKLLGSTDPVVSASQ SVGITGISHHAWATICYK
8418	22319	A	8479	59	166	NVNTCLCLHTHTHTHTHTHTHNYFKE TPIHQYI
8419	22320	A	8480	394	253	FLLLLLESQGFCHVAQAGLKLSSCDLPA LASQSAEISGVSHCAQPLA
8420	22321	A	8481	379	184	CFSLPKCWDFRGVPISPGDFWNFIKLG VCPFCQGGFELLAPNDVAASGFQNAGIS GINFWAWAL
8421	22322	A	8482	367	170	CGLSSGLGGRSGRESERKKERERERDRE KKKEGGERKREKRESVSSYKDTNSMG SGPHPYSLI
8422	22323	A	8483	324	136	QRSSCLSLPSSWDYRRMPPHLANFCIFC RDGVLPCCPSPWSQMTTSLSLNFLICLV GIILGRG
8423	22324	A	8484	1	57	GERRYGTCTYQGRWLWAFCC
8424	22325	A	8485	35	339	GWLLRFFFWQWKNGNLNVSLIDGNLSY DTLGYNGILNCHMYILTEGDSQKKKKKK KKKKKKKKKKIDPAGNSKIYNRKIFKT' PRGFFKWALGPLLILFF
8425	22326	A	8486	330	66	RPGVSRFNPWPLIFFLRRVFLCRPGWNA VVQSLLTKISASQVQAIPLGGGGCSEPR SCHCTPAWATTAKLCFKKNGKNFTDIM FSK
8426	22327	A	8487	3	209	CLSLLRSWDAQAPPPHPANFFLMFNFCR VGVLCCPGLASSDPPPLVVSQARITGM SHCTWTIFLSFK
8427	22328	A	8488	3	216	GQSITVSTATNSDVGSSNLVSWYQSSN LVSWYQHPGQAPKLIYEDNKRLSSEK KKKKKKKKKKKK
8428	22329	A	8489	326	62	PAYFSIGSFFLFLFFFRTECHSVTRLEC SGAISAHCKLRFPSSNSPASGGGRSE PKSHHFTLAWTTRAKLHLNKNKIKTVKE FLSS
8429	22330	A	8490	2	156	SSAGIGRTGCFIATRIGCQQLKARGEVD ILGIVCQLRLDRWVCGCKQGQQR
8430	22331	A	8491	399	254	KMNKRNTINNKITNKLIIKLKNISFLY FFFFFFFFFFFFFFFF
8431	22332	A	8492	2	130	FRRVGQAGLELLTSGDLPASASQAGIT GVSHRAQPTFLKSC
8432	22333	A	8493	3	94	HLPAEFTPAVHASLDKFLASVSTVLTSK YR



1067

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EHDRPTALINGHLNSLQSNPLLPDQKVC
8453	22354	A	8514	99	262	MNKRFLLNKKKKKKKKKKKKKKKKGG PFKKNPGGAQIFPGGEKKIFFLKGGL
8454	22355	A	8515	85	2	GWGWAQWLTPVIPVLWEAEAGGSRGQE
8455	22356	A	8516	244	423	VFAVFNFLGWVMDMLINLAVVITLQCAC ISNHHVVHLEYIQFLFANYTSIKLGKKP SKSV
8456	22357	A	8517	3	114	KINGEDKQKILDKCNEIINWLDKNQVCV FFFFFFFI
8457	22358	A	8518	413	91	GGVRGKISFRGGGFLKKKKKKLLKKKKK WGGGPKEKKKRGGFFFFLLNFFFWGGV KKKKKKKKKKKKKKKKKKKKKKRRK GRKEGREGRRKEGEGRQEIINMTA
8458	22359	A	8519	1	163	SRLPGRSRRRSRGRRRRRRRRRRRRR SRVLIFFWDQNLDLNIVYIIEDVDAA
8459	22360	A	8520	191	21	RFTTHVDAWATVTVFLIESVFLHVGQAC LELLPSDDLPAASENARVTGVSHRAWL
8460	22361	A	8521	2	144	AAATSQAWWCMPVVPATWAEV GASLKP GRLQLPLTMIALVHLSYAI
8461	22362	A	8522	90	8	KPTPFLPTLIARTTLLLPISPLILIL
8462	22363	A	8523	305	146	VFRHSCGIRGSVDVKITDGLLVIRRIE NVPPGPNNKNKNPYAIFQSSSIESQ
8463	22364	A	8524	176	2	LAWPFLFLPKCWDYRHEPLQPASLTTFV REWDKIGWAWWLTTPVIPALWEAEVGRSQ GQ
8464	22365	A	8525	2	200	CLIPSSWDYRHMPPRPANFCIFFFFLGD HVSQVGLKLLTSKDP LAWTSQRAGITGF SHHTKPQGFF
8465	22366	A	8526	2	217	SFSLFPSPSFLLLPPLASLLLPPLPSF SLLFPSPSFLSPPSPSFLLLPSPSIFL HPTFSHLYPPSPSFI
8466	22367	A	8527	2	186	IRGLRPLEKRGIRVGVSFRFSRYHLSRLS FARKGNSPTPCASRVRCPSLLHGLHPL SDKPQ
8467	22368	A	8528	3	153	CLGFLSGWDCRCIPPCLANLKKLFVEMG SLFWPQWILPPWPLKVLGLQV
8468	22369	A	8529	2	388	RTAVHTFILVLQVCVCRHLSLAALTPA HLVCSSHRILSYLSIRGSWDHRCMTTTP GLVISIFFVEMKYRYAVHAGHILLGSSY PASAYQSAEITGVSHWAWPTDSLWQKPH MVIWCISCFLNVLIGTM
8469	22370	A	8530	293	64	YRISIKVSKWFKGWVSSFWIFFFFVFFF SFFFVFFCFMFFLKQYLFIIIIIL TQALYICTTSKICYSFLYFR
8470	22371	A	8531	2	250	SCLGLPSSWDYRGTLPCLANFCIFNRDG VSLCCQGSQTPGSQVIDEAVYSIYAYY ILALLIVYVAQWEVWLKHFCILKYT
8471	22372	A	8532	2	201	FHHVGTGLELLSSGDLPAASQAGIT GVSHCTWPSILYRMNFKNLSAVFIWVI EGNYTNKTCI
8472	22373	A	8533	319	200	TFTFFLQRWGLTMLPRLVNSWAQAICL LQPPKVLELWA
8473	22374	A	8534	160	297	KTETLALVAHACNPSTLGGIGRQVSSAH EFKTI LGNMTPILYTKL
8474	22375	A	8535	333	228	PNRGHYIAIVKSHDFWLLFDDDDIVEVSS FLISYF
8475	22376	A	8536	3	325	PPSSLLPCSWILDCCASNERDSVGVGPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EPGAGYNLLVCCFLSLEKRSIRVGVTR FSRCRLSPLSLTRKGNLTPCASQVRRCLALLRLAHSALHPLSCSYCLALP
8476	22377	A	8537	216	5	KLGFVLNVLVEFQVKFFFLFFLEILLIE MRSHYVAQAGLELLGSGDLPASASQSAE ITGMSHHALPNYSF
8477	22378	A	8538	136	22	RPRRLVLNPNWPQAILLWPVPKVLGSQV WATCGRRPAS
8478	22379	A	8539	136	22	RPRRLVLNPNWPQAILLWPVPKVLGSQV WATCGRREAS
8479	22380	A	8540	8	319	YIYMSMYMLIYVCIYVSIYICVCIYINS ISFNTYMIYMLIYVYVMCVYICVCVY IYTNISISFNTHITPIKHSVDVHTVSTTRC NLGGRGFCHTWPLPHLAGW
8480	22381	A	8541	331	156	SVNGLLSLPACLPVCLPACLPFLPSFL PSFLSFFLLLLLLQKPVNSLIFSQSLIS
8481	22382	A	8542	72	1	KIGQARWLAPVIPALWEAEAGGSP
8482	22383	A	8543	2	83	QAGVQWRDLGSLQALPPGFMPFSYLG
8483	22384	A	8544	293	2	KTVWHYLVNAPEVEIQAIYSQETCKSMY QETCTRIFIAILFIIAPNWKQRQDTMNP GNKENGKVATLDSGFLVRFQSLMRSNCL PLYPFNKFPILLK
8484	22385	A	8545	314	122	LVETGFLHVGAGLELPTWSDPPTSASQ GAGIAAVSHRGQPVDFKNNISTQIQGRP IICNYKTF
8485	22386	A	8546	316	123	LVKTGFLNVGRAGLEIPTWSDPPTWASQ GAGIAVAVSHRGQPVDFKNSISTQIQGRP IICNYKTF
8486	22387	A	8547	3	247	GIMATERLANYTGGIYAEYQDTTYINHV VSVAGWGISDGTETWIVRNSWGEPWVRC FHFLKVI PRKKT SWYSSRLNGSVYV
8487	22388	A	8548	289	25	QRREKFFKNGPPIFFRGPFQIFVVSF PFFPKIGVFFVFFRFSLVKGDFFSN FLKINCFEEEEEEEEEEEEEEFIKN RPCL
8488	22389	A	8549	289	2	KKKIGETLCKLCKLCKFLDVT PKAQFIK QKKEKLINWQFIKIKNFRSPKALLRRGK GKPGTGRKRANHISDKGFLCRIQKNS RGRAQWLTLLV
8489	22390	A	8550	290	187	RQENPLNLGGGCSEPRWCHCTAAWVTE QDSINK
8490	22391	A	8551	293	183	RDEGRGISYMLPRLVLNSWPQAILLPQP PKVLELQA
8491	22392	A	8552	364	87	MLPLDFFLGPDLDFCPFFCESGSGGIKV PESTTPRASAFLPPGAANLHHLQLVGA PRVPPGFHHVGQDGLDLVDLVLRLPRPP KVLGLQGG
8492	22393	A	8553	57	225	KWQKWPWAGGVAHACNLSTLGGRGGKI ACAEEFKTILENIVRPLCLSKNKWISFS
8493	22394	A	8554	326	2	KSKRGYSEPLVFSIC SARAPRSHSVSQA TVYGHAASTQPFPPRLNRSSYLSLLSS GDYRHDPPPLAYICISVIGNDVEHLFLC LLSTCISSVNRSHVYSTLVPIFGP
8494	22395	A	8555	372	148	YICFLRSSVRQILFTPDSCDCSMWVPCN IRLPGSTHWCASASQAGTTGARHHARL IFFVVVFFCIFSIFSRNH
8495	22396	A	8556	422	269	AADQERLHTYQLNYYHFCRWGLTTFPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LVSSSWVQAILPTWPHKVLRLQA
8496	22397	A	8557	669	407	AGVKWRNLSTLQPPPPRRFKRFSHLSLPS SWDYRCPLPCPANYCIFLVEKEFRHVKG AGLELLTSGDPPAWVSLIAGITGVSHRA HPD
8497	22398	A	8558	195	352	LGLQAGTTASGYSTVILGMLKPRSWAW WPVVPATREAEVGGSLPEGRSKLQ
8498	22399	A	8559	345	219	MLARMISISLPCDPPASASQSAGITGMS HHGWLNLFKSIHL
8499	22400	A	8560	137	2	VKYCLPTRSLIKTVRPLSPSQATASEPT CTYTPRWPEVTEESQKN
8500	22401	A	8561	324	193	RSSGNLPASAAQSARITGVSHRTRPKCI ISKEYVAENNLKSTS
8501	22402	A	8562	326	121	HNHTHTHTKNHKKHQPPQHTHTYHTQTD IYVLQAASQKSLILISSLAV
8502	22403	A	8563	3	85	HEHTHTHTHGHHTHTHRHTHTHTLCARM
8503	22404	A	8564	2	153	ARDRHTPPCLTNFSVFWRDGGLAMLPR VSKLWAQAVHPWLLKVLRLQA
8504	22405	A	8565	2	177	ARVGFHYVGQAGLGRITSGDPPASASQS AGITGMSHRARPMSSLTHLILQDTRWAY AG
8505	22406	A	8566	353	212	AGFRHVGRAGLELVTQDGPRTSACQSSG ITGMSHCAHPEKSTAFILF
8506	22407	A	8567	76	191	ELIFCRDGGTLVFPKLISNTWPYAVLPL WPPKVLGLQV
8507	22408	A	8568	1	142	GTRGFLHVGQAGLELPTSGDPPALASQG AQMGTGVSHCASQKKEFLEW
8508	22409	A	8569	250	95	SASRAPLPLPSSHLPPLRAAGLSPLCP LVSSYRPHVILLPLPPKVLGLQV
8509	22410	A	8570	3	226	HEHTHTHTHTHTHTHTHGHHTHTHTLV LVYSLCEHIWRFIVISRARVCCIYVVVF FECGYADRRVADKWLWIH
8510	22411	A	8571	1	216	GTRGLGVGVSHLVSKNTHHTHTHTHT THHTATASQLSVFKIWAQRLDKGLT YISNSYCSSKFYLYNH
8511	22412	A	8572	356	268	LTMLARLVNFRPQVQPWPVKMLGLQ A
8512	22413	A	8573	12	175	RWGFHPVGQAGLELLTSSDLPTLASQKA EITGMSHCARPSFFSFFLSFFFWKHL
8513	22414	A	8574	1	163	GTRTGFFHVGQADLELLTSGDPPVASQ SVGITGVSHRAWPVGLCIALISNEY
8514	22415	A	8575	344	176	EFLVETGFRHIGQAGFELLTLGDQSTSA SQNTEITGVSHAPGLAIFKSGNQAFF
8515	22416	A	8576	2	179	ARGILCHSGTFKLDSPSMVAHTCNPST LGSQGGRIACGQEIDTSLKVARPRLYG QIF
8516	22417	A	8577	1	100	GTRGFTMLPRVVSWSAQVILLWPVKV LELQM
8517	22418	A	8578	3	114	HERHEILSIYLTIIYLSIYLSIYLSIYLI YLPITITRI
8518	22419	A	8579	1	264	GTRPCRTLYRVVESLAKAQETSGEIS KFYLPNCNKNGFYHSRQCETSMDCAGL CWRVYPWNGKRIPGSPBITGDPNCHIYF NVQN
8519	22420	A	8580	1	245	GTSGTSGILGFYLEREDRLLQIRTDIT LSHGYSTFSLNRCDSRHHMNRMFQMLYQ SPFLGYIQLSHEVLAFGISIYINTE

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8520	22421	A	8581	1531	1457	QARNETIARRLWDVSCDLLGLPID
8521	22422	A	8582	191	2	TITSYFSPTPAPGSHYATFCFYKFDYSR YFIKVELWEAETGGSRGQEIETILANTV KPLRSRA
8522	22423	A	8584	2	212	ARAGIYPKEYKSFYYKDTCMRMFIAGLF TIPKTTWTQSKCPSWIDWIKMYRQGPIL SPMLECSGEVSGFK
8523	22424	A	8585	2	192	ARGNSPASSSRVAGITGAHHHARLI FVF FLFVRFFFSFLKTGFKLVAHSNFQPLTL FAPLHFK
8524	22425	A	8586	277	66	PLDFRLGHKRRLPFPKKKKKESKFVCVC VCVCVCVCVKRQCLVTLPRIVSNSWAQA ILLSWPPKILALQV
8525	22426	A	8587	395	286	PHLGLPKCWDYRREPPCLAEEVVLKKYVW VTYFSFRR
8526	22427	A	8588	307	177	RYPSTINYSILNRDKIMPKLDRMVYKAR PRVMCLPWPPKVLGL
8527	22428	A	8589	167	349	RNLRELGEFFFFFFFWFFFFFFFVGKFS VFLLVGNLFLFFGGGIFGLSRVMCFKEF RCFS
8528	22429	A	8590	375	240	LLSRFSWFVFRQGLTMLPRLVLNCWA RGILLPWSPKVLGLQA
8529	22430	A	8591	347	215	ETGFPHVGGQAGIKLLASSDPPASASQSA QITGMSRRAQPSAKRF
8530	22431	A	8592	340	114	HRTAHCSLYLSGSSDPATSSSQVTGTTG KDQHTWLLFKYFCRARVSKINKYKSKINK FYFLNTQTTPSEYGKASPG
8531	22432	A	8593	86	253	LRLCCGLSCSTAKKKKKKKKKPKKKKI KKKNLHPKRGGFEEILFFPKGGKNLF
8532	22433	A	8594	3	135	GFCHVGQVGLLELLTSGDPPALASQNAEI TGVSHRAWPPVLFFF
8533	22434	A	8595	2	274	PRVRTISLLGILVYRSHLISLLCLEGI ILSLFIIATLITLNTSHLLANIVPIAIL VFAACEAAVGLALLVSISNTYGLDYVHN LNLQC
8534	22435	A	8596	3	316	SIPYSWGEKEGIPCMAPPQIQGTSRLND FTALSLHLNTHTHTHTHTHEIQHLPP QGITALILNSLLRHYCPSLAFPSLSPKQ NLTVRHCLSRDTWLATASK
8535	22436	A	8597	385	291	KAPPLFFFFFFFFFFFFFFFFFFFFKPV KKILGV
8536	22437	A	8598	275	369	GVQVLKLLTSGDLPALASQSAEITGVSH RAR
8537	22438	A	8599	98	344	VHYEEFMCVCVCVCVCVCWPRVRGVD MNPVEHPFGGTHQHGKPTIRRNASA GRKVRMLAALWTVRIGTKTVTLRKT
8538	22439	A	8600	328	195	THVPPSLAKFVFLVKMGFLHIGQAGLDL STSGDPPALASHVFKR
8539	22440	A	8601	2	214	HVDVVMGTFAILSELHWDMLHVDPENLR LLDSVLNCELANHFDTFTPPVQAAYQK VVADVANAHAHMYH
8540	22441	A	8602	89	181	GLRHNRLNSGGGGCSEPKLCHCTPAWA TE
8541	22442	A	8603	340	57	KEGHQEMEQAEDGGHGRKAPGTSPWTLG ELPKSARGHTGLFVSYRCRTQFRFKKV LFGGDRNRGLAMLPRVLNNSWPQEILLP QPSKVQGLQK

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8542	22443	A	8604	330	132	TGFLHVGQSGGLKLLTSGDLPTSAFQNA ITGGSHCTRPFSLFHSYLVLFYGCSSSQ VSLSLARM
8543	22444	A	8605	546	279	RPGPTVSPRLEICMIMAHCSLDFPGSG VSPTSASRVARTTSTHHAWLIFYSSVE TGSHHVAQAGLELLGSSNPPIASQSAG ITAL
8544	22445	A	8606	3	249	NRFNLGSGGCSEPRSHHCTPSWATEQET CITYLEYCFPPVSHNTLVYFKPLNVYTR SDYCILGLHASSIGGSDSLIIDCW
8545	22446	A	8607	159	324	VIQYRTNHLHLCEVLVFWFLPYFFLK KTYTGIGQMRWLTPVIPALWEAEAGGS
8546	22447	A	8608	334	179	TGFPHVGQSGGLKLLTSGDLPTSGSQSAG ITGVSHCTWLEVIYFLNISYPS
8547	22448	A	8609	278	202	QQPSTLRQDPFPAKRLHLSEGSDGH
8548	22449	A	8610	236	66	AASTFFLQIKRHLLSGTVAHACNPSTL GGRGIRISRGREFKTSLGNMVRPRVYK
8549	22450	A	8611	29	177	GKQVMALHCFIFHHFFRRSLAMLRLV SNSWVQEILPPWPLKVLQLQA
8550	22451	A	8612	1	215	HTSRTLFLVHLRLKFNKYLIWGLSMLP RLVLNSWAQAVLPPWPSKVLGITGMSHC TWLYLHLSTDLLKLC
8551	22452	A	8613	3	91	LRHGNCLDPGEGGCSEPRSCHCTPAWVT E
8552	22453	A	8614	2	167	FTISLLGILVDRSLTHHINNIPKPSFTRE NTLMFIHLSFILSTRKQLAIQHLSRLE
8553	22454	A	8615	2	281	FCILVETGFHCVAHAGLQLLSSGNPPAS ASQSVGITGMSHCTSPNLSLLTQSKSFC LLIQNHNPYAFINSQLTFSILFLLSYFI FYDSLFLLF
8554	22455	A	8616	282	182	GQAWLTPVIPALWEAEVGGLEPRSSR PAWST
8555	22456	A	8617	379	207	SNQTTKKYINFFFVEMRSHYVAQGLKF LGSSNPPTSASQSASITGISHYVWPISP S
8556	22457	A	8618	705	483	DKSFALVARAGVQWHHLGSLQPLPPCFK QFSYLSLPSSWDYRHAPRPANFCILSR DGVSPCWPGWSRTPDLR
8557	22458	A	8619	359	220	RQSLTMLPRLVSNWSAQAILPPWLSRL GLQALAPIPGKSYNEKTP
8558	22459	A	8620	3	186	HEVSWVKRKQDEWIEFDDTIVSIVAPED ILRLSAGGDCHIAVLLYGPRRVQILEE ESEQ
8559	22460	A	8621	1	116	GTSFCRDGGLTVLAQLGSSFWPQRI LPPWPKVVELQA
8560	22461	A	8622	369	188	MYSLEMGFTGNHAGLELLASGDLSALA SESAGITCMSLRYRTRFSFKRATCGLDL SLQS
8561	22462	A	8623	202	22	YILGFYFMPVICYQERKKDKKNWEVT TMSFVGICMELGAILSLKLMQEQT KYHIFSQV
8562	22463	A	8624	387	315	SNLGGGCGSELRLCHCTPAWATE
8563	22464	A	8625	2	135	TRDLCSLVYLLTFPPLSHDPAKSPSVR NTQELSIKKKKKGRPF
8564	22465	A	8626	3	232	HASAFEEPVIKSRQKRKESNPPKLVSS QPHGLKKKKKKKKKKKKRGRGLKKKKK KHKKFKKKGQKKYNFGRGAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8565	22466	A	8627	97	373	QHGFLLKKKKKKKKKKKKGGPPLLKKPLG GPNFTGDGKKKKFFPKKGGIKKPPGEFLK KNLFLGGKKNGKNPPKLNPLGEKKNFK GKKGKNPP
8566	22467	A	8628	2	188	RYGCPPPYHTFEFPVYIKSRQKRKEWNP PKLVSSQPHGLHDFKKKKKKGA AVLKD PSGGPS
8567	22468	A	8629	287	68	GEEGRTOQGERNGGGSERKEGEEHEAR RTGRGEGGGGEAKGRPSARRRGSRG SKSQTPSRHLPAHIITN
8568	22469	A	8630	364	136	VSLLLGLEYSGTITAHYSLNFFLLFIVET GSHYVAQTGLKLLGSSNPPTS DSQTFEI TGVSHGAQPKVQFWSKNLDT
8569	22470	A	8631	355	70	LFPPRFFPFSPSLSPLEFFSPKGFNF REFFPIFSPPKRVL SKNSPGGFYKPP RGKIFTFPFPVKFGPPRGLFKGPPPPFF FFLFFFFFFLVI
8570	22471	A	8632	2	266	AFTISLLGILVYRSHLISLLCLEGIIL SLVI IATVITLNTSHSLANIVPIAILVF AACEAAVGLALLGSISNTYGLDYGHNLN LLQC
8571	22472	A	8633	1	186	LTHHINNIPKSF TRENTLMFIHLSPIIL LKKKKKKKKKKKKKKKKKKKKGGALKKK PGGGQN
8572	22473	A	8634	2	80	VLEIAVALIQAYVFTLLVSLYL RDNT
8573	22474	A	8635	713	333	EGPPPPRSKKKGTQGGKDDPPSPPEPKT PGNPQGRKTGPPPPGRPYTGPRPPGSGP TRGGGSRSSSSNTNAPGEKIFFSKNPGR KIFPPRAILVFFSPFPLKNFFFSRLLI FLGGCAPFFPPPK
8574	22475	A	8636	389	1	FIFSFLFLIIFFFLNINFFFIYFSSLSF FFFLNFNLLKHTPPIILFFFSLSPIFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFGTKKELY LLRARGCKQYKNQKLIWYLT
8575	22476	A	8637	2	192	VRTLGLRDTAIPGRLYQTFTATRPVY YGQWYEICGANHSFMPIVLELLALTIFE IGPEFTL
8576	22477	A	8638	1	87	PTRPLEIAVALIQAYVFTLLVSVYLHDN T
8577	22478	A	8639	2	132	INLASTLIIFTILILLTILEIAVALIQA YGVTLVSLYLHDNT
8578	22479	A	8640	2	113	LEFFIAEYTNIIINTLTITIFLGT TYDA LSPELYTTY
8579	22480	A	8641	375	22	FIFISPLAYLFFLPFPFFFIPLCFFFF IPLFFFLFSLFSLIFFLFSLILIFPPS LFFFFFFPFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFCWLPHRVMIKVGISVSVSKKI
8580	22481	A	8642	180	34	WFISDSLWLG MVAHTCNPSTLVGGGWI TCGRSRPSVPKRTPSQTCAPA
8581	22482	A	8643	338	133	NLPLGLFYSLQKKKKKPLRPGTLGAPK GNFQGA PLFGKFAFFFFFFFFFFFFF FFFYGFFFFL FK
8582	22483	A	8644	156	287	LTYPIKPPLCSQKKKKKKKKKKKKKK KKKKKGAFKKNPWGAQI
8583	22484	A	8645	1	325	LHHCHTHNFVNKVCVIRKKKKKGKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKREKKKKKKKKKKGGGPKKKPPGGPK FSGGGKKKLFPPQGGYKKPPGGFLGKTL FLGGEKMGENPPKKIKPLGEKKIF
8584	22485	A	8646	370	3	PVRASRLCLPKQAWAMAGAPPPASLPP CSLISDCCASNQRDSVGAGPSEPGAGYN LVMHCFLSPSEKHSIWGVTRFSRCCPS PLSLTRKGNLTPCASQVRQCLALLRLV QGAGTHRTRG
8585	22486	A	8647	341	88	KKKKIFSPPIKRGPPSVYFICPPPPFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF PIWHKLCGDL
8586	22487	A	8648	1	108	PTRPRTRGVASVLYFTTILILIPTISLI ENKILKWA
8587	22488	A	8649	3	96	EICGANHSFMPPIVLELIPLKIFEIGPVF TL
8588	22489	A	8650	457	297	SPSFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLFYFALF FIYLI IKDNYMFQC
8589	22490	A	8651	84	352	YEKTDVKIISILFNTDYMLEYNVLHILG QIKMLLISKKKKKKKKKKKKKKKKKINK FFWGGLILTLGIVLYSPLEALKISPSF GFLEK
8590	22491	A	8652	2	111	NNIKPSFTRENTLMFIHLSPIILLLSLNP DIITGFSS
8591	22492	A	8653	1	305	RQQQQQQQLRNLDRFLVYNRMTELCFQ RCVPSLHHRALDAEEELHSCAGKLIH SNHRLMAAYVQLMPALVQRRADYEAS AVPGVAEQPGVSPSGS
8592	22493	A	8654	129	268	LSEVLYLFPPKKRLIILCLFFRNPGSS NLQKITKEPIIDYFDVQD
8593	22494	A	8655	281	117	CTITLSFINTLQAYIWL VVFSEVCLYV SLSIYLSIYLSIYVFERYIKISFHL
8594	22495	A	8656	3	177	DLHAHKLGVDPGNLNLSHCLLETLAGH LPGEFTPAGHAFLDKFLDFVSTVLTYYK R
8595	22496	A	8657	3	270	RRRGRAHCSLDLLGSRNPPASASRVAVT TGRHLAWLIVGGFLFFVLRDVLVRFH ATDKDIPKTGQFTKERGLMDLQPHMAGK ASQS
8596	22497	A	8658	107	11	QEHTKPTPFLPTLIALTLTLLLPISPF LIIL
8597	22498	A	8659	21	136	VPIEHDPVPNSRAELLMFGIDRDATA QAVRGLITKA
8598	22499	A	8660	1	395	LVTALYSLYIFTTQWGS LTHHISNLEK KKKGKGGKKRGGALFKGIFGGSHFFGV WELLFFFLKGGIKKTLGFLGKTLFFGG GLLGAPLPRKIKGLREKKNFKGELGVKN RVFFFFGNFSSLGVYLKKY
8599	22500	A	8661	1	255	RTRGRTRGRTRGLTRGKKKKKKIMKKKK KKKKKKKKGGAFLKNPWGGPIFWGLPKF YFLPNKGSFFNLIGDFLKRPFFWGGAYF G
8600	22501	A	8662	136	358	FHIVKGVSIKFKCVILKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK NKIFFWVGFFYKRVWGYF
8601	22502	A	8663	198	368	LINLVQFTCILGTLLGILFIYFLRRAI



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TMLARLVLSWPAVLLPQPPKVLGLQA
8602	22503	A	8664	407	82	KFLPHLGFPPFKRFFIKKEPFWFFFLLF GFFFFRRSFFLLPRVQCNGAISGPCNL LNVKVRLSFKKKKKKCDYTFEPLCPAL HFSFINKTEDCLFVCFTVYWP HGF
8603	22504	A	8665	166	293	KIIAKHNIARTNPYTFICIMKKKKKKKK KKKKKKKKKKKKKKGGAL
8604	22505	A	8666	1	164	RAKAKRRNTTVSCMRHLKIVYRRFRYR LYVGIIIGPGLNETLVFTCKKITVP
8605	22506	A	8667	295	85	YIYMSHICTLSLSLSIYKRVKCFCKFT WSHVAQAGVQWRDLGSLQPPPPKWILC ISVFFTVL FVMKKK
8606	22507	A	8668	2	131	INLPSTLIIFTILILLTILEIAVALIQA YVFTLLVSLYLHDNT
8607	22508	A	8669	423	107	HCALPKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKK
8608	22509	A	8670	432	301	SQILGRFSQKQHLSLGGGCSHPRSCHC TPAWARGRLRLKKFIK
8609	22510	A	8671	1	106	LKILTSSDLPASASQVAEITGMSHCARP LSRIYMC
8610	22511	A	8672	383	252	CPANFVFSVEKGFLHVGQAGLELPTSGD PPGCWFCFLQQQLHW
8611	22512	A	8673	560	135	SSWGMDSITPTSSNMEETQOKSNLELLH SLLLIESRLEPVRFLRSTFTNNLVYDTS DSDEYHLLKDLEEGIQMLMGRVEDGSHL TGQTLKQYTSKFDTNSHNDALLKNYGL LPCFRKMDKVVETFLRMVQFRSVEGSCG F
8612	22513	A	8674	2	326	SLLMCVHRCVCVCMRACLCAVCMCIAS CLGLPMNVVECYTWRVLVFHQFQDEELH DTVLDLETIPLERQPRDVQHPVSTRILYL HVYFVAVTLTIRILQLWTEAFSP
8613	22514	A	8675	171	272	TQCCLLKAEEKKKPKKKKKKKKKKKKK KGGPF
8614	22515	A	8676	60	409	LIVWLESHEDVGPLIKDSKQEKKKKKKK KKKKKKKKKKRGGAFKKKPGGGQNLRG GEKKNFFFLRGEKKNPRGNFGKKTFFWG GENWAKPPPKKSPEGKKKILKGKGKK YLNFLGE
8615	22516	A	8677	106	286	LFWNKEGNNWKKKKKKKKKKKKKKKK KKKKKKKGGALLKISGGGPIFPGGGKN FFFFFGGGF
8616	22517	A	8678	1	97	IIGQVASVLYFTTILILIPTISLIENKI LKWA
8617	22518	A	8679	1	141	NEHQPGQHGEPPSLKIQKISWAWWSMP VIPATQEAEMEKEQSISIM
8618	22519	A	8680	499	140	GVFFFSSRRKRCGVSPPPPKPVFFPLPG FFFWGGCPSAPPPPGGGFPNPPRGFF YPPPLKGNFFFPAGGGPPRGFFWAPP PPFFFFFFFFFFFPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP
8619	22520	A	8681	60	224	KQTKYIKEITKHICTWQGRYHDHEGGFP RVKLIHCTPDMLTPVISPDVGNSTTV
8620	22521	A	8682	252	383	SQXKKKKKKKKKKKKKKKKKKKKXGGGL LKNFWGGPNLTGGGKI
8621	22522	A	8683	405	145	KFFFSGGCFFFWGPPGKNVPPPKMFFF LIPPPKKKKPPPKKIFPPPPGVFFPPP PPFFFA PPPPPPPPPPPPPPPPPPPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFF
8622	22523	A	8684	1	406	LYYFLTKSTTTYLAVPQFPPTPSTPSR AKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGGGPKKKTRKGGGQKKKKGR GPEKNRGGGETTPGEKKKKKKGGGGKK KKKKS GGGKNGGKPGRGGGGGR
8623	22524	A	8685	391	265	GRFFFFFLDGVSLLLPRLECSGVILAH NLCLPGPSDSPSSA
8624	22525	A	8686	2	177	DTALYSLYIFTTQWGSLSHHNNIKPS FTRENTLMCIHLSPILLLSLNPDIITGF SS
8625	22526	A	8687	479	366	GLPKCWDYRREPPHPAANFCIFSRDGV PCWPGWSCL
8626	22527	A	8688	35	161	SNPPSSAFQVAGTTGVRHHDQLTFFFF FLGGTGILCRGGD
8627	22528	A	8689	1	122	THHNNIKPSFTRENTLMFIHLSPILL SLNPDIITGFSS
8628	22529	A	8690	2	152	NTLAFTISLLGILVYRSHLISLLCLE GILSLFIIATLIYPTPSFSCY
8629	22530	A	8691	541	85	IFLROFLSPRLEYSGVIKHC SLNLLGS SDPPASAFKVAGTTGIRHHAWLIFVFFF AETGFHYVAQGGLELLNLRLPATAFQS AGIIGISHHDLGIQITTWLQKLSYLQ KKICKDQETGLLHAFHLHPYPMPSSP QLLQGPDIITNG
8630	22531	A	8692	122	38	GRVDHSFMPIVLELIPKIFEIGPVFTL
8631	22532	A	8693	276	77	GVSPCEPVFFFI LGRCPNPAWGVPKGRD FFVLSFFFVVFYILLFFFFFFFFFFF SFYCFNGSNK
8632	22533	A	8694	3	70	FMPIVLELIPKIFEIGPVFTL
8633	22534	A	8695	230	3	GSGIPSHPGHPSLPYHLEREWLAKTGIR DTSNSVHLELCLRSQRHGRARWLTPVI PALWEAEAGGSRRQEIEPI
8634	22535	A	8696	401	240	PPPPPPPCGSEPRPPHPSLSPPGSREMF VLALSQESQMTFFFFQLRKKLHLYL
8635	22536	A	8697	103	313	EKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGPKKKFEAIFGKTP GGVSQGGGPPPLNFFFLNPGPPFF
8636	22537	A	8698	354	110	KKGTLFEVSESFYTTEGVSAKINRIRSI VSVNKVARCIGEIFTDVQSAFQKEVGG VSDSMVHKYAYAGCVDVKA VCSHGL
8637	22538	A	8699	2	164	FLVETGFLHDGQAGLKLLISGDPPASAS QSAEITGMSPHACNSSTLGGRRGRIT
8638	22539	A	8700	191	371	PPDSRWAIQGGHLELTPTTRQDLAQAPR RKLALLEGSFQQAQWLTPVIPALWEAE ASGS
8639	22540	A	8701	2	170	ARAGLYHVGQAGLKPLTSGDPLASASQS VRITGVSHRTRPKIIFKLIFLFFFFFFF
8640	22541	A	8702	31	229	MEKYNVHPHSGILRSHEKQQAALFTIAK RWRQPSYPSIDEWINIMWSSHTVEYYTA MKRNKQLYSQ
8641	22542	A	8703	3	126	LQELRDP TLTFRLLGSPRPVVVETRPVD DPTAPSNLYIQE
8642	22543	A	8704	438	31	SEPCAGYNLLVCRFLSPLEKHNIRVGVT RFSRCHLSPLSLTRKGNLSLTPCTSRVRQ CLALLWLAHSALHPLSCMHCLALPSEM N PVPQMEMQKSPIFCIAHAGSCTPELFLF GHLGSTPLTHLLSLRINVFLRTSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8643	22544	A	8705	429	319	PGATIAHRSNLNLPGSSDPTASQVAGN TGVSYCARP
8644	22545	A	8706	426	245	RAATPSPIKLTKKKKKKKKKKKKKKKK KKKKKKKKKKRGAPLKKTLGGPQINRGK KKIFFFF
8645	22546	A	8707	1	108	KHPRGGSFGYCFALAWAFPLALVSGI YIHLRKRE
8646	22547	A	8708	3	146	QIEGHTISALGDGAAWPVQGLIRHFRPE LEERMQRFAQQHQARQAAS
8647	22548	A	8709	2	83	LVLEIAVALIQAYVFTLLVSLYLHDNT
8648	22549	A	8710	1	81	RPLSKTVRFNVLKVTKAAGTKKQFQKF
8649	22550	A	8711	156	4	RPLSFHPGCKKRLFLKKKKKKLCAVAHA CNPSTLGGRGGRIMRSGDRDHPG
8650	22551	A	8712	440	233	TPSYFVLLVERGFMSLPRLVSLTSGDPP ASAFRSAGITGMSHHAQPERTGRSKAYLP FLEEDLKHIFPF
8651	22552	A	8713	92	302	AMHPTMGPDQDQGHGTGLYAHTPLPHPSH THANTLIHSHIYAHASHTIPATCPKGP TQPYLCLLSPHIEL
8652	22553	A	8714	2	166	KKINSFFSQGLTQAKVHGGPRSSSLGPQT PVLKRSSCLSFSSWDYRHEPLYPAN
8653	22554	A	8715	1	129	GFRHVGQADLELLTSGDLPASASQIVRI TGVSPCAQHEFFKSN
8654	22555	A	8716	381	105	RRSLHLSVLNGAQAGVQWRDLGSLQPPP PSSLPWPPKVPRLQPLGRHPVWEVRSV SARPPIVWDVRSPSAWLPSLESEERLCL AATPSGK
8655	22556	A	8717	385	125	FFFFLPPAFLLSGXFWFFFFYIFSSFFF FFFLGSPPPPIFFFFFFFLNKIFFFFFF FFFFFFNNLFFFFFFFYYFFFTFFFF FFF
8656	22557	A	8718	409	264	KTDQRWSSTSSSKIMSQSQVSKGVDFES SEDDDDDPFMNPSSLRNR
8657	22558	A	8719	3	269	KKHVKRVLSHLKASCPEELLHFSWQPQL LELQLMGGGSHTHMDQHTHMHPIYT HAHTHTVAKLNELPWVEMNLLSLGAFAQ QRLP
8658	22559	A	8720	430	141	LFFFLSFFEDGVLLCHPGWSVVAQSOLT ATSTSKKKKKKATPPGIPKFLIGKSGK PPRVLLIGHWAPKFFFFFNRLAFFF
8659	22560	A	8721	386	290	RWGLTMLPRLVLNYWLQAILLLWPPKVS GLQA
8660	22561	A	8722	3	157	HEVFLVETVFLHVGQAGLELPTSGDLPT SALWEAEWGGLLEDRSSGPWET
8661	22562	A	8723	493	186	FSPQGGKRAILGLRNLCPGKVDPSAR PPKEVGNRVPKTKLEFFVLKKKGFP IGRGGFKSRPWESPPRPPQKGVQRLNP PPGFFFFDLIWPNRNGS
8662	22563	A	8724	3	186	GGGTTPPPGVWGKNGGGTTPPAKTLPPF PSPLFFFSPPSPGEGGSREPLSTPLA CICI
8663	22564	A	8725	370	67	FADPKNFYKGAPPIFFIFLFFILFIYFF FFFFIFPKFLVFLLETGFHHVSEQEDLDL VIHLPPQPKVVGLOAWATTGQFFVFLI ETGLHPVNQDGHNLTL
8664	22565	A	8726	966	652	LGSLKPPPTGFKRFSCLSLPSSWNYRHA PPCPANFVLEETGFLHVGQVSLELLTS GDPPTLASQSAGITGMSHRDWLGQHLIV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NHCYLFYQGHIKTTTSLPPP
8665	22566	A	8727	85	425	HMHSFAHELHTFLHTHTNSHTNSQNQSP TYTSKSHTHSYMRFTDSHDSQMQQTHR SLLHMTQLYTCTHTHTHTRTVIPLELHS VKGWLN TKVALGGRTSHGRESHIAGRLL A
8666	22567	A	8728	393	124	LGSSEPQLFQSPSPSGGPPGPKSHWNSWG NANPPVPVPPYIESAPPPPHFPFGAQS SGGQAARLCPCPFFFLKKKKKAPGSGT GTFSFQ
8667	22568	A	8729	25	217	AVQPIRVQWRRSLQSPQEQIILAPSLAK VDMEMTQLTQENADFATRDRYHSSLVN REQLMPHY
8668	22569	A	8730	1	611	PGIFYSALLSLDTSILNQLCFIMHRYRK NLTAACKNELVQKTKSEFNFSKTYQEF NHYLTSMVGCLWTSKPPGKGIYIDPEIL EKTGVAEYKNSLNVVHPSFLSYAVSFL LQTS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSPSPEERTVNVSSIRGKKWSWYLD YLFSQLGLKLFIRSSVHSSIPRAEG INCNNQY
8669	22570	A	8731	120	378	VEKTOASTLGCKCSTPRAALGFRERTLP LRRCPCCGPPEAQMELEKRALGSQAQWL MPVFPALWEAEVGESLEARSFETSLGNI A
8670	22571	A	8732	2	68	VYVCVCVCVCVCVCVCRAKVG
8671	22572	A	8733	382	258	NYHSSLHLETPGLKQSSCLSLPKSWDYR HESPCPALIFNSL
8672	22573	A	8734	479	326	PPLYGFFFFFWGGGFFFFFYFFFF FFFFFFFFFFFFFFFFFQTT
8673	22574	A	8735	422	2	GRRPPGLYFFFFPPGKKNFQGRGGLFF FPPKGFPPFPPIGFFFSSELGKDWP PKKKVFSQRFPFFFPPLFLFLFFFF FFFFFFFFFFFFFFFFSFFFFFFFFF FFFFFFFFNKQVFIERLLCARHCFRPPAS
8674	22575	A	8736	7	75	IAVALIQAYVFTLLVSLYLDHNT
8675	22576	A	8737	2	176	NFGLLAETGFLYVGHAGLEVRSSGDLPA SASQRAGITGVSTAPGFNRYFYKQTIYK YG
8676	22577	A	8738	408	111	GSSPPPRAGGENFLKKNAGGKNFPGGEG GGGFYPLYPKKFFSPKGFIFWGGGGGK WPPPKKGGFSKKPQKVFTTPQKKKKFF WPPGGNWGPKNF
8677	22578	A	8739	5	249	YEGKKLHMQASPFQRGHPVNHKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK EGALGKFLAQTSPKGEKQKVFIKY
8678	22579	A	8740	1	226	FFLRQSLSVTQAGVQWCDLSSLQLLAFQ GSSNSPTSASQVAGITGVHHHQLIFIS LVETGFHHVAQAGLELNLQ
8679	22580	A	8741	4	96	DGLIMLPRLVSNWPQGILPPWPSKMLG LQV
8680	22581	A	8742	19	112	FGRILLVREKKKKKKKKKKKKKKKKKK GGGPL
8681	22582	A	8743	362	234	KMDQKCLSEVLQRWFPCCCCCCCCCCC CCFSLPFIPEPSRS
8682	22583	A	8744	3	419	LTLRRFQLNLALTATKKKKKKKKNLKKK KKKKKKKKKKGGPLFKNSLGGPIFP GGKFIFFFFWGGFLKPPGDFLKTFFLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GEIFGPPPPKNTPLGKKKIFKGVGVGKN PPLFLRRKKFFSGGFFKKIFSPGLGF
8683	22584	A	8745	444	1	KKPSKEILYPENSRRFFSPLSPLKFFFS KGFNFVGGGGPLCPPPKERFFSKNPPGG FSPPLKEKIFFFPPPVNLGPPRDLFKG APPPPPPPPPFLWEMFYWLSLSSGSQR LPQQVPTVEPSELGGMGAYFVSKRSTYL QRGWRPER
8684	22585	A	8746	104	222	NKTFCLLKKKKKKKKKKKKKKKKKKK KKKKKNWGGAL
8685	22586	A	8747	403	201	MEKYNVVQPHSGILYSHEKEQAALFP IAKRRQPSCLSIDWRNIMWSSLTVEYIT AMKRNKQLYSQ
8686	22587	A	8748	1	90	RTRGAVYAALERMGLDGCVEDLRSRLQR GP
8687	22588	A	8749	444	85	SPPPPGLFFFFFPKKKTSPPPTKKGFF SPPPPQKFFFLKPPFFLGGLGPNFPPP KKNFFSKNPPRFFFPFKKKNFFFP FFFAPPKFFFLTPPPLFFFFFFFFF FFFFFFFFL
8688	22589	A	8750	2	309	EFFPPYWEFLKINACMFSPKKKKKKK KKKKKKKKRGPPLKKTGGPQIPRGGK KKIPPLKGGQKKPPRGFLEKNPLFGGGP FGPPPPKINPPEKKKNF
8689	22590	A	8751	3	76	TASVSEGGGLQGITMKDSDEEEEG
8690	22591	A	8752	433	145	SFFFFFFFFSFFFGKKSSFFFTPL
8691	22592	A	8753	2	124	GHLLMHLIGSATLAISTINLPSTLIIFT ILIKKKKKGRPF
8692	22593	A	8754	80	201	FINANSKKKKKKKKKKKKKKKKKKK KKKKGGGLLKKTPGGAQF
8693	22594	A	8755	415	1	IYFPTPEKFGPPKETLKKCAPFFFFFKQ KPPFFGPGKQKGGFGLQTLPPGKKKI SRPNPPRKGFKDAPPPPGKFVFLKKKG VFPGGQGGFKTPTPRDLAPPAPLNPAL FFFFLQSLSLSLRLECSGTILAHAS
8694	22595	A	8756	3	136	FTATRPGVYVYGCSEICANHSFMPIVL ELIPLKIFEIGPVFTL
8695	22596	A	8757	80	326	KKFSLGSQGGGRAGVFPRLGLQTTAL NSGAKGTPPFLFPEPRKRGGPPAPGWE GIFCPHFFPMGQKGEGLWHTGEGPH
8696	22597	A	8758	1	164	SLISSTQGHKQCRRPQGPLPRKTRDPCS HVYLLTFPPLLSYDPAKSPSLRNTQE
8697	22598	A	8759	431	79	FFFFFFIFLKKVSTQSPPPQFYFFFLKT FFLFQPLLKEGGSWGGRGDKPPPLAPFK KWGVFFFFSFFCCFVFFFPPLFFFFFL FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFPRCVLTRL
8698	22599	A	8760	60	194	ARPTCPATAVTQKKKKKKKKKKKKKK KKKKKGGGVLLKKKQGGKRY
8699	22600	A	8761	383	38	CASMTFPKKKKKKKKKKKKKKKKKKK KKKK
8700	22601	A	8762	399	164	HITVKSLLVPMDDPPKKKKKKKKKKKK KKKKGGGFKKNLWGGQKLTGEKKKIFFF LKGGKKKPLGIF
8701	22602	A	8763	353	48	NFFFKVFFFLKDFSHKGAPPKGGPPKK TPPRKFFFLKIKPLFFIAFFFFWSLFG FFLIFSLFFFFFFFFFFFFFFFFFFFFF FFIVFTITLMHFKIYLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8702	22603	A	8764	2	93	FAMLPGLVSNWPEAICLPWPPKLLGLQMM
8703	22604	A	8765	398	63	PPPPVFFFFSGGFFFWGGGQKSPPRER CFFFKMHPGFFFIIPFVGGKKVFFVLEGV VCPLGFFFLSGGAFFFFFFFFFFFFFFFFF FFFFFFFFGFFFFFFFFFPGPSVSHL
8704	22605	A	8766	3	83	ILEIAGALIQAYVFTLLVSLYLHDNT
8705	22606	A	8767	450	306	QKKKKRRNKPEGLGTVAHACNPSTLGG RGRWITQPGQQEGNFISKY
8706	22607	A	8768	1	111	WSLALVAQAGAPGFKQFSCGLGLPKSWDY RHEPPCPGL
8707	22608	A	8769	385	261	FLAEMGFCRVGQAGFKLLNSGDPASAS QSAGITGVIAPVL
8708	22609	A	8770	3	293	SLGSKPLGLSLSPVKWFRIFGKERNKV WGKGGTDRNQSSSAFKHLQRGDSDPKQ NKIKACSSKPYLRRCVKRSFLLIKKKKK KKKKKKKKKKKKKK
8709	22610	A	8771	2	281	CVCVCVCARVYIYIVYIYIYTYMCVY MYICIYIHVYIHVYTCVYVYIRIHMYIC ICVCIYTCIYTYIYTHYKHSVYYLHNF YINPKLLQS
8710	22611	A	8772	295	161	THHTHTHTHTHTHTHTHTTTCSLPPS LAQLLGNCCIKAAISILYIL
8711	22612	A	8773	1	318	FFFFVRWSFTLVAQARVQWRDLGSLQPL PPGFKQFSCLSLLSSWDFRHTPPCLANF VFLVETGFLHVGQAGLELPTSGDLPALA SRGAGITGVSHHPQPPLCFLFL
8712	22613	A	8774	3	70	FMPIVLELIPKIFEIGVFTL
8713	22614	A	8775	369	191	TYKINKIGWAWWCAPLVPAAWKAEVEGL LEPGSLRPASVIQDPLHKKGTYSRVLT THL
8714	22615	A	8776	2	124	GFRHVGRAGLEFLTSGDPLASAFQSAGI TGMNHHVQPIVE
8715	22616	A	8777	1	162	LKYTTADENGKTSRLLPQRPSDECGAGV FMASHFDRHYCGKCCLTYCFIKPEDQ
8716	22617	A	8778	346	138	YNSPPYKEKTIPLQARVNFPGPRDSLKR PPFFFFFFKRQSLTMLPRLVLNSWAHGI LLPWPPKVQVLQA
8717	22618	A	8779	2	117	LNLDTTAVQVRNYPRIRESYKVSFLSAL EETTKLNTQ
8718	22619	A	8780	2	97	WDLTMLPRLVSNWAQVILPSWPPKVLG LLA
8719	22620	A	8781	403	276	IISTVFQRGSCPIPSRKEVCSEPRRLQ KDSLTFPHTVYKH
8720	22621	A	8782	2	119	QAGLELLTSSDLPASATQSAGITGMSQR ARPHFQCKNVP
8721	22622	A	8783	245	101	ELQFKMRSGWRRSQPISWGLTLVPRLLS NSWAQVILLTWPPKVLGIQA
8722	22623	A	8784	2	124	AKLEKKKKKTGRAKRRMQYNRRFVNVP TFGKKKGPNANS
8723	22624	A	8785	3	355	VGPSEPGAGYNLLVCRLLRPLEKHGIRV GVTGFSRCHLSWLPLARKGNSPTPCASW VRHLLALLRLTVCGLHPLSCTHCLTSPS EMNPVPQLEMQKSPVFCVAHAGSCRLEL FLFGH
8724	22625	A	8786	238	9	PVKLGAGPPQAPFWLRKWAPLIKPFFKG PIGSLQIPLFFFLRQSLTLPPRLECSAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WLTESSTSWVHAILLPQPE
8725	22626	A	8787	336	10	CLSLPSSWDHRRLLPPHPASFCIS
8726	22627	A	8788	1	147	IFYLLETGFHYVGQAGLELLTSGDSPAS ASQSAGITGVNHHALPEIHVF
8727	22628	A	8789	3	130	DLEEGIQTLMGRLEDGSRRTGQILKLDH SSEFSKTRELYPVF
8728	22629	A	8790	206	3	VPPSGPIKKGDKKKNLYLIFLIKNVENK KLRKGVSPLAIPFFFFFFVFLLETGFHH VGQAGLELLTS
8729	22630	A	8791	124	390	RAGAQSNNLMPPPSGVKAIFFPNFPKKW GNGTPPPAPLIFGGLKKGVSPCGPGGS EPPAPGGPSPLAPPKGGNNGDRLLPPPP DKFLN
8730	22631	A	8793	2	301	HEERERERERERERERERERERERERER ERERERDALFAFFPPRGARPPPEIERGV FVGAGSVREIYPTLSIFFSPPAHRCRE LRSRCVSHSLHLISRA
8731	22632	A	8794	1	285	ARGERERERERERERERERERERERERE RERERERERERERERERERERGAPPP PLFFLGRGGALRAHAISPPPF LGAPPYI YIFFHMRARPPHYLCAQRETRPAL
8732	22633	A	8795	1	321	ARGERERERERERERERERERERERVS RIPRGDLRDQFPPLARSRDSFCGSADH FGRGVFNKVSVDTPPTHRTSSLGGGV ERDLLTSLGGGTYPWKNMCATGEDQ
8733	22634	A	8796	2	140	HEERERERERERERERERERERERERER ERERERERERERESLPPAGCAKAGAGW E
8734	22635	A	8797	2	223	SARERERERERERERERERERERERVS RNLRSRGGGVPPPLQNVRIHSGGPARGT LHHIKKKTSLTDVGLAQ
8735	22636	A	8798	1	176	ARGEREREREREREREREREREREKISF LGGGRGTQFAIERGVIOFCGRRYTTGRV RN
8736	22637	A	8799	335	27	PPTKFFFFFFLVEMGFCCIAQGGLELLS SSSLPASAYQSAKIIGVSHHAWSVF
8737	22638	A	8800	342	191	STSLSLPKCWDRREPPCPANLSYFFKD PFSKCNPLRLRYWGLGLQHRNFG
8738	22639	A	8801	104	332	AVPLTMVKIQPLWKRVWRFHNKSKLELP CDPAISLLSMYPKEMKSLCQRDVCTPRL STGPLTIAGMWNPPKRSSMD
8739	22640	A	8802	563	258	PFLNLETRS WYVAQARVQWLF TGT VTH YSLDLLASSHPPISASGVAGITDACCAG LTLPLFLKGLGLGGGVGYPSYFGLLEG FHNDCSRVRVLCMWSYQ
8740	22641	A	8803	2	199	ARGLLVRRFLSPSEKRSIRVGVTRFSRC RPSPLSLTRKGNLTPCASQVRQCLALL RLAHGACTH
8741	22642	A	8804	266	108	KLVVSKCVALPPSFSSSCSSHIGCACFP FTFHYDCKFPQASQAMLEQAVEP
8742	22643	A	8805	1	140	KVVWFKRPGVYQGQCSEICGANHSFMPI VLELIPLKIFEIGPVFTL
8743	22644	A	8806	2	90	SSAAAEENNDKKEEAETEDDMEFGLF D
8744	22645	A	8807	229	34	KKKIFFFFPGFFWPPQKFFFKAPPPFFF FFFFFFFFFFFFFFFFLDFIYLIILSYTK LISIRAAPI
8745	22646	A	8808	43	173	NADSGHAQWLTPGMPALWEAEAGGSQDQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ETETILAGAGKPRLY
8746	22647	A	8809	259	134	IYMI FKNKFFNRDRGLPMLHRLVLNWAQ VILLSWPPKVLGL
8747	22648	A	8810	391	193	VLPKIPGIQFPPPCRFKKRPRPRFKKPP PKRKKISFSNPPKIWPQGYFKRGPPRL FYFFFFVVL
8748	22649	A	8811	304	3	TTPPTNIFCFLFFIFIFLWYFIFIFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF QCFIGHDDQKMMVHTHTQTSSHLLQGG NPQGGKQSPGWVLWCA
8749	22650	A	8812	395	268	FLVETGFHHVQGAGLELPASSDLPALTS QSAGITGVSHHGWS
8750	22651	A	8813	782	1174	LSRLFYFCVLFCLYMKTTQLPYFRGLVC LFVLRQGLTLSSRLECSGMIAACCSLNV PGSTDSPTSASRVVRTGVRHHTQLIFV CFVEMWFHYVAQAGLEPLGSSSPALSS QGAGITDVSHHTPLELCF
8751	22652	A	8814	95	236	ATMPGLKNIYFLKNKDKGLTMLPSLVLK SWARVILLPWPVKVLGLQT
8752	22653	A	8815	381	58	SCLLFPPFWGARGGGPPRAGGSNPPGPP GLTFPPPKPKNYWARGGGPFIPPPREG WAGGFFLPRRGVPLAPGSNNLELGLPLP SPPGYQKKTFFSKKKKKEKKRKR
8753	22654	A	8817	441	158	FFFFLRTDGYLTMLPRLVSNWPQAILL PQPPKMLGL
8754	22655	A	8818	415	342	RLVLDSWAQEILLPWPVKVLGLQV
8755	22656	A	8819	400	171	NFFFPFGVKFLGGGGPQFPFPQKRGFQ KTPGGFFKPPPKKKKFFPPPKIGFPQ GIFKKAPPPPPPPPPPPPPPP
8756	22657	A	8820	2	268	INIILAFITISLLGILVYRSHLMSSLLCL EGIILSLFIATLITLNTHSLLANIVPI AILVFAACEKKKKGGAVLKDPPWGGQSLR VLAR
8757	22658	A	8821	2	258	LCLPNQAWAMAGSPPASLLPCLISDC CASNQRDSVGVGPSEPGVGYSLVRRFL SPSEKRSIRVGVTFRSSWVRWLRTVIPAT
8758	22659	A	8822	250	456	GGGDKFGLIETFPFGLKPFLLNLLSGW ELGPLAPPFKFCFFKGRGFPLPRFVF VANLLLTCKKRD
8759	22660	A	8823	492	376	QENCLNPGGRICSELRSCLCTPAWATER ACLKKQNKTNQ
8760	22661	A	8824	1	116	LTPLPSPAPPSVDDNLKTPPEWVCSLFF HPQRMII SRN
8761	22662	A	8825	2	191	FLVETGFHHFGRAGLKLNSGGALTSFAF QRAGITGVITGVSHCFEVNRVWTGTQYF LCYILKS
8762	22663	A	8826	393	75	PRFFPPPPKIFFPPPPFFFLGGFPPI PPPPKNFFPKPPPGFFPPPLKKKIFF PPPPFSPPNFFPPPPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFSI
8763	22664	A	8827	81	380	KIITKHNLARTNPYTFCTMNYLKKKKKK KKKKKKKKKKKKKKKKKKGGGPFLLK NPGGGQNNPGGKNFFFFGGGKKNPPG FFKKKPPFGGKFGAPPPKN
8764	22665	A	8828	354	13	TKPKTPPLTKGPRRGFLAPRVPGGGGPI TPPPQNLGEGKTLARKKVFPGRPAKP RPPRKNKGFEMRPLKKNPGPWKFLGFF



<b>SEQ ID NO: of nucleotide sequence</b>	<b>SEQ ID NO: of peptide sequence</b>	<b>Meth od</b>	<b>SEQ ID NO: in USSN 09/515,126</b>	<b>Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence</b>	<b>Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence</b>	<b>Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)</b>
						LANPPGFPGPKKKKBPENQTHKKKCQRKRPRF
8765	22666	A	8829	1	215	KHSTTHSHCPRTIKLKKKKKKKKKKKKKKKKKKKKKKKKKKGGPPFKTLGGPPFPSPGKKKKFFFFLGGL
8766	22667	A	8830	1	127	ILFFWQRRGLALHLRLVSNWSAQVILPFRPPRVLGLQVIYFK
8767	22668	A	8831	264	55	FFFXXFFFFFFFFFFFFFFLVFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFWCSCSYVLIFIQPFIKSFH
8768	22669	A	8832	399	85	PPQKNFFFFQAPKISGGGGPQIAPPQKKGSGFKTPGGFFIPPOKKKKNYFPPPGKMGPQQGFfKRPPPLFFFFFFFFFFFFFFFHNRHLfKVKhLQNSFHLVQLRL
8769	22670	A	8833	47	288	NCLYRTKKKKKKKKKKPPYKKKTLRGPNFPPAGPPAPLPPLSGGEKKPSRGLLRPP TLGGAAGPPPPPKLTPLRKKKIF
8770	22671	A	8834	1	146	INITLAFTTISLGLIVYRSHLISSLLCL EGIIISLFIIATLITPSTLC
8771	22672	A	8835	2	79	EDPKTSKPKEIIQTTRRGPLPPSVSN
8772	22673	A	8836	1	156	PTRPPIITPILTLFLITQLKILNTNYHLPPSPKPIKKKKKKKKKKKKGGGP
8773	22674	A	8837	152	292	AKTFNFYKVEFINVFNGLCLLTIKNTLPKKKKKKKKKKKKKKKKKKKK
8774	22675	A	8838	1	122	VASNSTHPKAKENTAPHHTHTHTHTHTHTHTHTHTHFMAlFK
8775	22676	A	8839	2	106	HVGQAGLELLTSGDLPTSASQS SVGITGV SHRAWP
8776	22677	A	8840	364	224	APLCGRQCICDCCTYPSPHTYIHHTHTHTHTHTHTHS
8777	22678	A	8841	266	1	NSLSVEFLILFPPYNYS PKQCICSHQNC LNFWVIKCVNTPHPNFLNLMP LLAKRG AHACDPNTFGGGGRWITRSVDRDHPGOH NETP
8778	22679	A	8842	343	52	KTGFRHVQGPGELLASSDLPASASQSAG ITGVSHRVRPGLHILDNSSPLDTSFADIFSVELYLKAGIASLLHIYIHFLPLRDLL LVSSLTVSFPPTAV
8779	22680	A	8843	256	35	LFIFSLSLQYIFCVCGVCVFM SLCLFLV CAWHVQLHVCSVRMCVCENDVCVCGW VQMCFCIKNFQKEVYQI
8780	22681	A	8844	333	11	PIIKKKAPPPKGRAFFFFFLKKKKGGPP PPQKKTGGGGPKKRGGVKPPPGFFPPGF FGPLFFWGPPFLPPFFFFFFFFFFF FFFFFFFFFFFFFFFNFI STKNLF
8781	22682	A	8845	15	288	RCGLTVLPMLVS DCWAQVILLAQP PRVL GLQAGASASTPITSVNCSQA IYPEVGT TGSTIIAAASSGGEFD SVLQNDICM CFL TQQHFH
8782	22683	A	8846	1	397	ECAHHTQLIFLFLIESSLHHVQGAGLKL PISSDPPTSASQSAGTTAVSHHA
8783	22684	A	8847	1	179	ARERERERERERERERERERERERERER EREREREREREREREKKKLGGG GG GPQFPPIGGGLTQGGGGG
8784	22685	A	8848	2	233	HEERERERDRERQRERERERERDRERER ERETFSSSGGPKETTLFFETGAPKEGYQN MHARLIPS AVPFKKRG RG
8785	22686	A	8849	2	180	HEERERERERERERERERERERERERER

<b>SEQ ID NO:</b> of nucleotide sequence	<b>SEQ ID NO:</b> of peptide sequence	<b>Meth od</b>	<b>SEQ ID NO:</b> in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ERERERERERERDFVFYRWGEGHTDRQYCSELFPGWCHCPM
8786	22687	A	8850	2	79	PEERERERERERERERERERERERERERE
8787	22688	A	8851	1	178	ARGERARLFARGEKKKHTGGGPFLFYLYI
8788	22689	A	8852	3	76	TRRERERERERERERERERERERESP A
8789	22690	A	8853	5	227	EERERERERERERERERERERERERERERDFFFFFFLEKKYLFSPIGELKGRGGGSLTPLLTKWNPCPPPH
8790	22691	A	8854	1	189	ARGERBRHSRLFRESVCVARAGGASSPPRG
8791	22692	A	8855	2	271	HEEREREREREREREREREREREREREREREREEPRGEKYCIRVPPQKILSPACDSL LYVTHNLCVSHSTPRGERYVALFNSRETRCF
8792	22693	A	8856	2	309	HEQQQQQQQLRNLRDLFLLVYNRMTELCFQRCPVSLHHRALDAEEBACLHSCAGKLISHNRLMAAYVOLMPALVQRRIANYEAA SAVPRVAEQPGVSPSGS
8793	22694	A	8857	44	203	GYSTCVGMHAHTHIHTDTHTAHTYIHQCLIQIGLCTFATCTSQNKS SMAEL
8794	22695	A	8858	329	182	IIFVCLVERGLHYVGQAGPELKASDDLPL ALASQSAGTSGVSHCVSKMS
8795	22696	A	8859	1	175	GLTLPPRLGCHATITAHYSNLNPGSSNPPTSASQVAGTTHSRPCETQTALQRGPHD
8796	22697	A	8860	3	350	HEATGLRSNIKNGLDHFPLGTPTTPLIP ILAMIETILLVQPIALAVRLTANITAGHLMLRNGSATLAISTISLPSTLIIFTI LILLTILEITAGALIQA VFLLVGLYL RNA
8797	22698	A	8861	139	3	TFKEADIKGGGPPHLASF CFIGRDGVSE CWPGWSRTPD LKRSTRA
8798	22699	A	8862	3	134	SPTPPPSSKPSSI PRKSSVDLNQVSMLS PAALS PASSSQRHES
8799	22700	A	8863	346	219	RLVPPCLDNFLNFRCRYSCLTMLPGLVSN SWAQVI FLPPPKD
8800	22701	A	8864	1	147	GTRFFFFERGIDHVQGAGIQLLTLGDFFT PASQRAE ITGVSHHTWPNFI F
8801	22702	A	8865	267	132	KKKFWPFFFFFFFFLRDGVSL LLRLVSN CWAQEILLWP PKLLGLQV
8802	22703	A	8866	343	215	LAQGLKTPIPKRVPPHQKKKFC SERPTR IQTDRCWVSPLS
8803	22704	A	8867	1	242	GTSKKIDKLDYIELKCFCTAKETISR VKRPVEWEKI FANSSPEGLISRIN KEAKK LNSSAIAAHNCNPSTLGQVRRIT
8804	22705	A	8868	1	219	GTRRP TWATWQNPA STKKN SFFFETE SRTPVQAGGQGN LGSLQSLP GLKRFS CLSMGAPKGQSGSLMG
8805	22706	A	8869	1	181	ATGGII LLLDDVVSLAYESKHLL EGAKSESAEELKKRAQELEGKLNFLT KIHEMLQ PQDQ
8806	22707	A	8870	1	255	AAAPPNA PGPPGPQPAPS AAAPPPPAHALGMDAE LIDEALT SLLELGL HRVR

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						ELPFLFLGQSEFDCFSDLGSAPPAGSVS C
8807	22708	A	8871	383	233	ATTFFNPNGFLFVRLFVLVQWPDHEPPGF KQSSHFSLPSSWDYRHPPPPP
8808	22709	A	8872	211	294	AXKKKKKKKKKKKKKKKKKKKNIIWGG
8809	22710	A	8873	398	100	QKERPPPGFPFKPGPPQKRGKGAPPKD GEHYFFWVLEKSTGFPPPKTKRVYYPSPV YPHPAPQKEGFPGGSPPPRPIASPFQG KKKEKKSYLEKENLF
8810	22711	A	8874	3	214	DANVLGIIVYRSHLISLLCLEGIILSL FIATLITLNTHSLLEKKKKKKKKKKKK KGGAFKKNPGAQI
8811	22712	A	8875	2	254	PRVRPEGRNRTPQSWFQANPMACMTFSK KKKKKKKKKKKKKKKKKKKRGGGFIKKM GGGNFREKEKKNFLLIRGKIKTGGDF
8812	22713	A	8876	2	135	TINLPSTLIIFTLILLTILEIAVALIQ AYVFLLVLSLYLHDNT
8813	22714	A	8877	2	296	LARGAEVLGYGSHSRGPVGALVGQGAG RLFTEHPGSSPATLAITYPTPEGTSVAVS ISAPPKARSRPYPPSRSCHNLFLAGSSV LVPPGPGVHRWGRP
8814	22715	A	8878	164	29	RKIGPARWLTPVIPALWETEAGGSRGQE IEIILANTVKPGACEVL
8815	22716	A	8879	381	219	GEKMTREEVHMLVAGHEDSNGCINYECK R
8816	22717	A	8880	2	156	ANGNSFATRLSNIFVIGNGNKPWISLPR GKGIRLTVAEERDKRLATKQSSG
8817	22718	A	8881	3	402	SGFNIEYAAGPFALFFIAEYTNIIINT LTTTIFLGTTYDALSPELYTTYFKKKKK KGGRRPFFFFFFLKKKKIPPPKKKNFGKK GETLKGRGGAPIFQPKKILSPKKKKKK RGGAFKKSLGGAKFNGGGRN
8818	22719	A	8882	1	406	RYSTPSEGEVGERYSTPPGETLERYSTP PGETLERYSTPPGETLERYSTPPGETLE RYSTPPGETLERYSTPPGEALERYSIPT GGPNPTGTFTKYPSKKKKGGGRFKEPLG GPREFGVGRVKVFSLWGCVLNAR
8819	22720	A	8883	484	307	KKILNRRVRWLTPVIPTLWETEAGSSRG QEMETILGNTVKPPASASQSAEIKGMRI IIF
8820	22721	A	8884	1	131	GSLTHHINNIIKPSFTRENTLMVIHLSFI VLLSLNPDIIITGFSS
8821	22722	A	8885	406	106	KGGAGPKIAPPKKKAFSPIDPPFFFWPPP VFLKGPPPPSPFNFFPPPVFFFGRGLFF FFFFFFFFCETVVLPFRPSNLVFTLPHVF AWLIPIDQYLFIHSC
8822	22723	A	8886	425	325	SSTHTHTHTHTHTERTSHLLAFEPSAG ELWMAM
8823	22724	A	8887	394	278	VVCVCMCVYICITYPCWLPCWHMCLELY KVFKGIMKGV
8824	22725	A	8888	2	86	YSRTAAALIQAIVFTLLVLSLYLHDSAY
8825	22726	A	8889	400	62	FLYLKSFPPPPERGVFSLPPQKFFFSF KALNFLGGGGPKFPPPKRFFFKYPRV FLYPPHKKNYIFPPPDDFGPPRVFFKA PPPHFFFFFFFFFFTTTTTRLEWVQ
8826	22727	A	8890	3	100	SLEPGTSGLGFSCLTLPSSEDYRHEPP CPAN

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8827	22728	A	8891	32	142	VRPTRPGQVASVLYFTTILILIPTISLI ENKILKWA
8828	22729	A	8892	3	382	TPHNPLSRPSYEPKPASTPSRAPKKKKK KNPKKKKKKKKKKKKKKKRGALLKKT LGGPKLPGGKKKNFFFFRGGKKKPPGDF LKKTLFLGGGNLAPPPPKKNPWGKKKI FWGEGGKKNFFFG
8829	22730	A	8893	368	199	KKKRISPPSRKRAPQGDFLRPTPIKNI YYLSFFFLILYIFFFFFFFFFIFFF
8830	22731	A	8894	3	136	TINLPSTLIIFTILILQILEIAGALIQ AYVFTLLVSLYLDHNT
8831	22732	A	8895	1	144	TATINLPSTLIIFTILILQILEIAGAL IQAYGFTLLVSLYLDHPYN
8832	22733	A	8896	153	375	PQKKKKKKKKKKKKKKKKKKWGGGF LKNSSGAPIFGGGGKFFFLGGGFKTP RGFFGKNPFFWGGKKKN
8833	22734	A	8897	332	400	WLTPVIPXLWDAEAGGSFEVRS
8834	22735	A	8898	215	359	TELVNPAVLFCLPCSSGHHLLCAIAHAK RVTIMPKDIQLARRIRGERA
8835	22736	A	8899	414	73	PRLLCFHKKAWAMAGALPPALLPPYSLI SDCCASNQRDSVGVGPSEPGVGNLVVR RFLSLSEKRSIRVGVTRFSRCCPSPLSL TRKGNSLTPCTSRRLRQCLPLLWLAHGARTH
8836	22737	A	8900	374	88	VSPSPPLKIFFSPKAFNFWGGVGPHEFP PQKRVLPQKPPGGFFSPPLKKKKFSFP PVKLGPPKGSFKGPPPPPPPPPPFFGL DFMYTGSSNVW
8837	22738	A	8901	433	56	PEGPPPPPGFYPGKRGFFFTPLVVFGGP KRDPPPRGKKNPSWRSGGKQTPRFPRDP LLKAFFPGGPPQRLGKAQGFWFFFGPK KGKTQTGPPFFFKLGDWPCKKPPPG GAPRLGPPKKKFL
8838	22739	A	8902	3	73	IAVALIQAYVFTLLVSLYLDHNT
8839	22740	A	8903	3	149	PNLSYIIGKDTWVEHWPEDEQCDEENQ KQCQDLGAFTESMVVFGCPN
8840	22741	A	8904	351	137	FPPEFFAAPKSGILFFSKTWMEVEVLF LSQLMLGQKTQYCMFSLINGRLIIPAG SLKGDHHPPLGLLEG
8841	22742	A	8905	142	5	KIFLQKKKKKGLGTVAHACNPSTLGGQ GGWIMRSRDQDHPGQQW
8842	22743	A	8906	367	244	HVPQARAKFFCIFS RDGVSPYWPWSRT PDLMICLFFIVEL
8843	22744	A	8907	146	248	SQILGRRLRQENCLNLGNGCSEPRWCHF LAWAKE
8844	22745	A	8908	2	197	AAASTHHARLFLCVCLFAYLLVEMEFHH VAQAGTELLDSSNPPPLASQNAGIIGMS HHTQPQYIC
8845	22746	A	8909	1	127	KKTRLERAQWLTPVIPAFWNAEAGTLL ARSLRRLPWPNNVL
8846	22747	A	8910	368	280	LTMLRLVLNSWAQAILLTWPPKVLGLQ A
8847	22748	A	8911	355	211	QQQNLHLFWPGTVAHTRNSSTLGGQGM ITGAYEFETTLGNTARPHLY
8848	22749	A	8912	325	190	KKKKKKGGGPGQKKKNPPPPPTSKKKK KKKKKKKKKKKKKKKKKK
8849	22750	A	8913	1	411	VNVPAPRGGAYRGRQASFSSGGLHPVPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YRPLCLPNQTTNSAMAGAPPLASLPPCS LISDCCASNKRDSMGVGPSETGTGYNLL VCHFLSPLEKCSIRVGVTFRSRLSPL SLTKKGNLSLTPCTSRVRCIALLRRL
8850	22751	A	8914	258	9	GAIPCLHCETNPSSHISSTQELQTPPEPQL PGVPLELPPPGSCFKCRKSGHWAKECQ PGIIPKPCPICAGPHWKLDCTGPRL
8851	22752	A	8915	326	42	EKIHRYFCYSFFVFLVEMGFYFVGQAS LKLASSDLPASPSQSARVKAMSHCVRP VLVIFKNKILQNTENSTKIYVYPPNNQ ILTFCHFCFK
8852	22753	A	8917	3	106	GLELPTSGDLPASASQNAGITGISHHAR PIMTYS
8853	22754	A	8918	320	171	AASTDGSYKCLCLPGYVPSDKPNYCTP LNTALNLEKCPGLPHLSGSS
8854	22755	A	8919	1	201	VKPSDRYHLMPIFTAAYPHQNSTYNVPV STRMVMAEEFKQKRLSLCSDLYRKDLR TIVDPVVSCAT
8855	22756	A	8920	3	182	LLRPLEKRGIRVGVSFRSRYHLSRLPFA RKGNSPTPCASRVRCPSLLHGLHPLSD KPQ
8856	22757	A	8921	142	1	SCHPGWSAVVRPQLLRLRLRYENCLSLGG SGCSELGSCHTPAWTTEG
8857	22758	A	8922	1	117	LEFNAYAGWSTLLSRLSLNSWVHVILT PWPPKELGLQA
8858	22759	A	8923	357	121	LGAFSDGLAHLNKGTFATLSELHCDK LHVDLENFRLLGNVLVCLAHHFGKEFT PFVQAAYQKVAGVANALAHKYH
8859	22760	A	8924	343	133	LEFNFNLETRLREWLIFVFSVETGFPI KRAGLKLQASSDPPARGSQSAEISGMSH YAWPCKSNRAFKCS
8860	22761	A	8925	321	44	PDSGGSPASASQVAGTTGACHDAWLMFI FNMDININIPPSAKRDKLSMDKINEIIF SLLINRISSFQIMYFLCSSRIESRKRWL KQTGRKKE
8861	22762	A	8926	335	106	HFVFLIETGPHRVGHAGLELLTSTDPPA LAYKSSGITGVSYRSFTKLHLACVCLC ITYTLGLVLSFTPGSWEKKT
8862	22763	A	8927	2	160	LSRVPPRSANLSISVFAEKRCFTMLPR PISNSWAQGILLPSQAPKVLGLQA
8863	22764	A	8928	3	140	RVITEEEKNFKAFAASLRMARANARLFGI RAKRAKEAAEQDVEKKK
8864	22765	A	8929	126	59	NSGGGGCNELRSCHCTPAWATE
8865	22766	A	8930	3	104	KNMACYCRIPACIAGERRYGTCTYQGR LWAFCC
8866	22767	A	8931	311	112	MENYLSKMQQELEKNITRELKEAAAELE SGSIASPLGSTDESNLNQLVWKASREY VQVLKKNYMI
8867	22768	A	8932	345	134	GGGSSPWFPFWRPRRADSLRVGVNLPP GPGGAPFFLNPLIGWGGGARLWFQLI LLRVRPENSFDPR
8868	22769	A	8933	262	39	RPRRPHPGNFFFFFNSGSHYVAQGLEL LDSSDPTLPSQSAGTTGMSYQAWPLDHT FENRDCVLLHCSSPVSNT
8869	22770	A	8934	84	22	TPAWVWWLTVPVLPALWEAKAG
8870	22771	A	8935	277	111	ERIINHAAGSHGVSGIFMKYDLSSLMVT VIEEHMPFWQFFVRLCGIVGGIFSSSTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8871	22772	A	8936	2	106	DSAIPIRRLECLKEDVQRQEREKELQHR YAEFVF
8872	22773	A	8937	1	193	LMWDFSPSGLDGAFQRGYYWYNYINV KKGSISGFTMVLGAYMLFIYCLSYKELK HERLCKYH
8873	22774	A	8938	240	69	DSGNQLKRSFSGRARWLTPVIPALWEAE VGESLEVRNIYIILQNMNIGNIHLIK
8874	22775	A	8939	329	177	RWNLAAMLPRVLNSWAQATCPSWPLKML GLEAEPSPARTNFKVTSPLRH
8875	22776	A	8940	358	120	HPSNFFVFLVMGFHHVQPGLELFPAR YVPTLAFRSGGITGISHCAWPKEWALPR KASPLSGRRGSPHCATCSSKAW
8876	22777	A	8941	333	104	PHVYSNGHICLSILTEDWSPALSVQSVCLSIISMLSSCKEKRRPDNSFYVRTCNK NPKKTKWWYHGKQFEFVITF
8877	22778	A	8942	1	241	APLVAFTQVNLEDKGGLSKLVEAIRINF NDRYDEICHHWGGNVLGPKSGTRIAKLK KAKARELATNWIKCTLLSFLYIKR
8878	22779	A	8943	1	240	APLVAFTQVNLEDKGGLSKLVEAIRINY NDRYDEICHHWGGNVLGPKSVTRIAKLK KAKARELATNWIKCTLLSFLYIKR
8879	22780	A	8944	306	150	AASTLCPRLECSGAIMAHCSLNLGSGD PPASASQVGARGSLPEGRWRLQ
8880	22781	A	8945	284	2	GKSRSPDLCTSGFTGSTHFTLLICWV PRYVATCPPIGLNFVFIKTWWSHYIVQA DLKLMVSSNPPVSASQSAGNTGMSHTW LENRLLTTKK
8881	22782	A	8946	1	226	WSFALFAQAGLEFLTSGDPPASASLSAG ITGMSHHAQPAVSLNSIFSASTFCATSS YCAKMEKELKFMLIVDAA
8882	22783	A	8947	363	96	NTAPGYMPLLSIPFLVLSKAVFLFLGMEFTAALLIIAQRWEQPKCASTDEWINKMW HMHTMEHYSTCCGVHAAVNISIQISEWN CWEW
8883	22784	A	8948	1	208	GRVGQPLRLLTSGDLPASASQSAGVAG VSHRAQPTPALNCVLTWCVLQHYIKHNH GKRSEYFTIFNDM
8884	22785	A	8949	69	298	SRGHQRVADAALLSFPDVICLGLMLWGS SSIVCILHRHKRRVQHIHRTSVSPSTSSP ESGATKTILLEQERTSRPS
8885	22786	A	8951	2	201	LYDLLNMRISLPLSLVCIHSHTHEHT YTHIHTHAHTYTHTHSHWVLSLKQKKMV KHRPRLSVWI
8886	22787	A	8952	1	285	GASPPASLPPCSLISDCCASNQRDSVGV GPSEPGAGYNLVRRVLSPEKRSIRVG VTRFSRCRPSPLSLTRKGNLSLTPCASRV RQCLTLLWLHV
8887	22788	A	8953	341	256	LGLGGGGCSEPRWHHRTPAWVTERDFIS L
8888	22789	A	8954	227	43	ILFFIGKHTHTHTHTHTHTHTRAKCLFP PARFPTSPNSTTNCFTPEPAANPRGLV RAGIG
8889	22790	A	8955	310	79	RPRRPGLMERVNVFIFSLRESFYKIRI TNQAQCCMPIVPVTQETEAGRSLEPKSL RLAWAIQQNSISKNNNNFF
8890	22791	A	8956	374	198	FFFFLPNRHGLAMLRPMVLHWVQAVLPQ PPKVLGLQG
8891	22792	A	8957	138	10	RPRRPRLCQAQWLMPITIPALWESVAGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LEARSLRPAWFFNT
8892	22793	A	8958	354	216	AGPRVFPGGEGGFRPPPPGGSPQGPBK GGESGGKPPPAHWVFF
8893	22794	A	8959	364	223	LQAARSKKKKKKKKKKKKKKKRGGGK
8894	22795	A	8960	259	11	FEALKDPSNNLQSLFSFIVTLVTAHVY EKLSTLTSLAARRGLAMLPRLASNSRTQ TILLPWPSKVLRLQARATEPGLGLLL
8895	22796	A	8961	334	213	AASTKNFERMEWGLTTLPLVLNSWPQV ILLPWPPESMRL
8896	22797	A	8962	260	3	KGGFFPIPFIGIKPGFFSPALIFPKVF IFSQNFFVFLKKIFFFFVETVSSHVVK AGLELLASSNPPAFTSQSAGMTGMSHHA W
8897	22798	A	8963	425	248	ADEWIHKMRHIHMIYYLAIKRNEMLIH ATAGMHLENILSEKDHMYDSIYMKCLAW ANL
8898	22799	A	8964	1	118	GKLMELHGEGSSSGKATGDETGAVERA DGYEPPVQESV
8899	22800	A	8965	2	130	GRVGPRMALNSWAQVIHLPPPKVLGLQ VAMKRKIMILSTSY
8900	22801	A	8966	119	364	LGWYLIEKTIQCCSPCLGADPFQQMISP LRDGLSTVLPLVLNSWPQVFLPPQTRK VLGLQAEVTAPGHIIFMIIMINTFK
8901	22802	A	8967	238	333	TRCLRLPLRLVLSNWTQALLPSPPKVL GLQV
8902	22803	A	8968	297	169	NPPPHIYKFFFIENIFFFFFFFFF FFFFFFFMSKILIF
8903	22804	A	8969	2	212	RVRPRDRPLVRVRVGRNKDGAETTPSPG LLPAHLTFPLDYHLNQPFIFGLRDTDTG ALLFIGKNMDPRGP
8904	22805	A	8970	242	357	TLDTIKSFKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKII
8905	22806	A	8971	191	265	ILMPXKKKKKKKKKKKKKKKKKKKKR
8906	22807	A	8972	398	97	MFLYNRILWFFSPHPPLRFFFSPRATIF LGGGAPHFPPPKKGGFSKKPPGVFLSPP QKEKIFSPPPLFLAPPKDFKSPPPFF FFFFFFFVSTGSSVS
8907	22808	A	8973	370	265	YNSSLPSWDYRHVPPCPDNFCIFSRGW SQTPDLR
8908	22809	A	8974	3	119	GLKLLTSSDPPASASKTAGITGVSHHTQ TIFVFSSHKS
8909	22810	A	8975	1	110	VAQAGFKLVSSANLPTLASQSARVTGVS HRARSMKQ
8910	22811	A	8976	3	152	WNQPKYPSTGEWMEKMWIYTKLVQPM HGPHVAQDGFEGSPTQIHKLS
8911	22812	A	8977	375	193	FQDLPLGSTSNISFFKRWSPAMVPRLIS NSWPQEILLPQTPKVLGITGMSHCTWPG GHISI
8912	22813	A	8978	2	395	RAALPTQASAMAGAPPASLPCCSLSSD CCASNERESVGVGPSEPGAGYNLLVCYL LRLEKRSIRVGVTFRSRLSLTR KGNSTPCASRVQCLALLWLTLALYP LSCTHCQTLPSEMNLPQL
8913	22814	A	8979	120	19	ARVQWHDHGSTATLNSWPQVILLPPPK VLGLQA
8914	22815	A	8980	204	48	LNRDKGLTMLARFVRNSWPQATPLPWP KVLGLQALATAPCQMSFLRAPLS

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8915	22816	A	8981	335	221	FFFLFLFFCMITSHCSVNVLGASDSPTS VSHIAGTIGT
8916	22817	A	8982	360	150	LSHMPLLFVSLYPDHRAFMQVIFFFFT ESPSVTRLECSGAILAHCNVCLPGSSDS PASASYAGYSFYL
8917	22818	A	8983	346	116	GQGRGVETESCSVTQAGVQWCDHHSLLS LELLGSSDPSTSASPVTTGTHYHTSS HFLFSVSSSYFPTPVCLAYR
8918	22819	A	8984	350	263	LPMLPRLVSNAPQATFLWPVKVLELQ A
8919	22820	A	8985	3	159	EEYNLLVCRLSLPLEKCSIGVRVTQFSR CHVSPLSLTRKGNLTPCASWVR
8920	22821	A	8986	2	253	KHVVGELKNDLSICGTLHSVDRLNIKL TNISVIDSEKYPHMLSVKNCFIQGSVVR YMLPADEVHKQLLQDAARKEPLQQKQ
8921	22822	A	8987	2	115	GARIVGHLTHALKQGEYGLASICNGGGG ASAMLIQKL
8922	22823	A	8988	3	159	GFYHIGQAGLKLMSGDLPASASQGAGI TGLSHCAQAGIFFFLPYDIFTVF
8923	22824	A	8989	1	123	SHYVAQAGPKLLGSSNPPASASRSAGIT GVSHHAWPPSLFL
8924	22825	A	8990	462	303	LARTPSRPTRPPTRPPTRPPTSPTRPP FMLSVDCLLLY
8925	22826	A	8991	382	178	PPFFFYFFFFSFFFFFQKGFKGF PQKFFFFFGGKPKVKNFQKFFLRKKG GEKKPPQNKVF
8926	22827	A	8992	532	432	RDAGLTMLPRLVSNWAQVLLLPGPVKV LTLQV
8927	22828	A	8993	418	172	KKGKKKKKNIFLIFFNYFFLIFFFIFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFGGAWSLFRGGDSGEVKGTDSMS RQCFQGF
8928	22829	A	8994	2	722	AVRLNISYPPQNLTMTVFQDGTASTTL RNGSALSVEGQSLHLVCAVDSNPPARL SWTWGSLTSPSQSSNLGVLELPVHV DEGEFTCRAQNPLGSQHISLSLSLQNEY TGKMRPISGVMLGAFGGAGATALVFLSF CIIFVVVRSRKKARPVAVGVDGTGMED ANAVRGSASQGPLIESPADDSPPHAPP ALATPSPEEGEIQYASLSFHKARPQYPQ EQEAIGYEYSEINIPK
8929	22830	A	8995	498	323	EPKAELNEGDIADVHIKREEGWFKGTLQ RNAKTGLLPGSFVENI
8930	22831	A	8996	21	511	LIIDGVEAYALNASGVVNIIVFDPKGWA LFRSFKAVKEKLDTRRGSNSELETAVKD LGKAVSYKMGYGDVAIVVYSGQYVENG KKNFLPDNTMVLGNTQARGLRTYGCID ADAQREGINASARYPKNWVTTGDPAREF TMIQSAPLMLLADPDEFVSVQLA
8931	22832	A	8997	178	306	GAINATNWPPFNNVGMGKTLGFPNLMAL KQIPFSPVGEKTKRR
8932	22833	A	8998	351	211	SIQSLRMQPVPCYISGRHHHHYSHHHIH HHHYSSYFLKYPQEYLRPL
8933	22834	A	8999	1	381	FRLFKFALMELCSIEGTSDDQLFFVFGF FFFGKEASFGPQGGREGGKFKLMEPLAK GVKGISCCKPPHPCLNPPKPKRGESSP PEGPKKTGAPGPAKGLFFLTGKNPWP GPGKTRKKAFFPKNF



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8934	22835	A	9000	173	399	IKSEWAAKKKKKKKKKKKKKKKKKKKKKK KKIFFFGGGRFFFWGGDYFWGGGGVKK KGGGKKNPGPQKKNNGGGKK
8935	22836	A	9001	2	81	EFTPAVHASLDKFLASVSTVLTSKYR
8936	22837	A	9002	3	835	DAVRANDDLKENTIAIVERNNLLQAELE ELRAVVEQTERSRKLAEQELIETSERVQ LLHSQNTSLINQKKKMDADLSQLQTEVE EAVQECRNAEEKAKKAITDAAMMAEELK KEQDTSAPLERMKNMEQTIKDLQHRDL EABQIALKGGKKQLQKLEARVRELENE EABQKRNKSVKGMKRSERRIKELTYQT EEDRKNNLLRLQDLVDKLLKVKAYKRQA EEAEEQANTNLSKFRKVQHELDEAERA DIAESQVNKLRAKSRDITKGLNEE
8937	22838	A	9003	429	280	RGFRGHKFLPPGFGFPPIPGPPSPPF GSPPOKNFPLQPKPLGFKPPP
8938	22839	A	9004	2	108	LSAYQGTPLPANILDWQALNYEIRGYVI IKPLVWV
8939	22840	A	9005	3	158	SSTQGHKHCGRPQGPPLPRKTRDLCSPVY LLTFSPLLSYDPVTSPSPRNTQE
8940	22841	A	9006	3	370	LLLTGLNRLTDLYSLYIPTTTQWGS LTHINNIRPSFTRENTLMFIHLCPILLLS LSPDIITGIFSYTRHYVNSSTYLETNER GGSYKNRLGGPESKGLRIKDDSLCWGPL HDTSAAYENK
8941	22842	A	9007	363	76	KLFNVGGGGGLDKPPPPPKKFFFKKNGLF FFYPLKKKNFFFPRELLWGPFRFFIKT PPPYFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFVMIS
8942	22843	A	9008	1	87	KMLKKPKFELGKLMELHGGSSSGKATG D
8943	22844	A	9009	420	3	RFYFPKPRKRGGGVFFFPKKKKFFFL NPPPPFFFPKKKKKNIFPPRKGGRGS KVQTMGPPLFFFFFFFFFFFFFLFFFF FFFFFFFFFFFFFFFFFLRETSSNNV LAYQIENSLLKLDLQRQCLPLPGRV
8944	22845	A	9010	2	74	LHRLGGPEAGLGEYLFERLTLKHD
8945	22846	A	9011	33	132	IDRCRNSARAPLSLAGPHPGMGDASNH MGQM
8946	22847	A	9012	83	607	RRSGTPCGYNVTSQNGTIYSPGFPDEYP ILKDCIWLITVPPGHGVYINFTLLQTEA VNDYIAVWDGPDQNSPQLGVFSGNTALE TAYSSTNQVLLKFHSDFSNGGFFVLNFH AFQLKKCQPPPAVPQAEMLTEDDDFEIA ITGEGKPTRMPQSRKKSCHTISVLISAK LNRAFL
8947	22848	A	9013	483	364	PPPPPPFLNPAPGIFFPPLGGIGARPP PPSFFFFFFFFF
8948	22849	A	9014	74	180	LLSTYVGRLSARPKLKAFLASPEYVNL P INGNGKQ
8949	22850	A	9015	488	317	HVGQAGLVLLTSGDPPTSASQSTGITGV SHRAQPLRSFSFVLSLLQKRIVLC
8950	22851	A	9016	149	13	DERGGLOAVAHTCNPSTLGGRGGWITRL GDGDHPSCRILAGDASQ
8951	22852	A	9017	20	107	FDSTADSDQVNPIQGLASKWDYEKNEWK K
8952	22853	A	9018	448	239	VDHQQVIWNRERISNSQNGIVKEIKGAD TFIFGHTPAVKPLKFAQMYIDTGAVFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GNLTLLIQVQGEA
8953	22854	A	9019	3	209	CPPLSPGCTNSARAEPVHALPDALNNL RTHGSGDGPSSSVDNWRPEDVYPQGIY VISAPSIYAREA
8954	22855	A	9020	504	20	NYAQMSYSTARASANESWAYFMGRKRKFV ASRQASQMFLCWLEEAIVRRVVTLP RFSFQEARSAWGNCDWIGSGRMAIDGLK EVQEAVMLLEAGLSTYEKECAKRGDDYQ EIFAQQVRETMERRAAGLKPPAWAAAAAF ESGLRQSTEEEEKSDSRPAAGS
8955	22856	A	9021	3	168	LPRLEAAARIRHEERERERERERERE RERERERERERERERERAPPPTLCET
8956	22857	A	9022	2	89	LCSLVYLLTFPPLLSCDPAKSPSARNTQ E
8957	22858	A	9023	508	371	FFCRDKVLATLPRLLANAWPQVIFLPQP PKVLRQLQPCTTPSLKDL
8958	22859	A	9024	2	170	RTHSAGRPYQCNCQCEKAFRHSSTLVHK RTHVGRETIRNGSLPLSMHPYCGPLAN
8959	22860	A	9025	3	185	PFAATPQGGPSPINSPTKKKAKNKNRTK KTKKKKKPPPSKKKGPQKTPKKTMGGPL KTTT
8960	22861	A	9026	104	319	LVFLSKYTPPLLVSLLWIHGLSLLSFLPS LPSFLPSLLTYLLPSFLPSFLTSTVINPL PSLFFLVFKLSQFWT
8961	22862	A	9027	476	364	SLKRLTSGDLPASASQSAVITGVSHRAR PIIYFKYVQ
8962	22863	A	9028	36	154	FLVGQAGLKLTLTSGDLPASGSQSARITA VSHRTWRTHYF
8963	22864	A	9029	2043	1237	WLRTRVAPALPERLGACTQLGPVLPSCQ PYVVCRCQPEYRRQAAQPPHCPAPEGEP GAPQALGDAPSTSVSLTTAVQDYVCPLQ GSHALCTCCFQPMPPDRRAEREQDPRVAP QQCAVCLQPFCHLYWGCTRTGCGCLAP FCELNLGDKCLDGVLLNNSYESDILKNY LATRGLTWKNMLTESLMALQRGVFLSD YRVTDGTVLCYCCGLRSFRELTYQVRQN IPASELPVAVTSRPDCYGRNCRQTQVKA HHAMKFNHICEQTRFKN
8964	22865	A	9030	15	389	IVDHYPCGGIPTSGSVTQAGAQWHNLGP LQPRPLGLEGGSSCLSLICSWGHRHAPPH LARGHFSSEVEQLRSRLQHGAVFVKQRK GTPEDPRQGLRTLISLCLHLVALALWF SLPFGHPRIHMQ
8965	22866	A	9031	3	243	RHSLAFNRFSCLSLPSNWDCHRPSPCPA KFCTFVEMEFHHVGGAGLELLTSGDLPT LASQSAGITGVSHHAWTRCCCCF
8966	22867	A	9032	1	245	PTRPAGIATCICMCMKNHRATRVGILRT THINTVSSYPGPPPYGHDHEMEYCADLP PPYSPTPQGPQRSPPPPYPGNARK
8967	22868	A	9033	46	124	QELMTHGAKSPDGTRVHNAFLFVTTV
8968	22869	A	9034	235	435	KKKKKKKKKKKKKKRRPFKLGPFKPP LKPOGGLFEAPPFGGPPPPGFFAGGGA PPRGFFKKKGK
8969	22870	A	9035	333	70	CPYIQIPILKDQVNLSSISSPFSHLIKD LWKTFLISYITELIFVCFVEMMFHHVAQ AGLELLGSSNPPTSTFQSARITGISHHA CLNI
8970	22871	A	9036	297	411	NKTMFSFAATWMQLEVLISKLMQEQKTKY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CMSSLISGS
8971	22872	A	9037	461	167	NKNYP LLGGPPFGSPSPENLNGGFPLTP GGGGPINPNSPPPPPPGRRPFLKKKK KKKKEKETNTYILQDTCRCSAVLPIMQ VKIVMICLIMHRLF
8972	22873	A	9038	466	292	NGCLLEPASWNSLANIFIFCREEGLTML PRPQVILPPLPKVLRLLPPPLSS
8973	22874	A	9039	34	124	GIRNIKFSSLSTFIAHKYYCSSHAAEH VK
8974	22875	A	9040	54	239	RRRRKLRRWGLAMLPRLVSNWHQAILW PPKVLRLQACATTPGLTRRWLHGQIWSP GAGSV
8975	22876	A	9041	469	223	PWARVCVCVSVVCVCACVRVCARASES QTCAAVPSLGPAGAPALGCCAVCEDE VGSCPHARPLPRAAVDKAAGRRGLCF
8976	22877	A	9042	491	380	SPGVVAHSYNPSTLDGRGSHITVRKFM TCLATEGAV
8977	22878	A	9043	144	360	IHSHWGYWLDVSLIAAHLAINPDCFMVY YIFSQCTDKLTEKEFIEGTLANKEILRL IQFEPQVKKEKMKNA
8978	22879	A	9044	23	263	RWNSDGKGLRPAWATWPDFVSIKNTON THTTHTPHSPHTPHGQQPFLSPTPFPW PVSSPSPFPFHSHTCLSCLLPPGA
8979	22880	A	9045	461	287	PPSLANIYLFYILFIFGRDGVSLFPRLVS NCWAQAILLPWLPKVLGLQGEPPNLALK SL
8980	22881	A	9046	485	6	NNKNSWAWWRVPVLPATREAGAGESLES GRRRLR
8981	22882	A	9047	475	307	LFLRDGSLTVLPRLVSNWFPQAILLPWL LKGLGLQARATLHMACSSCINSTQNILQ
8982	22883	A	9048	483	338	LREGERQREQERERERERERDRERAH TTAFTQLLFQYVAIILLPCY
8983	22884	A	9049	680	303	NDLLFGSLYVKQFAASGTGRVTLPEPSE EQVVCRLCFQDLFGDDHNKNGFKMFDSS NYHGQDLLFKDATVRVAVPVGKTTYRGW LGLDYVALEGMSSQQCSGAGRTGPPCR LPWCYSDPFTPEP
8984	22885	A	9050	26	165	AFGYHRVQGAGLELITSGDPFASASQSA GITGVSHHARSQYFFVYV
8985	22886	A	9051	461	83	HKINLPSHKKKKKKKKKKKKKKKKKKK K
8986	22887	A	9052	475	209	MAAPPKKKKKKKKKKKKKKKKKKKI
8987	22888	A	9053	531	404	SVTQAMQWQKHNSLQGSTLEFKQSSLL SLPTIWDYKHADLS
8988	22889	A	9054	66	416	KKKTNKIKMGGGPLPFKISPPFLKKTLS WKKGAPKTPPLEMAPFFFPQGGKNSPF KGGKIFFFFPKKTFIKGPPGGEHTPPL GGGPQIFSLPPPVGVPQKNPPPLLRGGL FFTI
8989	22890	A	9055	1	104	ILAVNETLEGVTHEQAVAILKHQRGTV TLTVLS
8990	22891	A	9056	3	106	LKRWGIAMLTGLVLNSWAQVILPSWPPE VLGLQV
8991	22892	A	9057	1	299	PTRPINIILAFTISLLGILVYRSHLISS LLCLEGIILSLFIATRIYPIAPPLPPL EPEKKKKKKKKKKKKKKKKKKKNTKK RKIKAKRKNLGGGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8992	22893	A	9058	482	146	LTSSKKKKKKKKKKKKKKKKKKKK
8993	22894	A	9059	2	290	YFLFAYTILRSVPNKLGGVLAALLSILK KKKRGGPFKRTLGGPKFNRGGQGNIFFL MGGGLKPNLGLGRNLSLGGGKNWPNLP PKIKGFRENKNF
8994	22895	A	9060	413	48	PQKKGFFQKNPKGFLKPPPKKKKKKFFP PGKIWPPQKIFKKPPPPPPPPPPPPPP PKPPPPPPPPPPPPPSIRNPPSSYTKW LRSLDVCHLLPPIPTQVPGPTPVLLFST LPDCNHSLL
8995	22896	A	9061	2	274	FTISLLGILVYRSHLISLLCLEGIILS LFIIATLITLNTHSLANIVPIAILVFA ACEAAVGLALLVKKKKKKGRPFKRILGG PQINPG
8996	22897	A	9062	42	255	QEFRTTRERERERERERERERESSGVVR AKFRSNFSAGAIHTIRVMLPPSGIYSN EKSINKCGFALLFF
8997	22898	A	9063	20	413	YALRNSARAGDPHGQLGRDGAVGGRGW LMPREALHPWANVQAWAGSPGLFLGAP WPQGGVWLPWLCVMSASSSSINGLPPQ KKKKKKKKKKKKKKKFWGGGPGPQSPF WGGLKKFGGRFLKRGGEN
8998	22899	A	9064	6	306	ECEHSTTYSHFAGGGGPFVMVGDDADARS KALLGVCVSGSTEAYVLVDPHYWGTPK SPSELQAAGWVGWQEVSAAFDPNSFYNL CLTSLSSQQQRTLD
8999	22900	A	9065	463	126	AHYQLVYTCKVCGRSSKRISKLAYHOG VVIVTCPGCQNHIIADNLGWFSDLNGK RNIEEILTARGEQVHRVAGEGALELVLE AAGAPTSTAAPAGEDEGPPSPGKTEPS
9000	22901	A	9066	23	244	SCHAGIRHEERERERERERERERERE REREREIYFLALFSQKGRVHGFKTPRG GQKRELLSNRVNTLCTE
9001	22902	A	9068	396	143	KDIQNFQAWWLTPVIPAWEAEAGGSR GQEIETILVNMVKPHLSVLLAKNSSSHC PMCWLAELOWYDLCSFKIFFGILIPG
9002	22903	A	9069	828	99	VDREPVDREPVVCHPDLEERLQAWPAEL PDEFFELTVDDVRRRLAQLKSERKRLLE APLVTKAFREAQIKEKLERYPKVALRVL FPDRYVLQGGFRPSETVGDRLDFVRSHL GNPELSFYLFITPPKTVLDDHTQTLFQG EPLPGRSGCNLGAEEPAGVYLEPGLLEH AISPSAADVLVARYMSRAAGSPSPLEAP DPAPKSEPAEERGAALVPEPIPGTAQPV KRSLGKVPKWLKLPASKR
9003	22904	A	9070	20	427	DGTRRRERERERERERERERERLYLTEDT LHSLSLEGARSGASVCQSVYPTGASAP HSIINGHKRVLVLCVETEHTFPLAEKDR AFLGDTSVFVGAAPVGGANTGASAGGAP PSRGEPKEESGESHEMDMGFLFV
9004	22905	A	9071	297	126	CSIYDKRITPFGLEGVSRQRLLTLLP CLPPALTETPTSSDQSTDATPTLTNS
9005	22906	A	9072	117	286	VVLRGSEKMFQVQEQINEQYLQCLIKGI FLVKKKKKKKKKKKKKKKKKKPRPEYIK
9006	22907	A	9073	3	302	PPMETLRQWTTIVHSQEEEEHFEVIKD EVKVVARKHGQPGTPVAIATQLPPRTSA AFPAQQQPLQPLAPTTVLSVSADWNALL QRPNKYIWGLQYLEM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9007	22908	A	9074	437	79	NQKREEEEEEERRKKRRRRRRKKRRKKKK KILRQKKKKRRKAGSREKKKILRHLPEK NKRSKKHYELINALSRLQDTRLIYQKMH FYILAKNNWKIKLKIQVHLQALENKVPR HKWETYA
9008	22909	A	9075	51	185	CRADFMFFHDKIIVYLCSLVYLLTFPPL LSYDPAKSPSARNTQE
9009	22910	A	9076	452	310	QFSRCHLSSLSLDRKGNLTPCTSWVRR CLALLRLTLGALHLLSDNPQ
9010	22911	A	9077	438	326	LLHCWWDCKLVQPLWKSVMRFLRDLLE IPFDPTLHF
9011	22912	A	9078	37	169	GIPGFRHAGQRRQLQLITGDLPTSASHS AGITGTSDRARPPSTF
9012	22913	A	9079	1	408	RKGRLSKEETERMVQEAKEYKADEVQR ERVSANNALESYAFNMKSAVEDEGLKGG ISEADKKKVLDDKCEVISWLDANTLAEK DEFEHKRKELEQVCNPIISGLYQAGGGP GPGGFGAQGPKGSGSGPTIEEVD
9013	22914	A	9080	31	168	VRRNPRLEHTVTITAYCSLELLGSSNLP ASASQVARTGLQLLNLQ
9014	22915	A	9081	460	319	YFFVEMGSHYIAWAVLELLGSSNPPASA SQSAEFTDAHKPTDCRPLR
9015	22916	A	9082	465	326	PCVAEFCETHHTHTHTHTHTFKCVGSHL HTNND
9016	22917	A	9083	33	269	PGNSRPISSVRGHPPCLANFCFLNVFV EMGSHYVVLGAILGSSDLSALAVQSGR VTGMSCAWPEIFFLLENWIIIL
9017	22918	A	9084	47	300	DLITSLFLLKQSSLATMNIQTFFKNIFY DLIIKTFLRFFIFCFIYFYFLFFSYGG FFSFFFFFLKGSSFLPRLNGGAKIWNV
9018	22919	A	9085	437	220	NIAIKSLSLSLSLSLCVMCVCSACVC MCLSLSLFSPSSLSHSLFPSTPNMDIS HLPILSTQENMLLLQLQ
9019	22920	A	9086	227	23	DCPKANILGLTPRLVSNWPQVILTPWP PKGQSLLCRQGEGRDIWTHPWLLHPP PQARFPPTHTFH
9020	22921	A	9087	206	326	PHWAQWPTPVIPALWEAEAGKSQGGQFE TSLANTVKPRLY
9021	22922	A	9088	364	123	SRVVLPLKAPGEDTSLPLPASGGSRCSL AWGSIPPIASIPTWPSVLCPCEIFPLL FLLYGDCNLGPTLIPDDLIMRSLP
9022	22923	A	9089	373	205	MPRLANFCYFSRDWVSPYWSGWSQTPC WDYRREPPFPVPCVTSYSVQYACACAGL
9023	22924	A	9090	283	2	REFSFSAVVLAFKIFWKLFSPPFWRVRP EDWFI PGCGPNPNFPCCPPGVGKKGE PRFKKKKKKNFISSQAQWLPVIPAWE AKAGGSLEP
9024	22925	A	9091	16	261	CPEDLLVGQNVKVEDSDMGDPDRRPMCM FACFYLLVYRRCLAMLPRLYLNSWAQVI LLPQPPASLELLQAHATHPALCLSF
9025	22926	A	9092	17	109	RQGLAMLPRLISNSWTQANLLPWPPKEL GL
9026	22927	A	9093	282	114	KKGGKGALLVFLKTKGRKPPFFFLRQGLA MLLRVLNSWAQAILLPWPPKVLGLQA
9027	22928	A	9094	205	337	NANLHGRMQRLTPCLPEIWEAETGGSQG QEIETILANMVKPCLY
9028	22929	A	9095	62	287	EHSCAKLFCFAFESGPYSVAQAGVQWHD HSLLSQSTPGLKQSSCLSFPAAGFYKE

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						SESFYKDKSCHHLGKHSGA
9029	22930	A	9096	170	9	AASTGYCIGRFCTKLKIQSGQVRLSP VVPKREAEVGGLLLEARSSRPIWATW
9030	22931	A	9097	2	104	RRPGGRAEPRARVRGDRDPVLLRHYPH IFEECG
9031	22932	A	9098	350	142	LCLSCP KGGYRAMAPWRGNFCSFGKNG GFPMLGRVVLKWPQMGPPLPQPPKRVGFQ GLSPPPGPPFLV
9032	22933	A	9099	494	342	YFYFYFVEMVSHHVTQAGLELLASSNPP ALISQHAVITSGSHHTQPKLYF
9033	22934	A	9100	30	232	GGIMLCHGRACFPFAFCHDCKFKPVFQ PCFLYSLQNCSEFLYKIPSLRSCRLQLAE LLSIIYLENPL
9034	22935	A	9101	26	171	RNSRRLRHKNRLSLGGGCGSEPRSCQCT PAWQTARLSLKNKKQQQKKP
9035	22936	A	9102	486	239	HHTCPHQVCVCVCVCVYRVCVCVCVCVY IYMYMCIYIYIYIYICICYICRERERERE REMWFFHHVAQAGLELLGSRDLPPAS
9036	22937	A	9103	487	344	TGFHHVGGAGIELLTSSDLPASASQSAR ITGVSHHAQPLFMIFCAKC
9037	22938	A	9104	470	221	TPGLKRYTCLSLPKCWDYRCEPHARQGA FLCAFSPLSSQPPWGRPHFHSYETNK VERGKRLPLRSPSTEQGFDFRCVLFQT
9038	22939	A	9105	468	259	YVFFCRDGGLTISSRLVLNSCPQSPCL SLPKCWDYRHEPPCPSCSNLLLMFHFT NVFLIDSECSHFTF
9039	22940	A	9106	466	329	RVAGTTGTHHAWLINIPSVETGFHHVG PQVIQPPRPKALGLQA
9040	22941	A	9107	409	306	AGFELLASSDLPASASQSAEITGVSHHA RPSLIF
9041	22942	A	9108	417	269	MVVAQADMESSEKPGLFNVVIINDSLVQ AYPELKEALYEEIKKAQRGA
9042	22943	A	9109	533	399	RGSLRHETRLNAEARRCSELNSRQCTPA WATERDAVSKKTKQKA
9043	22944	A	9110	16	239	LVHFEVRWNSHEVSLTADSRKSHLIFPQ PNYADTLINQSEYKSEPLLTQDLLET KGEPRQLQVSFFPPKREE
9044	22945	A	9111	68	219	BPPHLANFLQRLVFTMLLTILNSWPGV ILPPGPPTVLGLQDKLPVLLPS
9045	22946	A	9112	192	57	DRVPLCPDWSAVARSWLTAASVSQVKG ILSPQPTCAPPGNST
9046	22947	A	9113	21	201	TIVSVVEFMNLGGGTCGEPRWCHCTPDW GTERDSVSGEKKEDKDVARRHVWGSFYNG GPQ
9047	22948	A	9114	2	144	TFTIDRCAKDLFVAKQVGTKLSVNEPLS FSVESILKRPSSAITRVSQ
9048	22949	A	9115	156	316	MILNKKKKKKKKKKKKKKKKKKKKKKKK KGGGPFKKTGGAKITPGWKNYFFFFMG GV
9049	22950	A	9116	1	84	TKPTPFLPTLITLTLLLPISPFLLIIL
9050	22951	A	9117	1	176	HLNLGGGVCSEPRSCHCTPVWATEILSQ KKKKKNGFKFWEPRPQKGGGGGRKKPPG VP
9051	22952	A	9118	1	184	AAAGYPGQQQNFHVSREMFEQRIGLNN SPVNGNSSQMAFPSSQSLYRTSGAFVY DCSKF
9052	22953	A	9119	69	374	IIFSKKKKKKKKKKKKKKKGGPPKKKP

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						WGGPKIFVLRRLVLSFFIRGEKKNTFGDF LKKTTFFWGGGKLGKPPPKKTPWGKKKI FKGERGKKPPFLGGKKK
9053	22954	A	9120	405	93	EFSPLLLLTNQKRGFFPPSPPKIFFPPK RIYFLGGGGPHFPFPQKRGFPQKNQKGF FFSPPKKKYNLPPPGKFCPPQGFFPPP PPLFFFFSFPFFFFRCQIK
9054	22955	A	9121	2	380	WDYRCPPPHPTNFCIFSGDGVSPHWPGW SWPQVICLPQPPKVLLTPVWRDRTRDLE GGDLWYGACLGACLHLGPQAASFGHGIL GPASLLCCIPKHVMDTLPSPGVKLQSCD TGVALRVGEKREGS
9055	22956	A	9122	2	534	DMIREQKIYHKYLAQRREEEKAQEKEFD RILEEDKAKKLAEKDKELRLEKEARRQL VDEVMCTRKLQVQEKLOREAKEQEERAM EQKHINESLKELNCEKENFARRQRLAQ EYRKQLQMQUIAYQQQSQAEEKEEKRREF EAGVAANKMCLDKVQEVLSHQVLAQNI HPMPQGMPO
9056	22957	A	9123	389	46	GNFLPPPIFGFFSPFSELKFFFSPKTL IFLGFFFIFFPPPKSFFPKNSPGVFFC PPFKKKNFLFPSPLNFAAPPVFFKPPPP FFFFFFFFFFFFNFYRLYFIWVNGLAKV VW
9057	22958	A	9124	422	59	AQOKKKKKKKKKKKKKKKKKKKKKKKK K
9058	22959	A	9125	333	168	KGPPCIVVCMVEFHKLEAGSHSVAQAGA QWCDGNLLQTLTLGLKRSPPHSLPSR
9059	22960	A	9126	175	89	KPPPHFFFFFFFFFFFFFFFFFFFFFI
9060	22961	A	9127	368	250	CFNYLSRDRGLPLLPGLVLKSWPQAILL PQPPKMVGQQG
9061	22962	A	9128	392	157	FFSPKRLNFGGGGPKMPPPKKVSPPQK PHPGFFSPQKKKKKFFPPPVKMGPPKS FLKSPPPFFFFFLISSIRGLFL
9062	22963	A	9129	396	13	FFFFFFFFFFFFSPRRFFFRGGGSVALSP PKVFFLLNPPPVFFFSPPFKEKTSFFP PPFFCPPPQILFLAPPYFFFFFFFFFLF VFFFLFFFLPLLLFLGKTSFLLLLFLF IYLETGSCSVAWARVQ
9063	22964	A	9130	55	180	LLYNKLIPTLKKKKKKKKKKKKKKKKK KKKKKEKYEKTKAY
9064	22965	A	9131	2	95	SFVHMEHEKAVLLLSFQNTVDLGIQRE LTV
9065	22966	A	9132	172	404	KKKKKKKKKKKKKKKKKKKKKNWGGGF FKNSWGGPKKRGGGKIFFFSLLGGKKKT LGVFLEKPLFLGGRKMAPP
9066	22967	A	9133	1	125	QPVSYPTTIIGQVAYELYFTTILILIPT MSLIENKILKWAY
9067	22968	A	9134	1	120	QPVSYPTTIIGQVASVLYFTTILILIPT ISLIENKILKWA
9068	22969	A	9135	7	269	IATGQPRLOKLTLDPTLLKRLTKKK KKKKKKKKKKKKKKKKKKKGGGHHK KKPPGGPKTYPVKKKIFFFFGKIKKPP WGI
9069	22970	A	9136	1	64	LVSISNTYGLDYVHNLLNLLQC
9070	22971	A	9137	400	259	SQPLRRLRHKNILNPGGGHYSELGSCHC TPAWDTEQDSIHSWLLSSV
9071	22972	A	9138	3	310	ECFPNSPNMNGHCNLLVQSTSPSISTMP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CPKYVALEKVFLLNVLWFFYLKYRDNRP GSVAHTCNPSTLGGRGGWITGAQEFETS LGNIARPSLIKRRKKYKLF
9072	22973	A	9139	34	142	NCKKLNTHTHTLTHSHTHMLTHSDTFTH THHTTKYK
9073	22974	A	9140	146	2	PPPPPPPEGVSLCGPGWSAVARFRLTASS ASRVHAILPPQPPQQLPTRP
9074	22975	A	9141	3	102	PPASASQSAGVTGMSHHAQPIEPLRCSS HRTT
9075	22976	A	9142	245	51	NREGDLLCCPRWSQTFLKQSCGLGFPKC WEYRRGPPHLYAIMSMRKNILIQMIFY NNPCLLYS
9076	22977	A	9143	2	108	GAKCVSDRIKHAFLIKEQKIIVKVLKAQ AGSQKAK
9077	22978	A	9144	3	200	MGFLHVGQAGLKLPTSGDLPASASQSAG ITGVSHRAWPVSGFFCSEAKECFWEEQL INLDKNSQK
9078	22979	A	9145	405	227	WFFLGFPPLKGLGPPKMFFRAPRVYSPF FPPFFFWPPPPRIIFPPGFKFVFLAG PIW
9079	22980	A	9146	387	220	PLFFVGCFFFFFFFYFFFTTTTTTTTT TTTTTTTTTTTTLGGCERNFIIRKNINN
9080	22981	A	9147	539	220	VINFKHILIKTVIQSLFFFERGSCLP LECNMIMAHCSLNLGSSHPASASQV AGTTGAYQHTQLIFIFFAETGSCYVAQA GLQLLGSSNPPWPPEVLGLQV
9081	22982	A	9148	3	141	GGGGCCEPRWSHYTPAWATSACLKLLK KKRFLKESCLTPLLKA
9082	22983	A	9149	413	240	FIFCRDGGTLMPLGLTSNTWSQVILPPQ PKVLGLQAYHADELPHLATGWVLYGLT V
9083	22984	A	9150	395	193	LLFGPCLLNLITQFVSLHLLDIKLQMTL SEGYFPLNIQESPFYRAPLDDPSVRHAR GEILPISLGGP
9084	22985	A	9151	1	77	LVAATVGGGTGWGFKNIRGRSGGA
9085	22986	A	9152	365	181	IVDRPDPCRDAQREVFTLSARYPKIW VPPGDPAREFPFIQSAPVMLLAAPDELV SAQLA
9086	22987	A	9153	373	251	FKKIFFCRDRALNMSPLVSNRTQAIL PPQPLKVLRLQA
9087	22988	A	9154	204	95	DYHWSQPGMVAHACNPSTLRGRGRWITR SGDRDHPG
9088	22989	A	9155	44	280	AEIFGTLMREDGLSLGGGGCKEPKSCHC NPAWATEPDCLRKRRKESPYLLVTPPD SSYSPPFFLLLPAPDNNDYFLS
9089	22990	A	9156	2	117	ERLRHENCNLKGRGCSEPGWCHCTPAW ETKQDSISKK
9090	22991	A	9157	3	207	HASAHASADAWDYRRVPPCPANFCILYV SHVGKAGLNLTTSSDLPTSASQSAGITG VSHHARTPTVY
9091	22992	A	9158	117	267	NRVLLCCPDWQTPGLKGSSLSLLSSWD YRHIPPRLAARSSYLGPGFYH
9092	22993	A	9159	415	167	LFFFFPIKNXFFFSPPPLFTTTTTTTPPPX XFFFFFPFFFFFFFTTTTTTTTTTTTT TTTTTTTTTTTTTTTTTTTTFLELKQNF
9093	22994	A	9160	217	41	SSQIHRDRNRMVRQGAHAHACNPSTFGG KGEQITRAQEFKTSANMVKPRLYYKPC



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LY
9094	22995	A	9161	341	164	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFVCF VSVELKKWQNYSFVRIILRVEP
9095	22996	A	9162	190	402	IHTGKHPKCYRNSYSVLFLASKKKKKKK KKKKKKKGGGFKKKKNLNRGGGEIIFFF WGPKKIFGGGGLKKG
9096	22997	A	9163	108	209	LSVKRCAKNPKKGKVPAGIKEIRTRSHQ DSEDI
9097	22998	A	9164	2	145	KHCGRPRPQGPLPRKTRDLCSLVYLLTF PPLLSYDPAKSPSARNTQE
9098	22999	A	9165	170	402	ISRCHFPSTLSYVKITKTIKAPKSKSK KKKKKKKKKKKKKKKGGGPFKKKNF LGGGGGEIIFFLGAPKKKRG
9099	23000	A	9166	399	113	WRLRWEDCLSLGGRGCSEPGSCYCTPMW VTEQDQSSGYEGFQRPSSLSKARIPPSVA AERSMCQPACVCNLSVEHLSLYSCLLAQ QGKALYKLLNK
9100	23001	A	9167	3	138	SWITGVCHYAWLIFAFIVETGFHRVGQA DLELVTSGDATTLRSH
9101	23002	A	9168	134	301	EKLTSQSHSVTQAGVQRLNVHSLRPPPPR FKRFSCSLSPSSWDYRNLETVLQEETH
9102	23003	A	9169	201	1	GATILRFKTKKKKNVFFKKKKKKKKRKK GKGWSGTESRWNLSEGGSSGLRRRKLQA PAGPQEFEKLA
9103	23004	A	9170	2	191	FVPQPLPLGFKRFSCLSLSGWDYRCTP PHLANFCGFFFLKFFFKKKNFSPR GRGGALI
9104	23005	A	9171	2	191	GGTESCFVAQAAVQGCGLGSLQSPPTGF SETASQTVDPDKVKDPGKLRMTFVAELP KTIVTDS
9105	23006	A	9172	3	143	SWFLYVGQAGLELLTSGDPPALASHSAG ITGVSHRARLQTGIFRAV
9106	23007	A	9173	361	174	VLGIILSMSETEIFNTKCLDQSGTVAHT YNPSTLGGQGGRVIRAQEFETSLGNTGR PHLFKI
9107	23008	A	9174	493	351	LVETGFNVHGQAGLELLTSSDPPASASQ SAGITGVSHLALVLISRKSC
9108	23009	A	9175	1	115	FRKIWIYTYTMEYCIAVKKKEMLSFTITW MNLEDFMLVR
9109	23010	A	9176	286	96	PLFFFNRWGLAICLGSVAIAIHRDHSA LQSQTPLGRSSCLSLSSWDYRRVPPC LANESHY
9110	23011	A	9177	399	237	RNTKWLFFLRRSLTLSTGLECSGAISAH CNLRPLGSSDSLANGIFKDLALLDM
9111	23012	A	9178	427	101	GRTGRQGRGAPHISHDGRPGRDAPRFPD VMAAGKRSSLPRWDGGAETLLTFQTG QPGRGAPHIPDDGRPGGDAPHFPDGVVA GQRLQSQHFRPRQAAGRWRLL
9112	23013	A	9179	193	41	IVFLFIYLFCEFFVGTGFCYVAQAGLKL VSSGPLASAPQHVGITGMSHHT
9113	23014	A	9180	292	119	KITKINKQILNLSYTLDDMDLTDICRIF HPTATEYRFFSRAHGTFFRSGTKNSAWH I
9114	23015	A	9181	3	279	ALSPYSSSECKLGSFNRELSSPSPPGGQ KSEIKVSAGPRPLPRVQGDPSPLPASG GPRCSWACGQITAVSASGVTHSPPLH VCCVCLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9115	23016	A	9182	402	238	QMOWHNLWPLQSLPPEVTPFLFCLNLPNNWGYRWPPPPPTNFFFLKGVSLGRPGSV
9116	23017	A	9183	3	207	EFHHVGGDGLLELLTSGDPPASASESAGITGVSHRAQQACRFLHFFEGTCFLSQELS YLKLGRDTIIC
9117	23018	A	9184	3	106	YPHYVKSTIVASTFTIISLFPTTIFMCLDQ EVIISN
9118	23019	A	9185	110	248	GVLVGSPRLRTRFHSQQAEGAEIGVVT VVMGDGVLPVCVVLEVDV
9119	23020	A	9186	925	1132	KCPASAWAAHPTSEIRISQGGSQAAVVLV LFFLLKNPGDVIPALWEAEAGGSQGGQF ETSLANMAKPRLY
9120	23021	A	9187	399	292	ASQVAGTTGAHHHARLIFFVFLVETGFH HVSQDENF
9121	23022	A	9188	7	82	PCDPPASVSQSAGITGVSHHAWQIF
9122	23023	A	9189	1	117	LPISLPSFLPSFLPSLPSFLPSFLPSFLPF FFPSSVTPYLK
9123	23024	A	9190	238	46	NKAFRIKAFVSPSNKKFSSFFFLNEMK SHYVDQAGLELLSSGNPSILASQNAKIT GVSHHVRP
9124	23025	A	9191	2	282	LIFYFVDNMLVRAGLELLSSSDLPALAP KVLRFRTGVSHHTRPELYFQRL LAPGTL LINSQAAGTNFPIGLSRIKPTQSGHGM LQ EVWGTSGLR
9125	23026	A	9192	44	136	CLCVCVCVCVCVCVCSCQKTL MCCFLENF DV
9126	23027	A	9193	469	347	PCPANFVFLVETGFLHVGHAGLKL LISG DLPNSDQKFYVN
9127	23028	A	9194	427	238	PPARPTAFPIEFFVEMVFRYFGKAGLK VLISGDL CASASPGVGITGVSHHAQPK
9128	23029	A	9195	34	178	SLVHVVEFERGRAEWLTPVIPALWEAEA GSGRGQEMETILANTDFWTG
9129	23030	A	9196	22	338	CGPYSMWWNSIKRERKEGKKRKKRRRK EQKERERKERKERREGGREGKERGRREG KKRKKKKRKKVGLIGSPCIVFTWQAAYC EESGGVWPGGETEHTQEGLVQ
9130	23031	A	9197	3	91	QGLSLGGGGCSEPGSCHCTPAWATERDS I
9131	23032	A	9198	1	203	RTRGNKSIDDTSNFDDFPESDILQPVN TTEPDYKSKDWFLNYTYKRFEGLTQRG SIPTYMKAGKL
9132	23033	A	9199	2	144	PTRTMPCCCCCCCCCCCCRCLFMTGVL FTCCHNQFENHSGCLPRQI
9133	23034	A	9200	1	99	YAAKELVHDIRPTTEMERRRGLWWLVP RLSLE
9134	23035	A	9201	3	149	LNAVQRMWQLKVQELDPAGHKS LCVNE VPSFYVPMVDVNDDFVLLPA
9135	23036	A	9202	284	21	KGPPLFFFFFFL RQGLVLWHRLEYSGMT TAHCNLELLVSSDPPTLSSQNAETTGVS HCAQPASLILSKPYIGFLHQIQKSLPV TFL
9136	23037	A	9203	1	77	LRLVLNSWRQAILLWPPKVLGLQA
9137	23038	A	9204	529	340	GVLLWRQAEAGELSLGGGGCSELKVRHC TPAWATRAETPSQKINELIKSMAVELTD DFIT
9138	23039	A	9205	413	241	HPPPELKLFCISLISRWCHRHRPPCP YVFLLAETGFHVGQAGHKHTYCCVSLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						T
9139	23040	A	9206	33	152	QLQGLESWGMERCALPGYPVVFTNLCKY RSWIEETMRDK
9140	23041	A	9207	70	402	HVDWEALGNDPRLVNLGICKLKASGIHE WVHTRTCAHTMHMTHHTCTHCRSPRVV VNLGCTFELPGALKNARAYPHPNATKP MTSESVGIRPTRQVFKAPRAEQHCSTA
9141	23042	A	9208	46	262	GGIPPAAVRGGRSWLRDVLRLAAGRR RRGTRRGRGRAGGAGGGRDVRGSRREPA AARTAAEGERAVRGKC
9142	23043	A	9209	15	206	PIEPLSERTNSAGAPPPASLPPCSLISD CCASNQRDSVGVGPSEPGDSMQTSLWA KVPVSKD
9143	23044	A	9210	475	110	NLLAPHLVLSLEKHSIRMGVAQFSRCHL SQLPLARKENSLTPCAGSVRRCLALLRL MLGGLHPLSCTHCPTGPSEMNLVSQLEM QKSPVFCVAHAGSCRLELFLFGHLPL
9144	23045	A	9211	420	132	PPPPNYFGGAGFFPPPPFFFLRPPPPFF LPPKKKKLFPFRGPKKIFFLKAPPPSFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFF LVRSHFILTIM
9145	23046	A	9212	353	87	FFFEXKQXFFPSLFFFSPXXFSFYPF* YLKYPLLPSPSFFLFFFTPPPPXFFFFF FFFLFPPPPFFFFFFFFFFFFFFFFFFFF FFFFD
9146	23047	A	9213	2	276	FIQLLKRRLCELGYEVLPHPSYSHDLLP TNYHFFKHLDNFLQRKFHNQQDAESAF QEFAESQSMIFYATGINTLISPWQKQVD CSVSIFYD
9147	23048	A	9214	402	276	LSCLSLPSSWDYRCPKPGYFFYFFLF LVKTGFPHLAQAG
9148	23049	A	9215	386	37	GFKKRVCSPPPPPPPPPPPPPPPPPPREG FFLQKKKVTCPNPSSNKLTLGLQKKKE IQPALMKKNSISQS
9149	23050	A	9216	1	142	KDFRVQVWNHSSLQPQPPGFKQSSRLS LPKYWDYRHEYLHCIALP
9150	23051	A	9217	402	181	FFFRXFFFXFFXFFXFFXFFXFFXFFX XXXXXXXXXXFFXFFXFFXFFXFFXFM FQQEKLLFIFYVNIIVTF
9151	23052	A	9218	2	87	SGSLIFGLIYICMVCVCVCVCVCVYPC
9152	23053	A	9219	420	271	YYCIFRETGFHHVQAGLELLTSGEPPA SASQSAGITATAPSPFLTFLLV
9153	23054	A	9220	139	413	SGYHSKTLFQKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKRGGGAFKKK IFFRGGGGNFFFLGPQKNIGGGGLKKR GGGKKPPPPQIFFVVG
9154	23055	A	9221	134	236	LHRWGPAMLPRIILNTWPQVILLPRPPK VLELQA
9155	23056	A	9222	364	280	STHLSLPKYWDYRHEPPCLAKKDAQSFS
9156	23057	A	9223	1	147	TLLPMLESSGTIMAHCSLNYLGSSDPST SASQSARITSVSHCTQPLPF
9157	23058	A	9224	1	208	AGAPPPASLPPCSLISDCCASNQRDSVG VGPSEPGAGYHLVVRRLSQSEKRSIRVG VTRFSSLLSSHA
9158	23059	A	9225	1	145	FQHVQAGPKLLTSGDLPASASQSAGIT VSNRVRPKTKNFYTGNTNPN
9159	23060	A	9226	396	210	KCWDYRHEPPYPALTNLLFIEMGSYGVA RAGLKLGGSSNPPIASASQSAGVPLSHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQPIF
9160	23061	A	9227	2	154	FHHFGQAGLELLTSSDLPTSASQSABIT GMSHHTQPRMVFFSNFSSTAQC
9161	23062	A	9228	1	238	FLLALGIFILHAIYLSIYLSIHPPSMH PSLSIYLSIYLSIYLSIYLSISLSLSLS IYLSIYLSIYLSIYLSIDFLSSAR
9162	23063	A	9229	3	65	RGDLITEPFLPKLLTKVKS
9163	23064	A	9230	25	188	YERTAWNQAWVYVPIVSATWEAEAGLL EPTSSRLRCVIAVNSYCTSTWAVS
9164	23065	A	9231	44	232	YDLKFNNHVVFYFLFETEFHSLSKVECN GAISAHNNLCLCDGARLHRRGGKKTCK KQTLPS
9165	23066	A	9232	3	195	FFVGLGSPYVVTGLELLCSGNPPASAS LNARITGMSHQVQPNTRLSFYLGSSIIY GSIHAMI
9166	23067	A	9233	380	244	SVPLAEMGFHVGQASPELLPPVIHSSQ PEKAIGLQARATAPSLH
9167	23068	A	9234	11	101	LLINTLMFIHLSPIILLSLNPDIITGF EG
9168	23069	A	9235	411	226	FFFFFATNSQGGPTSFWGPRNNAQVAGP LRNKIFTVPVGSPPKIFPSWETPVF
9169	23070	A	9236	404	262	QGLAMLPRLVSNWSWTQAILLPWPPNQSA GSGSVSHHTQPIFISENIH
9170	23071	A	9237	369	152	HAFVSVIWRSFHVSNSYMTVTVMYHNL SIPLDPHFFFRGGGLAMLPRLVSNPWP QAILPPQPPKVLGLQA
9171	23072	A	9238	389	190	RPKKKKKFFPPPGGKGVFFKGAPPYFL NFIFFFFFFFFFFFFFLIYTHNFIIL FLNCDKLYIT
9172	23073	A	9239	330	3	GGMEPPFFPPTGAQWGVFGSLQNSPPEF KQFLCLRLPNVLEYKSIPPCTNFCSFY KNGIFPCWPGWPFKFQKKKISWVWCA LAEAGGSLEPRWRRLQSAKMAPL
9173	23074	A	9240	122	248	KKKKKRGGLTPVIPPLWEAKGGGSRGQK IQTILAGGKAPLY
9174	23075	A	9241	2	286	FFVQTEFHVHAQAALQLVSSRDPPTSAS QSDITGVSHCAQPVIVSCDDQVTLVQR RQVTVTSLIAFCQVAYPKGAKSQWPQSF FFSSPFLFSL
9175	23076	A	9242	2	95	HMKKCSSSLAIREMLIKTTMRFFFFKLI TCY
9176	23077	A	9243	377	293	PLSPRLVLSSWAQMILLPLPPKVLGSQA
9177	23078	A	9244	422	147	KKGGTQGFSPPRVFKRGPRNFFGPPKK KKNPPPPRGKIFFFLKGPPSFFFFFFFF YFFFFFFFFFTHKYFLGLDLLLIYHLS KKNYSFF
9178	23079	A	9245	402	208	TIGRCHHTQLNLKFFVEMGSHYVQAGL KLLDSTNPSSAFQSAIGSVNPNYAWTE IMFLYSIPI
9179	23080	A	9246	314	168	EPYHLHFLPPHHYYYCRWGLIVLPMLVS NSWAQVILLPWPPKVQGLQV
9180	23081	A	9247	3	320	VVQAGLKLSSCDQPASASQSAVITGVN HHARPLIFLYEMDYGSRVLIIRKWDND EQSNRTIFLKKDELGNRSACLKYPMD INVNSGLGWRYRFGMHQCRW
9181	23082	A	9248	22	303	KGSYFSFTYEAQTESCSARLECRGAIS AHCNLRLLDSSNSPASASRVAETTHKKT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LVPERSCTPKERNVIQKQEESEEMS HLFTWLPILH
9182	23083	A	9249	13	174	LGLKVRHRLWLFVLSVTEFHHLGQAG LELLTSGNPSAGITGVSHCARPTSHS
9183	23084	A	9250	3	141	HVGQTVLRLLTSGDPPTSASESAGITGV SHRPRQIFISLFTICIR
9184	23085	A	9251	56	262	LRIPLTFGGVVKGEEEDRAVMHLRLCGD DSEMSSESLHFIKLPRTVLVDEEDARPEKK KKKKKKKKKKKK
9185	23086	A	9252	401	275	PADLFIFIWEDGGLTMSPRLMNSWSQA TLQPWTPKVLGLQV
9186	23087	A	9253	411	258	PKVFKYRCDPRLAWFLFFVQSLLPRLG LNSWAQAFLLPPWPRVLGLQA
9187	23088	A	9255	391	167	GLKILTSGDLPASASQSGANTGMSHCAR PLMSFKIRYFLFTIKMKLKLVLVPPVWSA GVHPPHFSCPIVITNKPRI
9188	23089	A	9256	9	255	FFCRYGGLAVLPRLVSNWTQAILSPWP LKVLGLQACTHHFFLMVNSNAARIKTIE MLLSEVDNFFVALLCPSFTISHFHL
9189	23090	A	9257	487	42	RYFIFLFYFIFKTETGSYYVAQARLRL GSSNPALAFQSARITAVSHRAQLTCIK YTFLFTHIP
9190	23091	A	9258	1	243	ILSSGGSFISLTAVILIIIFMIGEAFASK RKVLIVEEPSINLEWLGCPPPYHTFEE PQPKKSEIYKCFFFSVFVHFGGWG
9191	23092	A	9259	411	2	FFFFSPPVSLSLCVLESPPPPFFFSPP PKKGGFFSPPFFFSPPRVFPFVFFFP PFFFFPPLKKNFSPPPPGKIFFFFFRPP PFFFFFLLFFFFFRPFFFSFFFLRWE EVLYFIMCHHISDAYPPNVDMNKE
9192	23093	A	9260	417	219	SVEMGFLHVGQASTIKLPTSGDPSASGSQ SAGITGLSHCARPHSQLSIVCCYSVPVQ CLHSLAARY
9193	23094	A	9261	408	172	CPNHFRKWHRGCPPPRVFFVGRDGVY VAQAGLELLDLNSPASASQSNGTGMS HLGQPLLFI LNDVIAVIPLQGSF
9194	23095	A	9262	401	132	HQDNKPAPPGFFFFSPPKGGFFSKPPY FVSPRFFFPFPLNPAPLFYFWGPKKKI FFFPFPAIKFFFFKRAPLFFFFFFF
9195	23096	A	9263	393	220	LFFLNKIPFFPPGSGKGGDFGPHNTNPP GVKPIFRPHPEEGGPKGPPRPREFFL GF
9196	23097	A	9264	206	438	FPILKTHFRLGTVAHNTTTLGGPGGR NTCSKFKTSLGTWGDFFHKSENCLGWG VPNCGPCFWGAQQKSAWSEGL
9197	23098	A	9265	333	48	ALLAGPTPFFFLGKKKTRFGNRLFFFF FFFLNEVLLCNPWIMVVAIHRCDHGT QPPTPGLKRSSCLSLSSSNYKLPKPLHP ACVRFLDFVS
9198	23099	A	9266	3	275	TGFHHIGQAGLKLTLTLDPPLSASHSAG ITGVSHHAWPMHLESYWRVQYFMPQVL YFWAPSGAQHCAQIIENAIPTLLSRPQE EPASEA
9199	23100	A	9267	49	226	HGPEPCMDADAQREGINVSARYPKNWES TVDPAREFTMIYSAPLMLLADPDEFASV QLA
9200	23101	A	9268	159	236	PRLVLISWPQAILPPWPIKVVLGLQA
9201	23102	A	9269	1	208	IFNYCVFSSGVALAYGIYKQDLPALKEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PRGVVFVDMGHSAYQVSACAFNRGQLKV SIYFFSRRLLVVW
9202	23103	A	9270	1	209	TFNFCVFSSVVALAYGTIKQDLGALBEEK PRNVVFVDMGHSAYQVSACAFNRGQLKV SIYFFSRRLLVVW
9203	23104	A	9271	379	263	ESCSVGRLECSGAVPAHCNLCCLPDSS GSPASSSRLC
9204	23105	A	9272	312	3	FRREGLAALQPWWPNKVSSKKKKRKKERE RKKERKKERKKERKKEDGATADGISEAE VIRVHPYPVGFVGLSEGLIWTEDMRAGR RPHAGESGDTVMPLPQAQE
9205	23106	A	9273	405	246	PTKKNKYLHAPPLFHFFFTIPNPNFFFF FFFFFFNFFFFFFKTGCEFLYFSY
9206	23107	A	9274	2	227	LVETGFRHIAQAGLQLSSSYPPTSASQ SVGITGVSHQPGPSFHFERKSLGLKTL LCVKVGVRAFCALFFQSS
9207	23108	A	9275	70	304	NLFKLKASTYPSEHLYHLPPTPIVYIRKR LDAMAHACNPGTLGDRGGWIARTPDLKC SAYRGLSKCWDYRHEPPRPVLV
9208	23109	A	9276	2	260	TVFYHVGQAELLELTSGGPPALASESAG ITGVSHHAQPFLLILVLSLPCNQSFHI SPYRFSFTQLNHGFNTVLVPLVINISEI FF
9209	23110	A	9277	406	330	PRLVLNSWTQTILLPWPVKVLGLDV
9210	23111	A	9278	2	160	ELLTSSDPPASASQSARITGMSHTRLK YIVYRVSRSKKNIPKHHIGIQSFP
9211	23112	A	9279	1	91	GLTVFPRLVWNSWAQMLPFPWPKMLGL QV
9212	23113	A	9280	3	107	LGETGFHHVGRAGLELLNKVMHPPWAPR VLGLQA
9213	23114	A	9281	336	234	AHYKLLKIKLPGQAQWLTPVPIPLWEA EAGRS
9214	23115	A	9282	3	241	DRPEPCWDADAQREGINASARYPKNWVT TGDPAREFMTMIHTAPLMLLADPDEIESV QLAQSWPFGAIASLGRSPCKRN
9215	23116	A	9283	404	277	IFFVETRSHHTAQAGLELLGSSDPPYFF QVFTEMSLSQRALF
9216	23117	A	9284	399	231	HYVAQASLKLLYSGDPPASAFQSAETAG VSHCTWPTGSLNKIQNNIHSRISSM
9217	23118	A	9286	394	231	AFVFFVFFGERGFHHVARTVLKLLDSSN PPAVVSQSAGITDVSHDFLISLYRIY
9218	23119	A	9287	420	311	LNFCRDGLAMLPRVLVNSWAQAVLSPQP PKVMGLHA
9219	23120	A	9288	398	173	LLSFFYLFFYFFFLFFLFFFFFLFF LMFKALLFSCHYFPAMVTFKFSLSISGV VRTSGYIMLFSYLCCLKTM
9220	23121	A	9289	270	23	TPEQCRGIKLFYISLILYVRDGVLLCCS GWPVVAHKCDHSTLQHQIPSLKQASCL SLSSWEYRYAPLHLASANFLKVTVV
9221	23122	A	9290	273	46	HLINMPLFTEIWTTERLFLEYILCFVFLV ETGFFYITQAGLKLLTSSDPPAYASQSA EIIGTSHCTRPICYVNVNTNI
9222	23123	A	9291	424	230	CLPFTHSLSLSLSLSLSHTHTHTHTHT TIYMNK
9223	23124	A	9292	2	146	NLFLVETRSHHVARASFLLSSSNPPTS ASQSSEITGASHRTWPEVFF
9224	23125	A	9293	393	202	GRERERKREREREKERKKERKKERKPER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PSGSLTYCVREGITAANL GKRRHKASKT LISHKNKN
9225	23126	A	9294	252	193	GFCCCCCCCCYCCSCDKRHFG
9226	23127	A	9295	409	269	SQYFGRLLRRVDC LSSGVQDQPGQQGETP SLLKYKIYIHISWAGWHV
9227	23128	A	9296	2	213	FCCGLLIHLIYCKTEYSGQSTVAIHRCN HSVLQPQTLGFKQFSLHSLSSWDYRYS PLCPAYIFNLSIGY
9228	23129	A	9297	169	408	RFARHMNSPHEERLPPAGIRVRPPQP AASLGPPRMAPSISRREQMTPTYKHND F AGQAQWLMPVVPALWEAEAGGSSE
9229	23130	A	9298	199	51	LHPPPPSLSLSLSHTHTHTHSHTHTH TH TLWLGRPGPAQDVVLVWGNLT
9230	23131	A	9299	1	176	MGSHSLAQARMQWCNQSSLQPPGLKQ PSPFSLPSSWDYRHVPPCLASIFFLKLN YH
9231	23132	A	9300	412	209	MGFHHVGGSGLELLTSGDPPTSASQSAG ITGVSHRNWPHCGFNLVFLMPDDVKHLF MCILAICVSSL
9232	23133	A	9301	195	347	KIKGFRPGATAHAGNPSALGHQGGRTAI AWEFTISMNMGRPCLYRKYKN
9233	23134	A	9302	386	190	GFLFFFFPPPKKEVFPHFILGFGFFFP PPFKKRAPEFFFWGPKKKKNSPPRALN FFFFKGAPP
9234	23135	A	9303	27	173	SFQLWGHLLKVPRIIRPKRADHLRSGVQDQ PDQHGKTL SLLKKYKISRAN
9235	23136	A	9304	374	121	QWCDHGS LQPQTG LKQSSCFSLPKRWD YRREPPHPTSLSPYIVAWPCTLCPPPLS ALWKHLIHQKCDGVMVLQVPGRTHNVT L T
9236	23137	A	9305	70	196	PQVIHPGQAGLELLTSGDLPASASKSAG ITGVSHHAQPISHF
9237	23138	A	9306	378	256	QKWVSICCPGWSQTFGLQESSCLGLPKS WDYRRQPQCLTL
9238	23139	A	9307	206	3	PCHLGWSAVVQSWLTAASNSWPHAILPP QPPKVLGLQASLKLKAGITQVTFSDYN KILNKEIKRGR
9239	23140	A	9308	338	161	HFKKKIYIYIYVYIHTYIYIYTHIYIY HTYTYIYRIYIYIHTYIYMYVYIYIPS LPF
9240	23141	A	9309	503	288	FFLNLDKSQEWLMPVIPTLREAEAGGS LEVRSSRPASSDPPTSASQSAGIIGMRH HARPVVLRENGRIQN
9241	23142	A	9310	418	309	FFCKNGISICCLPKLVNSWPQAILQPQ PPKVQGT L
9242	23143	A	9311	442	275	VSPPPILGGGFLSPFPKPPPPFFNLKGGP PFPTIPFLIIGKKFCPPPPFFPGLF
9243	23144	A	9312	2	95	HENRLSLGGGGCSELRLCHCTPAWATER DFI
9244	23145	A	9313	318	154	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFF I FILFIYSLLYVVCVGLGS
9245	23146	A	9314	388	199	EQPKCVHRIKQIWHICALEYYAFAFKKK VLPAVVIQIKLEDTMLSEINQSWGKYCM IPLIGGI
9246	23147	A	9315	2	97	STPGLKRSSHISLPKYWDYRRGPPGPAS ILF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9247	23148	A	9316	3	235	TMVVNAEGIPIRTTLDNSTTVQYACLLH HLTMKAKSTVRDIDPQNDLTFRLIRSKK HEIMVAPDKEYLLIVIQNPCE
9248	23149	A	9317	253	71	LFFFFFFLFFVDTKFHHLAQDGFQLLSSSN SPTSASQSGGITGRSHQAWPYVHLLTLQ KLNLY
9249	23150	A	9318	425	95	CLLFCPKKKKKKKKKKKKKKKKKKKKK KKKGGPIKKKKKQP
9250	23151	A	9319	25	214	VRIDDRPEPCMDADAQREGINSSARYPK NWVTTGDPARECGMIHSAPLMLLADPDE FVSVQLA
9251	23152	A	9320	50	231	GHRPEPGRDADAQREGIIASARYPKNWV TTGDPARECTRIQSAPLMLLADPDEFVS VQLA
9252	23153	A	9321	401	226	QWLFTNMIIGHCSLELLGSPSNPPISASR LAATTGTRHHAQPSKFRNLKGWLCakra RT
9253	23154	A	9322	410	159	LGSILQLPPPGSKRFSRLSLPSSWDYRGC SELRLRHCTPAWVTEQDSVPPKKKKQIF RPFPPFSYGESLGVGLRHLCSKPSRRF
9254	23155	A	9323	310	25	KWGG LFFFSEPPKKRGFFKQVFFCVPFV FPPPPFKTGPGDIFLGPLKKKIIFPPPG GKKFFFKRGPPPPPPPPPPPPPPPPPP FSEVECVCCLCR
9255	23156	A	9324	406	289	PGFYHAGQAGLKLTLTSGNPSASASQ SAR ITSISQRT RPH
9256	23157	A	9325	1	116	LHSVLLPFFYFCVCVCVCVCVCVKHK YVRAGGAPGR
9257	23158	A	9326	2	158	FIFLFTVGGTLTGIVLANSSLDIVLHDTY YVVAHFHYVLSIGAVFAIIGGFII
9258	23159	A	9327	3	107	RGCSEPRLRHCTPAWVTEGDCVSKKKKK VPEAWG
9259	23160	A	9328	257	2	GFFSNISASVIIPPPISRKNLFFPPFRVY FGPPPKTFKGPPPPPPPPFLSPRLBCSG VIMAQCSLTLPGSSDLPLSASCVMATVS I
9260	23161	A	9329	66	384	GNLCGWMKSMADNPVVRKADWQGIRES LECQPNTGMLKKKKKKKKKKKKKKKKK KRGGPFLKISWGGPILGGRGKIFFFFFG GGILTPRGVFWKSPFFWGGKKK
9261	23162	A	9330	1	98	IIGQVASVLYFTTILILIPTISLIENKI LKWA
9262	23163	A	9331	33	412	NLFYVMAETILHTHIQLCCQVKLHLSVPR PSLPLLCWNFSLVLHEHSQPASEKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKKK FCGGGENFFFFFGGGLKKPRGVFGKNT FFWGGEKRP PPPPY
9263	23164	A	9332	401	311	PTRPVDLLVDDSVKESLIGYGPTEDSKE FS
9264	23165	A	9333	5730	452	TRSAPRAASWLEDPREVRSVCLSATFFT LSLQKPRLLLFSPSVVHLGVPLSVGVQL QDVPRGQVVKGSVFLRNPSRNNVPCSPK VDFTLSSERDFALLSLQVPLKDAKSCGL HQLLRGPEVQLVAHSPWLKDSLRTNI QGINLLFSSRRGHLFLQTDQPIYNPGQR VRYRVFALDQKMRPSTDTITVMVENSHG LRVRKKEVYMPSSI FQDDFVIPDISEPG TWKISARFSDGLESNSSSTQFEVKKYVLP



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						NFEVKITPGKPYILTVPGHLDQMQLDIQ ARYIYGKPVQGVAYVRFGLLDEDEGKKT FRGLESQTKLVNGQSHISLSKAEFQDAL EKLNMGITDLQGLRLYVAAAIIIEYPGGE MEEAELTSWYFVSSPFSLDLSKTKRHLV PGAPFLLQALVREMSGSPASGIPVKVSA TVSSPGSVPEVQDIQQNTDGSQVSIPI IIPQTISELQLSVSAGSPHPAIARLTVA APPSGGPGFLSIERPDSRPPRVGDTLNL NLRAVGSGATFSHYYYMILSRGQIVFMN REPKRTLTSVSVFVDHHLAPSFYFVAFY YHGDHPVANSRLRVDVQAGACEGKLELSV DGAKQYRNGESVKLHLETDSLALVALGA LDALYAAGSKSHKPLNMKGKVFAMNSY DLGCGPGGDSALQVFQAAGLAFSDGDQ WTLRKRLSCPKEKTRKRNVNFKAI NEKLGQYASPTAKRCCQDGVTRLPMMS CEQRAARVQQLDCREPLSCCQFAESLR KKSRLDKGQAGLQRALEILQEEDLIDEDD IPVRSFFPENWLWRVETVDRFQILTLWL PDSLTTWEIHGLSLSKTKGLCVATPVQL RVFREHHLHLRLPMSVRRFEQLELRPVL YNYLDKNLTVSVHVSPVEGLCLAGGGGL AQQVLVPAGSARPVAFSVVPTAAAVSL KVVARGSFEFFVGDAVSKVLQIEKEGAI HREELVYELNPLDHRGRTLEIPGNSDPN MIPDGFNSYVRVTASDPLDTLGSEGAL SPGGVASLLRLPRGCGEQTMIYLAPTLA ASRYLDKTEQWSTLPPETKDHAVDLIQK GYMRIQQFRKADGSYAANLSRDSSTWLT AFVLKVLSLAQEQVGGSPKQLQETSNWL LSQQQADGSFQDPCPVLD RSMQGGVGN DETVALTAFVTIALHHGLAVFQDEGAEP LKQREASISKANSFLGEKASAGLLGAH AAAITAYALTITKAPVDLLGVAHNNLMA MAQETGDNLYWGSVTGSQSNVSPTPAP RNPSDMPQAPALWIETAYALLHLLH EGKAEMADQAAAWLTRQGSFQGGFRSTQ DTVIALDALSAWIASHTTEERGLNVT SSTGRNGFKSHALQLNNRQIRGLEEELQ FSLGSKINVKVGGNSKGTLLKVLRTYNVL DMKNITCQDLQIEVTVKGHVEYTMANE DYEDYEYDELPAKDDPDAPLQPVTPQL FEGRRNRRRREAPKVVEEQESRVHYTVC IWRNGKVGLSGMAIADVTLISGFHALRA DLEKLTSLSDRYVSHFETEGPHVLLYFD SVPTSRECVGFQAVQEVVGLVQPASAT LYDYNNPERRCSVFGAPSKSRLATLC SAEVCQCAEGKCPRQRALERGLQDEDEG YRMKFACYPRVEYGFQVKVLRSDSRAA FRLFETKITQVLHFTKDVKAANQMRNF LVRASCRRLRLEPGKEYLIMGMLDGATY DLECHPQYLLDSNSWIEEMPSERLCRST RQRAACAQLNDFLQEYGTQGCQV
9265	23166	A	9334	46	324	SKYLPFPVITFQHEIWGVTNIQTISDWVL ICCPGWSAVTQSRLLAAASTSWAQAMSSS SCLGLSSSCYYRHTPPCLANFVAFVETK LYTMLPGLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9266	23167	A	9335	338	178	EVDIAVSHRRKQAFNLCLLKCKPHNNCLNLEGGGSSELKLCYCIPAWATDQSL
9267	23168	A	9336	396	254	KLSTDCTSKETINRHPTWEKIFANYAPNKGPTSTIHSSCLMFPYLF
9268	23169	A	9337	454	359	SSWDYRHAPPCPANFVFLVETIFIQGEIGLL
9269	23170	A	9338	540	328	IKKRGAPRRGVLFFFTRKKKKFSYYKSKTKERVSLFVAPGCIQGGKKKKPPTKKKKKKKKKKKKKKKK
9270	23171	A	9339	21	209	AEEFPDFKLYYKANQNTYRGQWNRTETSEITPDIYLGILVSNWPQVILLPWPPKVLGLQA
9271	23172	A	9340	345	2	KIFFFLIYILFFFNFFFFFFFFFFFFFFFFFFFFFLENRWFLMENFIKGRGHVKGPLGQARDHDISGRRWRRREQCRASQLPGVRRSLLQVQAGGPVHIRISGLQDARQGPRVAGA
9272	23173	A	9341	15	252	LERVIRQSAALTDSSFNFILLILFIYLF FETGSPCVSQAGLKLGSRDPPVSASQSARIIGVSHRAQPALTDFFPSISF
9273	23174	A	9342	484	276	RHAPPCQANFFVQTRFCHVAQSGKLIRSRYLFAFAFQSVRITCMSHCARPLYFLMFKRLQYLKSPTKS
9274	23175	A	9343	464	326	LVETGPHHVQAGPELLAPCDPPAPASQSAETTGMSHRARPPANFV
9275	23176	A	9344	486	280	SFSSHSCSLPSSWDYRCTSSHLANFFFKRWGFTILPRLILNSWPQVILLPQSHRHEPLCLETCLKTLNV
9276	23177	A	9345	276	179	DRDFTMLPRLVLNSWPKTILLPLPPKILRLQS
9277	23178	A	9346	45	143	RWNSRQENCLNLGGDCSEPSLCHCPPAWATE
9278	23179	A	9347	229	73	PPPHMIFFFFFFFLFFFYFFFFFFFFFFFFFFF FFFFFFFFSRLQVSVYCSSVLNKNVD
9279	23180	A	9348	391	139	IPSLKRSSHLSLAKCWDYRHKPPCQVTF SFLNVRIYATKFFLSTPLAASKYWLVL FLLSFSSKYLTPIISFLTHNVSSSIF
9280	23181	A	9349	53	191	IYVTYIWIYSEVSHAYNSSTLGGQGGRTGAQEFKTSLVNIAKPLLY
9281	23182	A	9350	373	235	EEGELLEPGVQGCSELSWCHCTPANGTEQDHCVSYNNSNTHNNVNY
9282	23183	A	9351	476	82	YLATYLPYLSIYLPYLPYLPYLYL GSHYIAQAGLKLGLWVGHNGSCL
9283	23184	A	9352	286	142	ELQFKMRFGWRHSQTISWGLSLLPRLISNSWAQVILLTWPPKVLGIQA
9284	23185	A	9353	3	102	FFETESHVARLEYSGAISAHCTPVIKLYLYT
9285	23186	A	9354	3	270	TAGAPPRPANFCIFSRDGVSPCWPGWSRTPGLRCDPPASASQLGLRLHENCNLG GEGCTGAILAHCTSTLRAQAILQPQSPC PAPQ
9286	23187	A	9355	1	112	GEGSAHCNLCPLGSSNSPASTSQVAGIKGVSHRARN
9287	23188	A	9356	1	63	VALIQAYVFTLLVSLYLHDNP
9288	23189	A	9357	244	140	QRRHHTHSHTYTHTHIPNKKIPILTILKCIA
9289	23190	A	9358	464	181	LGAGGMTGILFSLGASMVLGGAQMLAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KARTRRIQTDDNGKQNTYFSSLDNMVQA GNVLPVLYGEMRVGSRVVSQEIISTADEG DGGQVVVIGR
9290	23191	A	9359	11	469	IDLCRFRHEERERERERERERERERER ERERERERERERERERGRAPPPPLFFGGG GPPARAHALSPHILGRPPLYTYFFSYVR APPTERSARTQREARRALKSVCVVRERE THSLPRARCVCSHPTGCGGAPGARVSL QSAHCFLCVCAG
9291	23192	A	9360	22	172	GLSHEERERERERERERERERERD CPLFCPTGGFILREARVKSGLCF
9292	23193	A	9361	15	345	PPNRPPEAFRTHLISLLCLEGIILSL FIIATLITLNTHTSLLANIVPIAILVFAA CEAAVGLALLVSIISNTYGLDYVHNQKK KKTWGGGRAPNSPYGGRNNNRPAPV
9293	23194	A	9362	61	298	SCDSFLQECCHTHHTHTHTHTHTHT LFSIDIKHTWREWALSLLTTEEGGGT LFQGTLLIFGHTLFWDKPLWQKEF
9294	23195	A	9363	430	2	GGAGPPPPCWTQGGPVPPPTLSRVNGP SLCSDFPSPKFYKEKRKKKGNKTPKRKG KTLPLPTETIVLHVSPGESKPGAGSADR RAPGVDRDGGSDASSSGTRASELGDGPVR VNFVLGDPGEAGRGFSMLGHPPGTSGPR TS
9295	23196	A	9364	432	291	GITGLRHHSQLIFLFLVETGFHHVQAG LELLIHQHRPSKVLRQLV
9296	23197	A	9365	343	507	GQGLTLVPQGVQWGNLSQLLPPGLK QSTCLSLPKCWYKCGLPPASFCFVL
9297	23198	A	9366	417	128	MGWNPGRGAPFLDEMAAGQRRSSLSRV GSQAEGLLTSHTMGGAETLLTSQTGWR LGRGCNLGSLEGQGRRLGGGCGNEPSSR HCTPAWAPLSTE
9298	23199	A	9367	500	285	SLPRSWDYRRAPFRPANFLFLVEMGFHH VGKAVLELLTSGVELLTSGLDLPASASQS AGITGVSHRAWQIRE
9299	23200	A	9368	1	229	IVDLTTWGIPTHTIHKYTHIHKYIHTH AYTHHTHRHKHIYTYIHTDMVWLSPHPN LILNFSSHNPHVSWEGPNGR
9300	23201	A	9369	451	88	KQNTIYTCIYMYVYIYTCIYTVVYIYTR TYTCIYVCVYTCIYVCVYTCIYVCVYTC IYVCVYTCIYVCVYIRVYTCVCIYVYIR VCVYTCIYVYVYIRVYTYICIYTCISTY IQCIYTHIYKVTKCSG
9301	23202	A	9370	1	208	ADETIEQRGGIPKFFVHDNIVIRRTAVDR GIPLLTNFQETKLF AEAVQSKRKVDSKS LFHYRQYSAGKAA
9302	23203	A	9371	354	202	PAAQREGITASARYSKNWVTPGDPAREF TMIQSAPLMLLADPDEFVSVQLA
9303	23204	A	9372	1	336	KSLIKYKGYQVAPAELESTILLQHPNIFD AGVAGLPDDDAGELPAAVVLEHGKTM EKEIVDYVASQVTTAKKLRGGVVFVDEV PKGLTGKLDARKIREILIKAKKGGKSKL
9304	23205	A	9373	2	187	NILVATLYSLYIFTTTQWGLTHHINN KPSFTRENTLMFIHLSPIILLSLNPDI TGFSS
9305	23206	A	9374	96	240	ACWLMPVIPALSEAEAGRLVQPRRLRAA WATWQDLISTKKKKKGGPF
9306	23207	A	9375	3	293	STISAFTTSTTSATTTSTTSATTTSTIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						APTTSTTSLPTSTTTSTTTSTTSAPIS SNKLHKKKKKKKKQKKKKRKNDDTKQD TITKIHSGGGSL
9307	23208	A	9376	69	160	EHHTHTHTHTSHHTHTSHLPERFPCVLN SL
9308	23209	A	9377	336	199	EGITASARYSKNWVTTGDPAREFPMIQS APLMLLADPEFVSVQLA
9309	23210	A	9378	321	128	EPGFMTWASLAPTSSLQVIHRLGLPKCW DHRREPHPAYHSLYESGPSVQNGEEKG INPIIKMG
9310	23211	A	9379	440	286	SSDPSASASKSAGFTGMSHHTQLTSYS EGECLSYLVFLVLV
9311	23212	A	9380	392	154	KGSSPLSPPISLAGGKPPPPRKFFLNFF FFFNDRDVRSPCLPRLVSNWPQAILPPQ PHKALGLQAYATTASFIFLIVTV
9312	23213	A	9381	403	178	GRRHEPCRDADAHLEGIIFSAFYPKNWE TTGDGAREWTMSNSAPLMLLADPEFVS VQLA
9313	23214	A	9382	303	206	DPVSTKICSLQPPPPGFKRFSCLSLPSS WDHR
9314	23215	A	9383	215	116	SNNFVVCCCCCCCCCLRWSLTSLPRLH SCGTM
9315	23216	A	9384	2	285	ARHLLMQLSGGATLAISTIDLPLSTLIIF TLILLLTILEIAVALIQAYDITLLGSLY LGDNTYKKKRGAAFEETKFTSAGMQSK NFFLGLTNWR
9316	23217	A	9385	12	123	GYENFLPLTLHTQTHAHTHTHTHTHI HSKDPMEY
9317	23218	A	9386	3	230	KCWGYRCEPLRLAPLRCFFTPGGISLTS GPALLSNASALAEVRGQQLCPPTPFLPT LIAALTLLLPISPFLIIL
9318	23219	A	9387	590	396	ARVQWPDGLSLQPPPPGFKRFSCLSLLN SWDYKCAPP CRADFCIFSRDGVLSWPG WSQTPYLK
9319	23220	A	9388	224	79	GLGPVGHACPTLWEGEAGGSRGQIEAL PANTVKPRFLKRKKKKKKG
9320	23221	A	9389	249	72	LVYLIIVKKILFPVHIRTFNKIDHMHIGH KTCLNKLQMTEILQSVFSDYNRIKLEAS NN
9321	23222	A	9390	400	254	LRQPGSTNSPVSASRVAGITGTHHTQI IFVFLVEMVVHACNPSYSGG
9322	23223	A	9391	3	64	PPQKSDPPYKLVFVHLDLIL
9323	23224	A	9392	266	106	LTANFLFLVETGFPHVTRVGLLELASSD LPTLASQRAGITGVNHLQNFWPNGNF
9324	23225	A	9393	430	348	FGKPQPPPKGKSPPPRGNFPPQKAPKG
9325	23226	A	9394	481	311	LSLSEKRSIRVGVTFRSRRCCPSPLSLTG KGNLTPGVSQEIHSPWFGIAYSVCTH
9326	23227	A	9395	3	136	VFPRLVLNSWAQMIILCWPPKVLGLQAC TTRPSHFLPLLNSKYK
9327	23228	A	9396	143	347	NFVFLVETRFFHHVQAGLTLTSSDPAS QSAGITVRPEILTLKRYHFPSGILGTE GMVIMAYLLKV
9328	23229	A	9397	2	231	LELLTSSDLPASASQSAGITRGSHHARP SFTFRCVIHLEFNFMRGAREERLHFYCR WVIRRLTTFGRGYPSPAASD
9329	23230	A	9398	383	200	QHYLNRRLSLAQWMPVVPATQEAFAAGG LLEPRSSSLQCAMMLPVNSHCTLAWATH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REPHL
9330	23231	A	9399	3	416	GFLHVGQAGLKLTLTSGDLPTSASQSAGI IGVSHRAGCLKSIYLTFFTRKFFVQMSI CDFKVEIEGKIGFISVPISLQSIHIVN NFFFFLETGSFPPGWRWKEKFGLIAPLA SGVKGIFLPLPRENLGWRPSPIPPA
9331	23232	A	9400	400	151	FGYPQVFPPLPFLKPGGTFFLGPLKKN FFFPPLGLKIFSFKRAPPFFFFVRKGLI MLRLVSNWAQVLIIPPPPEVLGLQA
9332	23233	A	9401	324	154	FFFFFFKXXXXLFFFFFFFLFYIFFF FFFXFXKFFFFFFF
9333	23234	A	9402	413	312	PKLVLSNLQALLPRPPKVLGLQARAT ITQPK
9334	23235	A	9403	363	3	FKKKNFCLGGAGVFFFFYDPPPKKNIF YFPSKKIYFLSPASSSFFFLCFPPFIF FFFFFFFFFLENRWFLMENFIKGRGHV KGPLGQARDHDISGRWRREQCRASQL PGVRPRV
9335	23236	A	9404	401	82	SELPHDPINPTTGYIYPKKMKSVCFTDI CTPMFTTALFSIAKIWNQPKCLSKRITI FMFLVTYSQLFCTHYPIYPFPAPLS SSHNYHYTLTYENILLDSTYE
9336	23237	A	9405	382	219	WARWHGFLVPTSPGGEAGGSLEPGKRRV QLTQISPLPSSLGGKVLPLKKKNN
9337	23238	A	9406	3	195	YLYSLVETGFHHVQAGLELLISRDP LASESAEITGMSHSIQPKSAFYIQIPET FWQPAFK
9338	23239	A	9407	371	1	FRRLRLKNRLNLGNGGCSEPRLCCHCIPA WETRAKLGRKKKEERKREKGTMYNKMY KMYLELNLTCPEPASPQMTRQLEVLSS NPSPGTQFICKKQKFSCCFALRVSIY LLMSVFEVCSC
9339	23240	A	9408	326	229	RQGLTMLPRIVSNWAQVILPPWPPKVL GLQA
9340	23241	A	9409	81	231	LESASFPPGKVAHTCNPTLRGCAGWIA WAQKFKTSLGNNMAKPCLYKIK
9341	23242	A	9410	367	256	HPGWFWLVSVIPTLREAKVGRSLEPRS LRLAWDTWG
9342	23243	A	9411	2	192	VFLVEMGFLHVQAGLELPISGDPPASQ SAGITGVSHHAQALTFLNIPINPSHPPK ACCSKQL
9343	23244	A	9412	3	83	KNCLNLGGGCGSELRLCHCTLTWATE
9344	23245	A	9413	371	301	EDHPRMVILRLRLRYIVRLVWRMH
9345	23246	A	9414	486	337	AGLELLGSSNLPALTSHIAEITGMCHHT WLAYIFVCAFGWVLLDLCLAF
9346	23247	A	9415	378	254	IVAHCSLDLGGSDPLTSASRVAGPTGM CHHVWLVVFFVC
9347	23248	A	9416	160	309	VVRYSSNEFLPLFLFYLFKSNFTVFCCC YCCCCCWQSLTLPKLECGV
9348	23249	A	9417	162	339	RPSSFCEFLHDSVPELALPMKARFEKSR RSQVSWLMPVIPTFWBAKVGRYQARSLI PA
9349	23250	A	9418	1	147	GGGGCSEPRSCHCTPAWATRVKGLFKK KKKINFLVPPFIFLKSKTGV
9350	23251	A	9419	283	126	KMMYKGQAQWLIPIIPAFWEAKERGLLE VRSRPAWATEQDSTATKKNKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9351	23252	A	9420	133	3	ELMFSWAWWIMPVIPALWEAEAGGSRGQ EFKTSLPNMVKPRLN
9352	23253	A	9421	3	133	LRGLYSGAGTIRFEAKKNALALWAWDI AGDNCAICRNHIMDL
9353	23254	A	9422	409	291	ILILGGGSCSELRSCHCTPAWATRAKHR LKNKSPINVY
9354	23255	A	9423	1	210	RFFHLGLSKWDYRCESPHAGTRNEVLI YATIWMNSENIVPNEIIQTORTNIVSFY LYQVGRIGKPIDRR
9355	23256	A	9424	479	306	GVPTNQPWNSNRVKTPSPSTKNIKISWPWW CMPCPNPSCEGQGRRIALNPGRWRLQ
9356	23257	A	9425	1	209	GFFLFQGGGHHAGQAGLELLTSGDLPAS ASQSAGITGAGPNQGI FVALESPMESAA LLHLHVVLSSPCS
9357	23258	A	9426	628	433	RQGV AHLPGMECSGTITTHCSLELLGSS DPPASASQSSRLAVVSHCAQPSLLFSVL CLKPIFCCA
9358	23259	A	9427	417	125	FLRQSLTSSPRLEYNGAIPAHCNLCPLPG SSDSSILASQSIRITGVNHCTWPDAAVL RQNFFFSEKPPQFYSEGFQQTHIIKSNLL YLKSTKCTCYPYL
9359	23260	A	9428	366	256	SFFYRDRSLATLPRLGNSAWSQAILPPG PKVLRLLA
9360	23261	A	9429	3	140	GFCHVGQAALKLLISSDLPTSPSQSAGI TGVSHCARLTRLFSSHE
9361	23262	A	9430	368	3	VRASQLLCLPTQASAMAGTPPPASLEPC SSISDCCASSEQSGMGVGPSEPGAGYNL VVCSSLRTLEKCSIRVGVPPQFSRCHLSQ LPLARKGNSPTPCASWVRCLTLLQLML RGLYPLSCT
9362	23263	A	9431	3	131	LTMLPRLVSNWSAQGSSHLSPKCDWYR CEPLHSGLDIFLE
9363	23264	A	9432	384	274	LSFAMLPRLVLNSWAQESAHLGLPKCWD YRHEPLGLA
9364	23265	A	9433	431	273	PPPLGYFFIVKMEFPPVVDGFKLLNSS DCSTASPSGRISGVNHSTRPIF
9365	23266	A	9434	211	473	CVCTFFSFLSMHIFFLVGEAESHCVT EAGVQWHDLGSWQPPPRLRKFSCLSLP SSWDNRRVPPYPANFCIFSRTRVNSCWP GWS
9366	23267	A	9435	391	188	LPGSSDSPASASRVAGTTGGCRHTVLLG FEFKDNIRWIKLVEKAHTQYGNIIYICVI KYMPLFYVYHH
9367	23268	A	9436	331	115	SRDRGFAMLPRLVLNSWTQAICSLDSQ SAHLSLPKCWNRYRREPLCPASGEILSFI KPSSSKSFHNSTKKRQ
9368	23269	A	9437	3	109	IYGSYSLPACFFPSFLPSFLPSFLPSFP PFFLSFF
9369	23270	A	9438	2	167	ECNGAISGHCNLCLSGSSDSPAPAWATR VKLRLLIKKKKKKNQILFFYPPRKTLF
9370	23271	A	9439	648	310	VCPCILRHPAFLFAKSGNPLESSLSDHS SPTFKLTDRENLRHVKTSHSQSLPTSG FQPGLPDSTLCAWYPTRSPKLSPAGWVG GYRAPVGRRGPGSRNSWRLHWTPTISVG D
9371	23272	A	9440	1	170	YEIWFLDVGQAGLELLTSGDLSASGSQS AGTTGMSHHARPLKLTISVSSNKKVKC
9372	23273	A	9441	133	244	LFGYQTRGLAMLLKLDNSNWPQAVLPPQ

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						PPKVLGLLA
9373	23274	A	9442	365	176	RGSMDMVPSESTGYNLMCPLLRPLEK RSIRVGVTRFSRCHLSQLPLARKGNSLT PCASQVR
9374	23275	A	9443	368	231	VEAGFCHIAQAGLTFLSSTDPSALASRS ARITGVSHHARPIFLKE
9375	23276	A	9444	88	194	KMLEAKKKIEQQGGFTFENKGVLSAFNF GTVPSNN
9376	23277	A	9445	3	349	IRSGSYACYFCYPRECYALFHCYSMIVS YGPYYFMNIDQRHESRLSTIYIFKFEIG SKHVAQAGLELLCSSSPFAFTSQSAGIT SVSHHTRPQKIFNVIYSCDLHFHPGIEG PQR
9377	23278	A	9446	3	141	HAECSSMMIAHCELELLGSTDPPASASQ SAETTGISYHAQPYSTF
9378	23279	A	9447	2	282	ICPTRSRFPFPRVLKNGRKKDRLECSGAI SANCSLCLPGSSDSPASARVAGSTVAE EDSTRRAVRHQGSSRSAPSGRGSWAGKQ ERADRAQQS
9379	23280	A	9448	307	430	GLAWWLTPGIPILWEAEVGSLEVEFET SLASMEKPSLYYK
9380	23281	A	9449	2	253	IQCVVCVCVCVCVCLSVCLHFIAILGC SPWGSRLPCSVSSPSGRGPGGEDLSPLP PTMSVSPADFPPLAAAPGNIMTAIT
9381	23282	A	9450	1	166	NTGGGGEEIRVFSSCFAEDRLQKGKDRP GAVAHACNRSTLGGRGWITRSQIFFC
9382	23283	A	9451	1	123	NTRGLVMLPRLVSNWSAQVILQPLPPKV LGLQASVTVHINN
9383	23284	A	9452	396	291	SLCIKRVCAACVCVCVSGAKLRKLV LDFMRS
9384	23285	A	9453	1	147	FAIRARFSNTYTKIGTIHTYIYIYTYIY TYIYTHTHIYILSQVLEMEYEF
9385	23286	A	9454	394	235	TRSCYIAQSVVQWLFTGTLIHYNLQLL SSRDTPVSASQYLGLQAHTTTPDSC
9386	23287	A	9455	1	85	TNPVATLLEWQDALCFIPVGSAAPOGSP
9387	23288	A	9456	339	165	KTHWWGKKSFLKNPFFFFFFFETKRSRV TRLECSGVILAPKQKTKKQNDKTTINKT I
9388	23289	A	9457	3	209	LLILFSIKMRNRPDSPALLSTQLPPIFI YIHTHIYLYIYTHIYIFIYIYLYIYLF YIHIYVSLFPLK
9389	23290	A	9458	374	156	QAGLELLTSGDPPISASQSARITGLSQR AQLSELTLTVFTTRHCTCLCAHFLYYTV FLEGRNDEFISIPST
9390	23291	A	9459	287	3	EAGLLWRKATHKYAHTHTHTHTHTHTH RGLQNMNCKYITYQEIMTLAQAKNKG IPDSFPFTSSPPLTYPPALSFHQKHIP NKTTTYHGHC
9391	23292	A	9460	3	72	KTELKMKFTNILESFLMNNKS
9392	23293	A	9461	327	92	ISLFLVWGALFFPKKIYPPKKKSPLFF PPPPQENFNPPSFLAPPVFPQENPKF AGGRKIFCPPPPVFFVFFVFFVFFVFF
9393	23294	A	9462	3	173	ACRGDSGGPLVTRDLKDTWYLGIVSWG DNCGQDKPGVYTQVYYRNIASKTGI
9394	23295	A	9463	258	39	LKVILPSDPSSIFVCLFLENESRSVTQA GVQWHDLGFKRFSCLSLLSSWDYRRVPP PPAKFCIFRKHGVSPC

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9395	23296	A	9464	104	336	NHVSQCEEI FLFDEYYIFSRVASMFWV DAELGSDIYLDGKLKNSFLSFLGFFFF FFLGKKVFFFQNGGLGRPGQ
9396	23297	A	9465	410	0	LNLGGGGCSEPRLCPTPAWATE
9397	23298	A	9466	254	61	KKKKDAFFTIPLYPSSQNLFQFTQMDPD TNISQQLTWTVLPQGFRRHSPPTFLDKPF KQTSINFA
9398	23299	A	9467	403	255	PAPQLGGPPMPMPMAPPSWMMPMGCAP AMRLPIGGDI IWLVCVPTQISP
9399	23300	A	9468	1	1428	PARFKDLNLAGTAEVGLAGYFMDHTVAF RDLFVRMVCSSSTCYRAETNTGQEPGRGLY RVHHFTKVMFVGTGPGLEQSSQLLEEF LSLQMEILTELGLHFRVLDMPQTQELGLP AYRKFDIEAWMPGRGRFGEVTSASNCTD FQSRRLHIMFQTEAGELQFAHTVNATAC AVPRLLIALLESNQKDGSVLVPPALQS YLGTDRIATPHVPLQYIGPNQPRKPG PGQPAGPRVGYKALQPWPAQRLGPVGR PCRPEGQPLSCCCCGCSCWGLRTRCLAE VVTEVLTVGQVQRGPC TALLHKELCGTE PHGCASTEEKLLLGDFKKQEAGKMRSS QEV RDEEEEEEVAERTHKSEVQEQAIRMQ GHRQLHQEEDEEEEEEKEERKRGPMETFED LWQRHLENGGDLQKRVAKASDKETAQF QAEKGVRLVGGDRSLWQGAERGGGERR EDLPHHHHHHHQPEAEPRQKEEASERE
9400	23301	A	9469	265	170	GTESHVSTQAGGQWLNLSSLQPLPPGPK QFS
9401	23302	A	9470	289	110	RDLELASFLSFFPSFLPSFFPSFLPSFL PSFLSFSFLISFFPLPSFFSFISFSLSL FFE
9402	23303	A	9471	67	210	TVTTGQALHAYNPSTLGGRGQITRGQ DFETTLVPGDLNFSRVLASS
9403	23304	A	9472	2	186	TSLWRQAKNVEKKTDRKTEVLKTHGLL VCTQKSCSFLKNKNKAWLGKQANAPARK VEIRC
9404	23305	A	9473	417	265	FLSSFLFFFFFFFFFFFFFFFFFTV
9405	23306	A	9474	430	120	ASQKKKKKNKKKKKKKKKKKKGGAL
9406	23307	A	9475	1	150	PTRPVVQAGFKVLSSGNPPALVSQC FRI TGVSHRARPHLLNLRAPNLPVL
9407	23308	A	9476	404	109	PPPLFFNFGEFFLVEARLHHVGGAGLKL PTTSDQPSASQSAGFTGVSTRAQPTLI TLY
9408	23309	A	9477	391	235	PPFFFFCRDRGLTMLPRLISNSWAQVIL LWSPKMLGLQARATVSGLNKRY
9409	23310	A	9478	438	277	KRAPFFFFCRDRGLTMLPRLISNSWAQV IILPWSPKMLGLQARATVSGLNKRY
9410	23311	A	9479	399	279	PPPPVFKNPPPKKNKGAPKKKNISPPPG RKKYFFFKGPP
9411	23312	A	9480	247	26	LKAGDDSRVTLGKVHQSPCFLSLFFIQ VSCRDEGLTVLPRLVLNSRPQAILLPQL PKLLDHRCEPPLANHG
9412	23313	A	9481	2	176	HAPPHPANFLFFEEKESCIVTQVSIKLL DSSNPPALTSQSAGITGENQHGHMPMNCL SG
9413	23314	A	9482	2	178	HAPPHPANFLFFVEKESCIVTQVSIKLL DSSNPPALTSQSAGITGVSHHGQPMNCL SG



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9414	23315	A	9483	2	151	GRVGEGLVSLVSLVLDQHPVGTSDHRDA TQLGFQPLMSDLGSTGSTEGA
9415	23316	A	9484	420	325	FFVFLLETGFHHVSDGLDLVICPPRPP NTFV
9416	23317	A	9485	400	104	LEFFLFFFFFFFFFFFFWNPPKTFKKV EGLNFPTLLKLKFNPPPGPPKKKKEL
9417	23318	A	9486	117	280	SSTNQANNCFFFKKRGAILPRGALNP WAKGILLPWPCKGLKLRGGAIGPGQK
9418	23319	A	9487	76	353	VLWNTLEFCLLYLDLLFLFFNKEALIR KKKKKKKKKKRGGNKKKKKTPWQEK AGLFLGDTIIYSRGAVLKNSSGETPRHT PSGGLWPR
9419	23320	A	9488	3	122	HASEDNVFLHCSHSDLYVLLAGTASLQ DFSFFQKSPPP
9420	23321	A	9489	1	155	PTRPTVCSGAMLAHCNLCPLGSSES LASASQVAGTTACTSTDPFFFFSL
9421	23322	A	9490	3	212	BTGFHHVGLSGFKLLTSGDLPTSASQSA GITGMCHCVWPQFAYFCLLVLYDLHLKF TIIMLVLCLLFYD
9422	23323	A	9491	2	163	ETLFRHVGVQVSFEPLTSGDLPASASQSA GITGVSAMPSWMIKFFIAFYSCINC
9423	23324	A	9492	474	296	SQPAGTADCLLPLPPGSCFPTTIPCPAAL VPLPSFSPARLWPPQSLHQLPLPGTCS SCT
9424	23325	A	9493	7	151	LCAVEFVYMKPPAHEEAKAPSRGFVVR YAPWTASSEKGRDDGMGERA
9425	23326	A	9494	52	363	TTAPSLSVFLFTFTGELFVYWWVGTLE TSFISFFLFFFSFLEKDFSFSPAGRPWP NFGLIQPLASGVGGISRPNPPSRWELRA LPPPPGGLGFFFWKKGPPG
9426	23327	A	9495	383	118	WKPRPWVPPGAGVQTPPGPQGETPLFLK KKKKRGRGGPLFGPPSFGGGGEIPLTP APKGQEIYFPPPPPPGKKKSLFQKKK KRIR
9427	23328	A	9496	554	419	FFFETKPCSVSQAGVLWRDFGSLQPPPS QVQRDSPCPQASQVAND
9428	23329	A	9497	428	281	GSYVQLTFKYFSIYIYVHTLHVLYTH IYVYVHICIKYKEGYITGSVLA
9429	23330	A	9498	144	16	KVKKKVSQCPGIVAHNCNPSTLGRGGR IAWQEFETLSLQKN
9430	23331	A	9499	2	155	NLALLGSSDPPVSASPVSIGIRGVHHHAQ LIFFFFGKRAWFNPPGGRKGEE
9431	23332	A	9500	2	184	FIYGRDSLTMPLRLVLSNWPQAILPPRP PKVLGFRCEPPHLASLLFYRDILFTLG LKSV
9432	23333	A	9501	465	153	PHKVFLNKGPFETPQGEISRGWKTTRPP PPRERSRPFHRKGGFGSPPKLRQGPPFV FFSWPPWCPPPKKGARQQKGFFYFPP FFNPPFFFFCLFFIFEIV
9433	23334	A	9502	429	11	CRTLLGADCVCVCVCVCVCVKAFFPI SYSCHLVPSDLPLLVGVQFKCVHFGLSF LTCPPSPWPFGGAQPGSCYWGCLCL FACKLGARLTQTLGIPASGPGTWATPL GSCASVLRRLPGGSESDTLKVSVLSG
9434	23335	A	9503	436	202	LPGGYIFQEGEVKTKFSPLLRENNFFS NFFPPKNNGGGPRIPPPPPPPLFKKGV FFIPKFPAPRPKKKFKKKKK
9435	23336	A	9504	3	112	SFDLLSSDPPALASQASGITGVSHSHG

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						QKVYICNM
9436	23337	A	9505	426	208	VGHNLLVPRFLSPSEKRSIQVGVTRSSR CRLSPLSLTRKGNLSLTPFASRVRQCLTL LRLARAPTDLRPLSGTP
9437	23338	A	9506	441	189	CPANFFVFLREMGFHHVQGAGLLTSSDP PASASQSAGITGLSHCARPTVGSVDVLSL PSGQCTSALTGFMLGSTTVHSNAAARA
9438	23339	A	9507	117	278	NKALLCHPGWNHIKKVNGRLGMETHTCN PTTLGGQGQBFENSLGNIGRPHLYK
9439	23340	A	9508	3	126	FFVEMGFRCVGRAGLRLLTSGGLPVLAS QGAGITGVSHCI
9440	23341	A	9509	421	134	FLVERRSHHAAQASLEILSSSDSPTSAS QCAGITGMSHCARPKYTSFFRLHRHMPM ATPTKLPPTLASASPQVKVCLYPLLPST SKGEIFTLQLY
9441	23342	A	9510	2	200	PQPPTFYPSFLPSTPEPPAFYPRLPST PASRLLPQPPAFYPSACHLLPQPPTFY SLGNRARLHL
9442	23343	A	9511	414	204	ERDRKKERKKEGRKERERERKKEKKRKK KKERRKEGRKEGRKEASKQRVVIMVD T
9443	23344	A	9512	1	211	FHHVGWAGLGLLTSGDLPASASQSARIT GMSHHARHRHGFDNLSLCALAPSPPTPLW RRHRRRGHFTVPEK
9444	23345	A	9513	390	265	VFLVEMGFHHVQGAGLELLTSGDLPPLLE SQSAGITGVSSQQFS
9445	23346	A	9514	438	180	IGFRHVGHAGLDLPLGLDPLSLASQNA RITGVSHRAWPAMAFVNCHGAGGSVAMRT TRGHSCRHLGIGGFWPASLLQPVLASGS L
9446	23347	A	9515	126	11	RNLDFFLSLGLAMLSRLVNSWPQVIFQA WPPKALRFQV
9447	23348	A	9516	2	249	FLHVGQAGFVLPTSDDFRPTHPTQSSGI TGVSHRTRPLRCYFLRLNPIPLYVYAYY ILFIHSVISGYVGGCTAHYCHPRKVV
9448	23349	A	9517	403	57	PEGALVPQKKKKKKKKKKKKKKKKKK NIKI
9449	23350	A	9518	406	140	PHYNHTFVYNGVRLEDLQHMCLLTWWD REPLASNDFLVGVRVGVTGEIPSPILT CLKASCLFYSYHSRPPQTQSSSVMTVVF FFFS
9450	23351	A	9519	3	75	GIEWMVNCVVRNVHRPPRQRDIT
9451	23352	A	9520	183	6	LLTHLILTSALIGETIMVAPILQKNSGSE RECRLPRLVLNSWPQGILLPWPVKVLS QV
9452	23353	A	9521	89	339	LQCLQKSGKLEPGMTYTKLIDADVNVGN ITSVQFIWKKHLFEDSQNKLGAEMVINT SGKYGYKSTFCSQDIMGNILQNLKPC
9453	23354	A	9522	3	329	PSLMFPWLKLSFPGRPRGRQTYSRQTL ELKKEFLFNPYWTRKRMEVFHALGLTE RQGKIWFQNRMRMGKKENTRDNLPEAQN EEKVEEKGIEEKEKEEKEENRD
9454	23355	A	9523	1	156	AKTSMNVNEIFMAIAKKLPKNEPQNP GA NSARGRGVDLTEPTQPTRNQCCSN
9455	23356	A	9524	1	272	AKNSARALLGILGYRSHLISSLLCLEGI ILSLVITATLITLNTSHLLANIGPIAIL VFAACEAAVGLALLVISNTYGLDYVHN LNLLQC

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9456	23357	A	9525	1	62	GNDAWVCTNDMFRLALHNFG
9457	23358	A	9526	1	111	GDIHNNENMRQGRDKYKTLRQIRQGNTKQRIDEFEAL
9458	23359	A	9527	427	340	IPIGNIMSCDSHSHHELVMASQALNAIFHD
9459	23360	A	9528	439	27	PRRTDKWLTVEMIQDGHQVSLLSGELTV DQRASIIQFRDQGEKVLPTNVLCARGI DVKQVTIVVTFDLPVKQGEEDPYETYL RIGRTGRFGKKGLAFNMIEVDELPSPMK IQALFDGRNKQLNAEVPCQAAMED
9460	23361	A	9529	1	236	REVLITTNVCARGIDVKQVTIVNFDLP VKQGEEDPYETYLHSIGRTGRFGKKGLA FNMIEVDELPSLMKIQDHFRRKS
9461	23362	A	9530	437	240	QQVSSARPEPEAGEVSPFVAGVNSNSW AFKYGPGNPKQSGPEPKQTQVSFLLRR KGEASQPRQ
9462	23363	A	9531	413	260	LFDQVVKVASPSGLRTSTVRYGDPEKLK LEESLRQQAEEKGSALSVRISNV
9463	23364	A	9532	431	260	ASSGQMFVSKQAPPVRLPPFGISLFG GQIYDNISPRPPQGIAPPGGRGNIPNLG
9464	23365	A	9533	2	134	IHGVCVHMCVCACVCVYACVCVGGYDGR IFLALSSTVPSMVNIM
9465	23366	A	9534	419	53	LLLLTNGDRQTQREKIEACQSYFDAV VVGGEQREEKPAPSIFFYCCNLLGVQPG DCVMVGDITLETDIQGGLNAGLKATVWIN KNGIVPLKSSPVPHYMVSSVLELPALLQ SIDCKVRMST
9466	23367	A	9535	439	109	NCIVIIDSTPYRQWYESHYALPLGRKKG AKVTPEEEEILYKNRSKKIQKKYDERKK NAKISSLVEEQFOQKVLACIASRPGQC APADAYVIEGKELEFSLRKIKARKGK
9467	23368	A	9536	1	185	NTTSSHHFTIPCLVLYSTSTHTHTHTH THTHTHTHVRVFSYIPSDQVKEGCIPAP SVFSW
9468	23369	A	9537	168	280	NPNISIRLTSCCCCCCCCWKSPYNVYNR LLRTGFTFP
9469	23370	A	9538	142	324	KIVKMGFPFHAGQAGLELLTSGDTPGSTS QSAGITGVSHRSRARSIFLYPYLPSPVYL PWRRV
9470	23371	A	9539	3	139	YIGGMGQAWWLMPGKPRQNDYLSPGVQD QPGQHSETPSLQKGFKN
9471	23372	A	9540	383	318	MSTQNNIQSYPIGEDEESES
9472	23373	A	9541	372	207	YGLNMCRCQFRQYAKDIGFIKVGVCRR PCLGREGCGGYFFRERQTDSSLEW
9473	23374	A	9542	2	360	ARGDDHRSDDRDKDGLVEEQIERLQEKV ESAHSEQNLFVLVIFQRVIMILTEHLVR CETDGTSLTPWYKNCIERLQQLFLQHH QIIQYQYMTLENLLFTAELDPHILAVFQ QFCALQA
9474	23375	A	9543	379	75	TNLQQFAMSHGSAQVKHGKGVADALTN AVAHVDDMPNTLSALSDLHAHLRVDPV NFKLISHCLLVTLAAHLPAEFTPAVHAS LDEFLASVSTVLTSKYR
9475	23376	A	9544	380	56	RDLSMVRMKSMFAIGFCFTALMGMFNSI FDGRVAKLPFTPLSYIQGLSHRNLLGD DTTDCSFIFLYILCTMSIRQNIQKILGL APSRAATKQAGGFLGPPPPSGKFS

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9476	23377	A	9545	304	92	SKSRVTNNTLRSTRKDTMITLNTHSLLANIVPIAIVFTACEAAVGLALLVSI SNPYGLDYVHNLNLLQC
9477	23378	A	9546	394	108	KRIDFSLVDVTADDAGNYS CMMYQTKSPFWASEPSDQLEILVTVP PGTSSNYS LGNFVRLGLAAVIVVIMGAPLVEAWYSRNVSPGESEAFKPE
9478	23379	A	9547	1	335	GNAVGLNLHRINFDKYHPGYFEKDMKH YHLHRNQSF CPTVNLDKRLTFSEQTRLNAAKNKTGTAPIIDAARSVYKVLGKGLPKQPVIVKAKFFGSLIFCFRIWILID
9479	23380	A	9548	326	188	NFLRMGTVAHASNP SILGGLGGRTAGAQEFETSLGNITR PCLYFKK
9480	23381	A	9549	381	152	VTLLISL SLLQVVGIVLVVIARLN LNEVEKQWRNLNQLNNAATILVFFTVVINVFITAFGAHKTGF LAARASNPL
9481	23382	A	9550	170	65	IHRSKNKWK FHLKDGIMNLNGRDYTF SKAIGDAEW
9482	23383	A	9551	544	361	RRLRQENRLNPEGGGCSKPRSCHCTPAWATEQDSSSKEKKERKNLKGNTVKSVP LPLTSHA
9483	23384	A	9552	369	181	GVLGATSGDMQIHTFGSMIIGSITGMVS ELGYKFLTVSTADVMIQTLNLHLFSEHMSHQKKKSY
9484	23385	A	9553	1	516	SLVHVVEFGQAIARRLKPFQVQRFLYTG RQPRPEEAAEFQAEFVSTPELAAQSDFI VVACSLTPATEGLCNKDFQKMKETAVFINISRGDVVNQDDLYQALASGKIAAAGLDVTSPEPLPTNHPLLLTKNCVILPHIGSATHRTRNTMSLLAANNLLAGLRGEPMPSELKL
9485	23386	A	9554	386	56	LFPACVLRWQFASDGGDIGFVFLKTKMGEQQSAREMTEVLPSQRNAHMPEDGSLTCLQAGVYVLRFDNTYSRMHAKKLSYTV ELLLPDKASEETLQSLKAMRPSPTQ
9486	23387	A	9555	375	150	IVVGKTSFHVSIPLSLFFPGDVLVDLLQHILKQSKPRILFSPFFHPGNSIHTQPEVILHQTHEEGTGRGFSFLA
9487	23388	A	9556	3	354	CLPTQASAMVDTPPPALLP PCSLISDCCASNEQGSVGIGPSEPGAGYNFLVCRLLRPLEKHSIRVGVTQFSRCCLSPPSLTRKGNLTPCTSRVRRCLALLQLTLSELPHCPVPSV
9488	23389	A	9557	463	40	PIKVEDPEPVKKPPKEQRSIKEMPFITCDEFNGVPSYMKSRITYNQINDVIKEINKAVISKYKILHQPKKSMNSVTRNLYHRFIDEETKDTKGRYFIVEADIKEFTTLKADK KFHVLLNILRHCRRLSEVRGGGLTRYVIT
9489	23390	A	9558	338	104	NFKKKKKRRTKKKEIRTEEKGRGANKKTFRGPKKKETRGSNRSPEGKKNHGAKKEGERRPRKKKKKKKLLARYDFTCL
9490	23391	A	9559	1	152	NTCVCVCVYTGFC HVAQVAHELSSSNLPSSASQSAGITGISHHAWPGFGF
9491	23392	A	9560	517	238	SGPGESVPHPWSAVRTRPAKKPGSQCLLQSAFPLWCSSRRTTWAEERKLNTETFGVSGRFLRGRSSRGGRGGRNGTTPRNPTSHRAGTGRV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9492	23393	A	9561	709	280	NTSPALTAPCGRPRGIREMQCWARVPAPSSACPAWQLPSLCLRSTVPAPHPSPAHHQPCELSQHHRGGLEPALPGTRQRLCSRTWHRCVRFPLPGAQAEAGELGPAACATGRPLVSHSTDMEQAPGLTSLHQEPHSTARGGTATH
9493	23394	A	9562	3	130	YRGFCHVGQAGLELLTSGDRITSASQSAEITGVSHRAQPQMS
9494	23395	A	9563	409	160	NPGVKRSPCLSLSSSGGYWSMPPCLAYYKKKKRRFLKDGGLTMLPRLASNSCAQQFSHFGLPQSWDYRHEPLHIAQFFLFSL
9495	23396	A	9564	1	241	GICLGSNIGSGWMTSSLCPNYSNTLNQNLSTTKPFVPVSVGTNCGIEPWSGVTSGLGKMLFLYYYYLLLFQMTQPS
9496	23397	A	9565	2	215	IHWMMGWMDGWMDGWMGSCVRAVTGPGTSSPHTSTCGHAVCVCVCVCVYTCAHVFLALFGVEKNNYFLWKA
9497	23398	A	9566	244	117	DHQHLNWSVFISFSFKVIKARKNKKGILNPDSSMETSPDEFF
9498	23399	A	9567	414	77	FGGVPPGTLVPPTWLPVRVPPPPAFCLGELSPPPFFWRKGLAPLLNFFFSQGRGFPSPGGKGRPLPRPAGFPGFVAKPPFRPPGFSSTPSDCGGLPFFFFFCKKVF
9499	23400	A	9568	418	198	PPVSLTEIVSKSHKAELVFWMMPGTLEHPEGDNMYMEFIEVLTEALERVLLVRGGSEVITITYSYPTLNARA
9500	23401	A	9569	549	415	ROENRLNPGGRGCSEPRSCCCIAAWATEGDCLKKINNKKPKEQK
9501	23402	A	9570	546	1	KLECRGAIATAHCSLNLPGPGDPPTSATQAAGTTGTCH
9502	23403	A	9571	415	215	SRLRKKIYIYIMCVVYVYICVYICIVCVYICIVYICVYIYVYIYVYIYVYIYVYIYMHEFITFFSI
9503	23404	A	9572	374	138	LAASAAIQELFKRISEQFTPMFRRKAFLHWYTGEQMDMEFAEASNMNGLVSEYQYQDATAEEEGEFEEEAEEVA
9504	23405	A	9573	370	233	GSPFVRSVHQSGVSLSTQVDEGVRSGSKRMVAPPGGRYNITSL
9505	23406	A	9574	3	399	YSSPGPIALALRDPCHAGGSPNSLSLPAQGHPARAQGPQPQGGPSSLGSDLRPHVAHTRGALHGPAPAPASAPAGGSGSVAAASMSAPRPRAGGTGSLVLTAAHPASAGCAHRDAYVCKAPGRAVF
9506	23407	A	9575	314	48	SILPHSDPERCFSTIQPEEGTIHTAAPLDREARAWNLTVLATELDSSAQASRVQVAIQTLDENDNAPQLAEPYDTFVCDASAAPGQVSN
9507	23408	A	9576	505	264	IFVVEMEFHHFGQAGRLRLTSGDMPASASQSAGVTDMSHCTRPTFPNFKEPLGAVVTFLLCGMQVGRDELEDDWMAWS
9508	23409	A	9577	508	314	PATWKGCLSNFSSYLTKPADFIEHQVLSWEQVPDGFIFNERFKSFTVVVLNNVAEFVCKYKLL
9509	23410	A	9578	512	1	RMREAIFFSPGRLPRGAAPLRGPAGTLVPMPTPGECWLSLSVSAAGEKPYKCSVCESAFNRKDKLKRHMLIHEPFFKKYKCFSTHTGCSKEFNRPDKLKAHILSHSGMKLHKCALCSKSFSSRAHLAEHQRAHTGNYKFR

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						CAGCAKGFSSRHKYLKDHRCRLGPPQDKD PV
9510	23411	A	9579	3	487	WDLIYVGRKRMQVEHPEKAVPRVRNLVE ADYSYWTLAYVISLQGARKLLAAEPLSK MLPVDEFLEPVMFDKHPVSEYKAHFSLRN LHAFSVEPLLIYPHTYTGDDGYVSDTET SVVWNNEHVKTWDRAKSQKMREQQALS REAKNSDVLQSPPLDSAARDEL
9511	23412	A	9580	1	840	SKYLYDEGEEEEVFNDWEAAGGVAVPT LNALERGFSLSAMDWHLTYTDPREIFEVLS WLESCVAEQQRWRGWYTYTDLCLVLEEQ PTWQLALGSLCQRLVKLSCLLAVAYVSS VALAVASVAVIHQSLGLSCTPTPGPPDL GLTSRCLLEPCIPSVPPQLPLSLANVSSC LEGSMGLRSLWGSLLASLTTPPLPPDP PAPPTLLHNCHLCQKLQSDSPTCHACLH PNRTVPTALSSPWYHTYGLAPPWPWSPV PLSLPQPQQCSLFSVMELARLKSFFVFP
9512	23413	A	9581	2	158	IHAGFISVSVDNIIYICMCVCVCVCVC AHMCACISEHITHAPRLPEVFYTP
9513	23414	A	9582	3	144	YTAGVISVSVDNIIYICMCVCVCVCVC AHMSACFSEHITHAPMLP
9514	23415	A	9583	503	3	GKCVCLSAVWGSLLSAFRGSLSVCCLGQ FVCLSAVRGSFSVCCPGQVRVCLSAVRGS VSVCLSAVQGNVSVCLSAVRGSLFVCLL SGAVCLSFCLLSGAVCHLCRAPTPCLSR SLAHRRCNVNCEMTQLISVSYFFCWGW WRHRNNIHLQKCLRILMAYTGQGGP
9515	23416	A	9584	2	1358	AGLDSLHKFQVKIEKEKVYVRASQALQ LQRTKVMACISPSAGYSSSTNVLIIVG AETLRQEGFSDRIVLCTLDRHLSYDRPK LSKSLDTQPEQLALRPKEFFRAYGIEVL TEAQVTVDVRTKKVVFKDGFKLEYSKL LLAPGSSPKTLSCGKEVENVFTIRTPE DANRVVRLARGRNVVVVAGFLGMEVAA YLTEKAHSVSVVELEETPFRRFLGERVG RALMKMFENNRVKFYMQTEVSELRGQEG KLKEVVLKSSKVVRADVCVVGIGAVPAT GFLRQSGIGLDSRGFIPVNKMMQTNVPG VFAAGDAVTFPLAWRNNRKNIPHWQMA HAQGRVAAQNMLAQEAEMSTVPYLWTAM FGKSLRYAGYGEFDDVITQGDLEELKF VAFYTKGDEVIASVMNYDPIVSKVAEV LASGRAIRKREVELFVLHSGTGDMSWLT GKGS
9516	23417	A	9585	360	239	QCRKGLGKLVSFGLGIWLSLIDVLLIGV GYVGPVHGSSYV
9517	23418	A	9586	160	1156	MPRLTFAPKGWPHPTSLHPGQVTDQTT WWLFQELPTPSSENSMPPGLSTPTASQEG AGVPDPSPQPTRRQIRLSSPERQLSSL NLTPDPMEPPPKPPRSCSALARHALES SFVGWGLPVQSPQALVAMEKEEKESPF SEEEEDVPLDSDVEQALQTFAKTSGTM NNYPTWRRTLLRRAKEEEMKRFCKAQTI QRRLEIEAALRELEAEGVKLELALRRQ SSSPEQQKLLWVGQLQLVDKKNLSLVAE EAEMLITVQELNLEEKQWQLDQELRGYM NREENLKTAAEDQVLRKLVDLVNQ

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						RDALIRFQEEERRLSELALGTGAQG
9518	23419	A	9587	419	130	RRDPHLPRIMGRTRLNRKNAETRINAQL PLTDKGRMARHVLDNSGEWSVTKRQVIL LHTELESLLEYLPLRCGVLTGLAAIASL LYMLTHYLLPYA
9519	23420	A	9588	2	399	FSCEFNMENQCPLVVEPSYPDLVINVG EVTLGEENRKKLQKIQRDQEKERVMAA CALLNSGGGVIRMAKKVEHPVEMGLDLE QSLRELIQSSDLQAFFETKQOGRCFYIF VKSWSGPFEDRSVKPRHV
9520	23421	A	9589	19	205	LYCLVEWHDLCSLQPLSPGFRQFSCNL LSSWDYRHMPPRPTIKLSSYSIKLIYY LFMLVL
9521	23422	A	9590	500	407	KLTNEVRSVKRSQLFPEFSMCKEKLNT NII
9522	23423	A	9591	727	236	RRSRGLEGREALALCPGDGSHLLCRRTD SSFSSMAFFFTFMAQLVISIIQAVGIPG WGVCGWIATISFFGTNIGSAVVMILPTV MFTVMAVFSFIALSMVHKFYRGSGGSFS KAQEWTGAWKNPHVQQAAQNAAMGAA QGAMNQPTQYSATPNYTSNEM
9523	23424	A	9592	381	278	HPSVYKVASGLKEGLSLFGLNRCHCKW GEKLLR
9524	23425	A	9593	412	156	SQRCLSLGCHEHLANAYATIIICDNGFSA LLGPPLPGWIYDIAQKYDFSFYICGLLY MIGILFLLIQPCIRIIEQSRRKYMGAH V
9525	23426	A	9594	263	50	KHAAPPASLSLSLLHHGQKRACFFFAF CRDCQLLEGSPAMLPVQPAKLLVLEQV CLLCALLIPPSGRI
9526	23427	A	9595	432	309	GTFSERGPPLEPRSQTVTVDFCQEMTDK CTTDEQPRKDYT
9527	23428	A	9596	457	29	TLLPGWITAQASEGEIGASLPSSLPPLL YLPSSWRCSPSGALHPACPTGQRSSA LLPSLPQAPPFGCGMTGLRPLPSPSVGC CSAPSPQLLCPTQLPPAPESSEGGCSES RCVANVKYTRDLGDFLEKCTNGEASALE YP
9528	23429	A	9597	864	407	PSRRLSPTGRTTHGSSAACAPPPRRLER RSRTSRPPWGPPHSASARTQRACTTWYS RSWACSCSWITSRPSWMTTKRTCMIFST IPTTPRTALWRGLSLWKDAWLLTRLKLA PSSPTSMPTTTCTACSSTWMTGSPAR WASTPMPRSTT
9529	23430	A	9598	421	145	LTQHNGDAAASLTVAEQYVSFAFSLAKD PNTILLPSNPGDVTSMVAQAMGVYALT KAPVPGTPDSLSSGSSRDVQGTDAASLDE ELDRVKMS
9530	23431	A	9599	1013	604	PGRPTRPDICLLLERMEEQVKNVMTFR EELYNIEKAFAFEVERQELLASNKKKWEQA LQAHNAKELEYLNNRMKKVEDYEKQLNR QRIWDCEEYNMIKIKLEQDVQILEQQLO QRKAIYQLNQEKLEYNLAGAEER
9531	23432	A	9600	409	191	HHVGQAGLELMTSSDLPSLASQGAGITG VSHCARTVYGLSIVFSSHRGFASVRTP PSNENFPDRPISIAHP
9532	23433	A	9601	367	1	PPRYSPPLGGVRRGGVPPGPGVLAPPFPK GKPPFFFKNPNLPRPGGAPYSPPFGGV

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						GRGTSFNPGGQSGSPGQKKPPGPPRRGTG GFFSKKKKKESTKLPVTSHTTHCWFLPE ALDLELDPLY
9533	23434	A	9602	1722	394	GWNGSWNDNLVDTSPDKRDLQDICRRY MEDLKICFYRELNSKTTLKFFVHTSFHG VGHDYVQLAFKVFQFKPPIPVPEQKDPD PDFSTVKCPNPEEGESVLELSRLAEKE NARVVLATDPAADRLAAELQENGCKWV FTGNELAAELFGWMMFDCWKKNSRNADV KNVYMLATTVSSKILKALKEGFHFEE TLPGFKWIGSRIIDLLENGKEVLFAFEE SIGFLCGTSLDKDGVSAVVVAEMASY LETMNITLKQQLVKVYKYGHIKTSY FLCYEPPTIKSIFERLRNFDSPKEYPKF CGTFAILHVRDVTGYSQPNKKSVLP VSKNSQMITFTFQNGCVATLRTSGTEPK IKYYAEMCASPDQSDTALLEEELKKLID ALIENFLQPSKNGTSGRSCLGVPPNTV MTLCGAYGNRATRRNCHTLEPCG
9534	23435	A	9603	14	356	DFVERTQYTHQTHTHTSHAVRLSPRP VQSRPEASQTGPTRTKPALGPAHPSPRG APCPDDPGSLRMLGYGSRAHNSRRGRW GHGRCKDQRAMGPHSHMWEALPPGALS SP
9535	23436	A	9604	477	264	LVETGFLCVGQAGLELLTSGDPPTSASQ SAGITGVSHRTWAALSTFTVLCNYHYLF LEVFFHHPKLKLSPH
9536	23437	A	9605	1	378	EGINFSNLRRCVVMVGMFPFNIRSAEL QEKMAAYLDQTLPRAPGQAPPKALVENL CMKAVNQSIGRAIRHQKDFASIVLLDQR YARPPVLAKLPWIRARVEVKATFGPAI AAVQKFHREKSASS
9537	23438	A	9606	417	254	MVSLTQELCPVAMRVAEGHNKMLSNVAE RVTVPFRNFIRGALLEQAGQDIQNKLE
9538	23439	A	9607	404	272	PPKFLLESQPIRVVDWWSLGMALMYDMLT GAVGAQLKAACIIGLC
9539	23440	A	9608	409	205	HMNGSLSGDIDGLPKNSLNNISGISNP PGTPRDDGELGGNLFHSFQNDNYSPL PCSWSLFYSLPF
9540	23441	A	9609	449	263	VWICPCDPPASASQAGITGLSHHLPKC WDYRLEPPRPAHCFCFYSFTMRNRNLLS LVKYSR
9541	23442	A	9610	366	75	TPGLKRSSCLSLMSRWGYRIEKKRTIIR SVVEAIKEQDGREVDWEYFYGLLFTSEN LNLVHIVCHKKTTTKLTCDSSSIYYPQT RLKRKQPVKRQ
9542	23443	A	9611	1	801	PGYCGSWVFTCGALRQLSGGRDLSRGAR MGNSALRAHVETAQKTGVFQLKDRGLTE FPADLQKLTSNLRITDLSNNKIESLPPL LIGKFTLLKSLSLNNKLTVPDEICNL KKLETSLNNHLRELPSFTGQLSALKT LSLSGNQLGALPPQLCSLRHLDVMDLSK NQIRSIIPDSVGELOVIELNLNQNSQI SVKISCCPRLKILRLEENCLELSMLPQS ILSDSQICLLAVEGNLFBIKKLRELEGY DKYMERFTATKKKFA
9543	23444	A	9612	179	329	KGLAFCPPPGRGGGPPPLWPPPPSYKK IFGLKTPKSGALSPPPPPPCNF



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9544	23445	A	9613	410	298	PRFTPFSCLSLRSSWDYRCPPRPANFLSLSSVLHGT
9545	23446	A	9614	1	130	NPGSHCVAQAGLQLLSSGNPSASASQSA RITGVSHCAWPNTTI
9546	23447	A	9615	1	146	NTWRLHMVPRLVSNFWAPGILLSWPCKI LGLQKRATTMPGPEIYTSIN
9547	23448	A	9616	552	26	RLSIRNLLTHAFFAEDTGLRVELAEEDD CSNSSLAIRLWVEDPKKLKGKRDNEAI EFSFNLETDTPREVAEMVKSGFHESD CKAVAKSIRDRVTPIKKTRKKPAGCLK ERRDSQCKSMGNVFPQPQNTALPLAPAQ QTGAECEATEVDQHVRRQLIQREPQQHC SSVTGD
9548	23449	A	9617	420	48	FSQILRASIEFDSPFWDDISESAKDFIR HLLERDPQKRFTCQALRHLWISGDTAF DRDILGSVSEQIRKNFARTHWKRAFNA SFLRHIRKLGQIPEGEGASEQGMARSH SGLRAGQPPKW
9549	23450	A	9618	190	285	RQGLTMLPWLVSNSWPQVLLPWPLKVL GLQV
9550	23451	A	9619	392	308	SPIKPKIPLSAPRKNTNSVKYRLKFRFG
9551	23452	A	9620	166	23	FCNPISPSSLPSSLPSTFSPFLPCFLTFLP LPCFLPPLPFLSFMTLTF
9552	23453	A	9621	49	374	DRRGIRIMAAALFVPLGFSLLGTHGPSG AAGTVFTTA*YLGSKILLTCSLND SATQ VTGHRWLKGRVVLKEDS\LPGRKPEFNV GPHPPNGDKSSFVFPSPPCPRLTF
9553	23454	A	9622	85	472	SHVFPPLRLTLTLHSMVPETRPNHTIY INNLDKIKKDELKKSLEYAIFSQFHNLD ILVSRILNMMGQAFVIFKEVSSATNSL RSMQGFPPFYDKPMRIQYAKTYSYIIAKN KGTFLLSC/DRKLIK*TPQ
9554	23455	A	9623	170	2	IFFFCFERFGSCSVA*AGVQWRSYSL* S*TPG\SSNTASATS VAGTTGL\HHHAE
9555	23456	A	9624	2	469	RRLCSDRGLQRLSGMSAAVTAGKLARA PADPGKAGVPGVAAPGAPAAAPPAKEIP EVLEDPRRRRYVRGRFLGKGGFAKCFE ILDADTKEEFAGKIVPKSLLLPYHR*K MFMEIFIHRS LGHQHVL*FHGYF*EHDF MSEELEL\CRPRSFLF
9556	23457	A	9625	661	1393	ASPPPSQTTPAAPGCSAGEVSLA\GLCL QERRLDVAGFSIFIPSRYLDHPQPSKA EQDASIPPGTHEALLQTALSPPPPPTRP VSPPPQKAKEAPNTQAQPISSDEAS/RWG RNP*CS*SGSPHQWPLPHLP*GRL*A* PSPCCPG*VG/PVHSPQARRRPITTSIS QRSWKFWPKPTVFRETSGGPWAMP RPSM PSRASISLSPRTSRKQPRPLTLGCCVW HVVHTDGERATCGDVRRAHHSR
9557	23458	A	9626	1	286	PTMAKLIALTLMGMEALFWNHQASYQT RLNALREVQPA*LPCNLVKGF*TGSED F\EILNGLTFISSGLENPWI*RLDP\N SPGKMLLMDLNE
9558	23459	A	9627	173	491	EGPLPLESSSNWQQADLDKKSRELLWKT VYLL*LNIQLPYNPNPILGINPREHT C\HQEMCTRIFIATLFTKAKA*K*PRCP *AREW/IK*/IWNHIEHY
9559	23460	A	9628	351	1	VLGDALQSRRGSSRKAGSYLLSRSP/CS

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						EGGRGGCWAWNLGTMSSVASGHGAWVPR ELTS*AWPEPGPAGQREGRPPTPCPPT CAHGPPAQF*PRGKAAYPG/CLGLQWPD *SAFNP
9560	23461	A	9629	599	11	KMWR**H*AKSQIRNAIPFTIAHK/RDL KSLKIQLTKEAKDIYENYKIPL/NEIR DVTNKWKNIP\CS*IGYLYSTYKYKCIC LVNIYL
9561	23462	A	9630	226	1	KCDNLGYSTFFFFFFFFFFFFEIGSYFVA QVGV*WHNYSNS/DASAFQVAGTTGVCH HAQLIFNLFVEVGSHYVAQA
9562	23463	A	9631	241	1	VSGCPLPRG*RPQPQSPSTPGTSD HPCTPCR/PALRR*SP**LPCLDLPPAS GPPSTSGNSTGTMQPT*PKLNSSSS
9563	23464	A	9632	201	1027	MTLTAPAGQGQSSQCLWRRPL/PLPPG PDSEEPGSGAAG/PGSSL*SPDLPPAAP PKP*TSS*EMNTVGSTQEGSGLAQRITQ HCPVPPST/RVDILGTCLQFPALCLTS APWLVRMPSPQRSSREIP*RLEAF/SLR TPIPAHSAQPSHQEKEP/PSPR*DHGD* PPP*PKPPTHQTLAQAPRSGQGLARPT LPYPPSPLRVTPRICRVHV*GHLRRPRG PPSSARRPTWDRVGLPWEDLEVVLCR GPAWLLARTSAPFSSLPHTACTGKKTTM PF
9564	23465	A	9633	103	379	YHCITIIVLKCIFFFFFLKPCILSPRL EARGIILGH*NLCLT\SQLLRRLRKSP LTLEGGVCS DPRSPHCSPA WPTKGNFFS KGKKKILD
9565	23466	A	9634	155	405	VPAFRSVTNISISVSFFFFETEPEGFVTQ AEMQGLDIGNGQPPCKLSSFA*ASQVM GTTGPRH/HC*ALIFLVKTGFPHVAKTW F
9566	23467	A	9635	4	423	GAMRGDRCRGRGGRFGRSGGPRGRFRPF VPHIPLDFYLCEMAFPRVKPAPDETSFS EALLNRNQDLDPNSGEQASILSLVTKMT YEIDNLT VAPGTLDVLI EERQQGGPYIK GTMTT*RH/SVADLT VILQILT TWESVA S
9567	23468	A	9637	2	492	GSRAIGFGLAHELERHLIKIWLASTVR* DLA*LMNWSG\SHKDLAGKYRPILEKAI QLSGSEQLQAFKAFESMVNENVSLVIS RQMLTDFCTHLPNLPDSTVKEIYHFTLE KIQPIVISFEEQVASIRQHFASIYEKEE DWRNAAQVLVGIP*TGQKQYNVDYKLE TYLKIARLYLEDDDPVPAY
9568	23469	A	9638	1	417	VVQGLGLVMGSPSRRLQTKPVITCFKSV LLIYTFIFWITGVILLADGIWGVSLLEN YFSLKDKATIVPFI\LIASGSAIILFG ILLCIFSV*HYPV*LLLVTFLL*LLVFL NKWWISPHFLILTFNYLLFDIIDNSS
9569	23470	A	9639	125	451	IYRKPLKSIRRVGGLHLNKIFFFLKQI WGWARGLMPC*HFGRLLKGDCLTLGIGD /SRG/RVDHDPALQPRQSKTSLKINK IGWAQWLMGPAPWEG*AGRSFGAGI
9570	23471	A	9640	670	927	GHVLLPRRAGCAQPGTGPAAAPAAVQR LPGGGVQPSGPGGRAGQGGLRG*AGG NPGTGF/GGPHASALLPPSEAPGSLPS

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						QFR
9571	23472	A	9641	115	460	ISWIFLIICVGGFFGGGGGARVPLCHLSP RLECSAIRARCGDFPGSSDP*ASAS* VAGTT/G/SCHHVQLIF
9572	23473	A	9642	1	431	AMRAEVLVYCCRGALASGCVQAFRRY\ WVLIIVDPDNEQANASIIIVKLTDSEFTE QADQLTAEVGKLLGE*KVDAILCVAGGW AWGNAKFKSLFKNCNCDLMRKQSIWTWTF SHLATMHLKEGGLLTLAVAMAVLDGTPG MIGD
9573	23474	A	9643	154	408	IIMNAQSVEEDSILIIPTPDEEEKILRV KL*EDSDGKYGSKIIPWNHLEPENFRLL FKHVG YLD*SGLY\EILTKF*ILCVLCY Y
9574	23475	A	9644	3	403	YSQFFGGPKLEDPIRPGVFSQPGEHRGH PFQIF*KVGLGNGARPGFPVLGKVKCKD NLKLGQGQCSRVMHPRTSAWAIERDPV LKKKKRQR\EHQCSNEQKHTN
9575	23476	A	9646	3	399	ARAMVLSPADKTNGKAAWGKVGAGHAGEY GAEALERMFLCFLTTTKTYFPDFDLSHGS AQVKGHGKKGADSLTNAVAHVDDMPSAL VALSDLHAHKLVEGVPVNCILLRH*LLVT LGG\HFPWLTPGGIAFLEKF
9576	23477	A	9647	22	407	APSAWGMCHFTTEEDKATITSLWGKV\NV EDAGGETLGRLLVVYPWTPQRFSDSFGNL SCASAIMGIPKVKAHGKKALTS LGDAI* HLDDL*GTFAQLSELHCDKLHVDPENFK LLGNVLVTVLAIFHFGKE
9577	23478	A	9648	243	2	QIATTTTLGPGSEGVGKRLDGS SSRHHSQ VESVKH\PRDLAQDA*GHGSAPRPLCPP PAQSWHCLRGPC LAPHPTLCPSR
9578	23479	A	9649	283	196	SYFI*IIITTHSLI\ISIPLLFNQIN NNLFSCSPTESSDPLTPLLILIT*LLP LTIMASQRHLSSEPLSRKKLYLSILISL QISLIITFTATELIIFYIFFETTLIPTL AIITR*GKPTPLIQ
9579	23480	A	9650	10	354	QLRVITRLTVVNN* TSA*SRGVSY*AH \SSDALHL*RELTEQRFIVSVNCAIAHC RHQSASEDHVKLRNEVTEFAQTWDADES AENCDKSLHTLFGDKICTVATLRETYGE MAD
9580	23481	A	9651	2	404	AFGTTKWVTYISVLFCLSSAYS RGVLRRL DAHKSEAAHRFKDLGEENFKALALIAFA QYLOQCPF\EDHVDLVNEVTEFAKTCVA DESAENWDKI\LHTLFGY*LCAVACFRE T\YGETAAC*AKHEPVEDE\CFLR
9581	23482	A	9652	83	396	NIPGVGGGGVPIPLVWKNISHTQR*RE PYIQSLRSGNWSERM SHVAR*QRHHP YYI\LLQAQLSMA\SDPANVMDSVITA GVLVA/SRRARRISKLGHR
9582	23483	A	9653	67	954	REGNHNTERNCKRPPQDTGPTQ/RPGGP PPEVPWQDASSAPTAAAPVGKLLPS*G PPGSASCQGR*TLGSVHWL*GSPLSPS AGGRALPYGPAQGSQGHWENTGRGTPL PGSRET*GHELTGVEHQHKA PREPQA GQPRPCPVWQSLPPT\ARSPSWSQGERP
9583	23484	A	9654	1	252	RPPQLLASDSLPPSRPPSPFLLSLR PPLSRSLCLSHYLCPLSLIQLTSPFD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TFSPPKSTTSGPPQPEDSPSS*PPTPSP P\PPSLSSLPSSLSSAPPF/YVHSVSP TISAPLYP*YNS*PHFPFPFPRKVQHL ARPSPKTARPPWTIRRI
9584	23485	A	9655	1	394	SLRIYCFVIEVICFLYLL/FIMYSIS*G I*LLMNFTILCIGY*LLQYFFVVKSF YFNFIPIFILFLYLICLLVF*LIFFDL SYF/MCLRLIIFNLFY*LFLLYSICLWN MVLILLISKLF*F*FCGRFALIQ
9585	23486	A	9656	122	371	SPYLLLLQGGVSWIVWLLNVSTNSSFL FPETGSHCAVQGGVQWCGRSLQS*TPG /SQS*VAGITGMCHHAS*LEKFFVEMG
9586	23487	A	9657	425	3	KTSMNNSIVPHISIPTLNVNGLNVPLKR YRIAE*IKIHQPSICCLQETHPTHKDSH KLKVKGWE*IFHANG/QGVAILISDK/T DPKATTVK/RDKEGHYIIKGLVQQENV TVLNLCPNTGALKFIK\QLLLDLRNEI NANT
9587	23488	A	9658	179	373	VHSWLLWGSQS FVLFRPLTD*MRLTH/I MKGNNLESKSTSLSVNLIQKHPHRNIQN V/AQNIWVSWNS
9588	23489	A	9659	103	373	LKHVLRCLQSERKLHYLFNIDQWGKFY TWDDLYECISSKFTTHFFSFL/FFSF* SQGLALSPRLDCSDAIIAHCILEFLGSS HAPTSAS
9589	23490	A	9660	216	424	TDINVTTKTIKPLDENIGITLYDLGLGS GFLDMT*T/AQVANEKIG*WDFIRNLKL TCIGHYHEVKKNPW
9590	23491	A	9661	276	2	PRIGKLPTNMTEPLTIKEMLINLAMRFH LSPVRMAI/IKIKSNRCW*GCREKGI\ IYHYWWECKLVQPL/WKSSLK/FIK*LP IDLSFVPAIPLL
9591	23492	A	9662	239	356	ICIKRRK/WSGTVAHTCNPSLGGQGG IA*VQEFQPGQQ
9592	23493	A	9663	1	340	RHELMTPHAFGAMKRVTFISLLFLFNLA YSRGVISRDHRSEDAHPKDLV*ETFK ALVMIAFAQHLQQRPFEDHV*LLNE\VT EFAKTCVAEESAENCDSLHTLFGDK*C TV
9593	23494	A	9664	759	1039	KRIPFGRPRRVDHLRSGVRDQPLHDET PS\LKIQKLAGQGGICL*SQLRLRLR*E NHLNPGSRGCSEPRSCHCTPAWATE*DS ISKKNNTKIS
9594	23495	A	9665	1	355	ITDLYSMFHFG*VDLATITSLWGKGNEQ KAGR*TLERLLDVYPWTHRFFDSFGNLT SASAIMGNPIVKAHGKVLTSLGDAIMH LDD/LKGTFAQLSELHCDTLHVDPENFH ENPCDGS
9595	23496	A	9666	364	3	APNIPPSVTRIPALLAFRSQCLCGSCPL PLATEPVGLLSMSFQAAPCFTWWVTEA WLTGISWPPDFLISLLCI/HINYNAVIF RKYRPRVGAVAHICNPSTLGG*GGWIA* AQEFETSLGN
9596	23497	A	9667	1	357	PISNAMRHLGQEETATITSLWGKVNVED AG*ETLGRLLVIYPWTHRLFDSFGNLS ASAIMGNP*V\KAHVKKALTSLGDAIKH LDDLKGTFAQLIELHCDKLFVDPENFKL LGNVLAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9597	23498	A	9668	24	369	APRPDAMGHFTEEDKATITSLWGKGNVE DAGGETLARLLGVYPWTQRLFDSEGNLS SASAIMGNPKVKAHGKKVLTSLGDAI*H LDDLKGTFAQ\LSELH*DKLHVDPENFK LLGK
9598	23499	A	9669	12	365	LLLMDGERK*FLETDSAPCEDAMNTVEM TTKNLE*SINLVDKAVA/SGFERIGFNF EKSSTLGKMPNSIACCREIFHERKS/S MWQTSFSLSYFKKLROA/PAAATTLDHQ PSALRQDPSP
9599	23500	A	9670	346	2	YPYDPWSLINNMFFLKRQNFLLKEGT LTFPFKGFRGDLSLFFWPPYKLFNLKSF L/CKFLEI*RYFFG*IIFFFFFFFFFFL RQSLTSPRLECNGTISAHCNLCCLPD*S NSP
9600	23501	A	9671	121	364	HKKKTAGRVQWPLLVPALWEAKEADCL SSGVQGGPGQHSKTPSLP*PSKSWDYRC TPPHLASFCNFFSFFFGRDGVLLCCPGW P*TPELKQSA/CLGLPKWDY/RARATA PGLLFF\FMLKYVLVPAVNIANAN*KE LSEPDVKNEICFV
9601	23502	A	9672	437	223	EME/FSLLLPGLECNGTCLAH*NLRLG SSDFPASASPVAGITGVRLHAQLELYFL NLLGFFFFIISLVVYLS
9602	23503	A	9673	100	338	KSRPSAVANLTPVIPALWEAEAGGSPEL KQFSLSLSSRDHRFATPC/RG*FFIFF VEMEFHCVAQCGFELDSSSPPTSA
9603	23504	A	9674	161	1	SFLWKLCLRGAPSCMRCLA\LL*DVSQ LGY/SGVRDPLEEAVCFPSDLKLRAGR
9604	23505	A	9675	304	1	VPPLASQLGDKRRIFFQKKKKKKKNKDK IHIIISILKKFDKI*YSLIIK\TL*KL GME*TYLNI IKVIYDRPTASIIISGEKL KSFPLKSGR*QECPLL
9605	23506	A	9676	111	346	SKEGSKEGSLEIWGFLVLAFFPPFFPPF SFFFF\*RQAGRPRLECRSMITAHCNLE LLGSSDPASAS\QVAGTTGPTSP
9606	23507	A	9677	3	349	ARAGRIKDLWLGGFFFFFFFFFFPKKTP FTRDKGGKLTAKKNPNHPVKREKKKP PPGTRGGKNPPGNPFWGFQPRFFFGG KTFGGGAHPDPTLG/PSPQS*KRPF GK RGPPP
9607	23508	A	9678	38	368	QASLLKESESERKSPTSLTSLQKGMIR LCEEGMSKAKAD*RLGLLH/QVSQLVNT KEKLFKEIKSAISVNTLMIRK/RNSLTA DMDKV VVAVIEDLSSQNNPLSQSLIHSK A
9608	23509	A	9679	187	345	PFILFFETESYSVA*AEMQWCDLGLSQT PPPG\SSNPPVSALWEARAGGSRSQ
9609	23510	A	9680	192	468	ERTSLFTIHLKLLTITNSAAMSNHV*V FV*T*IFLSLGQMPKSVTAGNSGSLFR FFK\NCQTLFHGGCAMLH/SHTQLNAIP LFRNLWQHLS
9610	23511	A	9681	141	367	GSWAASPCSCCTMDDFAKESFTVVDYVLL ENCPNMGDYVAPQFMTDNYVRVTQLNW DGVGTQ*KDYI/SSERNL
9611	23512	A	9682	193	3	IFGERR*ILKIYKLTGHVGLRL*SQILR RI/RLNLGGGGCSEPRSCHCTPVWATER DSISEKKEK

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9612	23513	A	9683	1900	1988	NLVHFEHFPSPSLFTSPSLCHIF/CSRDRVSPY*PGWSRSPDL/RYLPLCLDLPKCWDYRRESPCPASSRFLMNFYLY*NTTLWQ*KTIPLLF*SGDC/S*FF*YNFLAHTSSTMVNSGISRNSRPVFKLADKAPSHSPLSILAFGVVEFF/NLGSQPPQLK*ASHLNCLSSWDNRHAPPCPDNFFFNIL*RWGFPILSRMVLNSW/PLCSLSTASQSSG/ITGVSHCAGPILVF
9613	23514	A	9684	69	358	ILIVKVFFPHTQKPNFVRLSLQSIQOMLLPERKWTTHAQKTCVSSENTERCHEKQVITSHWLGMVAHSCNPSTLGGGGWIT*GQVFET/SLANTVKP
9614	23515	A	9685	66	344	IGEKLLTDTKHRNWVLETE*APGKDSVNIDEMT/TR/DLEYIYN/TDKAVTGERTDFNFKSSIRGQSL*YSII/CAKGSQQKQQLSLVPYFKKLPO
9615	23516	A	9686	269	1	PKIQNGHCKTLPKNPSQSDTKTFPLFTSGSSPQPHKLSFCFSAGPTLPSKTQLKIH L\WQGTVP HAYNPSTLGSRGGRIT*GQEFKTIQ
9616	23517	A	9687	229	361	DRYYYKSHFKPGAEEAHAC*LVLASFFMCYRAIMINK*HLYHRKL/VYQVIRH*KYRD/I*THVTLTTTL*DRYYYKSHFKPGAEEAHACNPSNLGG*GG*II*GQEFKTSLANMA
9617	23518	A	9688	318	46	KLYALNDMASNTCKEYDNLIQYRYKIYKRLIQHD*VEFIPEME/NWFNI*/RKSNVIHYIHSLEWEEKNYMIISLDVADVSDKIKLTFLLIF
9618	23519	A	9689	168	3	GNSNTMIFFTILYLFYFF/LFFIFDMKSHSVARLECSGVLAHCNV*LPGSSNSP
9619	23520	A	9690	192	3	WHKASLSNPQAGCMQPRMALHEAQHTFVNFLKTLWAG\ PVAHAYNPNTLRGRGGRIT*GQEFK
9620	23521	A	9691	388	1	CRSAGVCWRSTDPVCLGITSSGCRTAEIVACSFLLWKLHSGAPARCQPELSCMRC\R*TLL*GVSQSGGTGVRDPLKEAVCPLAELNGARRSTALFRASRQDSLSLLKLRPQLPLLPGALSQIEGI
9621	23522	A	9692	226	3	WFLLPQVKLAITMPRLYFPNLPFFFF*DRV/CTVAQAGVQWRDLSSLLLSLLGSSSPTSASRLTGIILOHHA
9622	23523	A	9693	305	1	NHAITTVN*FGLIRHLVTKAAFNSGEVDIV/SIKDPLIALNYTVMFHHDSTHGKFRGTVK
9623	23524	A	9694	320	1	PRDPPASASQSAGITGISHQAWPDMILYIENPKDSSKNPLGLINKYSKVAGYKINTQKSAFL*TNNYLKN*P/MRTIPTIATKKKYLETYLTMEVKDLYTENYKM
9624	23525	A	9695	263	1	VRILLFSESLALSRLCSGVISAHCTLCLPGSRGALSLLSRVDY/Y*VFLVKAGFRHV/GQAGLEFLSSGDETPVSLPDFWDYRCKPR
9625	23526	A	9696	262	359	IRKIKIWSGVVAHTCNPSTLGR*TKAHEGSLYCLRVGKIVSNKVGTRS*FFRTQK*V/HLFFS*VYHINGSH*SRTSL*IRK

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						IHKIWSGVVAHTCNPSTLGGRVWGT*GQ
9626	23527	A	9697	166	473	TQDTSQPWKNIWISFGSLKVFENVDIHK LYLELDNRHRSWMTDILLFFYF*DGSFT VT\RLECNGAILAHCNLHLPGSSNSPAS AS*VAEVGGTLEPRRLRLQ
9627	23528	A	9698	456	59	LFLWKLHLRGAPGYVRCRLA\LLGGASQ LGYSGVDRDPLEEAVCPFSDLKLHAGRTT TLFKAVRYGHLCLQKFLLPFVRLCPAPT GGVFTVRQASMSCDGLLIV*\VSEHR*L PKPQQFWELVPKFVRPGLKSL
9628	23529	A	9699	4	375	VPCSSVTIVSEIAFLMWLSAQLLLVYRN ASDFCMSSLYPETSLSLTKVTQGGAL/H*N G*LT*EQYWKTDQKAVI/CQQSTGSS GQSSQAREIKGPGAVAHTCNPSTLGGRG RWIT*GQEFETSLA
9629	23530	A	9700	239	361	RNDTFFFFETESNSVA\RLQCTGVTLAH *NLCLPGSSNSPA
9630	23531	A	9701	169	1	IFYWKAIFFETESHVAYAGVQ*SNLGS LQLPSS\GSSDSPISASQEAGTTDAHH
9631	23532	A	9702	37	348	HAKNFDVSLPYTKTHEHFVKEDIWIAN KHVKRCSATLVTKIIPPQS/TLKWLKH* PPC*QGNRTGSPIP/C/WVECKIVQLW KIV*PFPKKLSIYL/PY/DPPIILLGI
9632	23533	A	9703	16	339	ARLNTFAMAAC*KSERKS/RN/SLTLNH KLQMIKLIBEEMLKAVNGQKRLRLLYQ/T SQFANAKDELLMDIISATPATV*MIG*Q NSLIADLEKVRVV*LDDQ/TSHNIHLSH
9633	23534	A	9704	276	2	GISRGGLSKPPFFP*DFPLDYLQSPFC KVKRNS/REFTTKSPLDFPIPLFFFFF EKVSQAISAHCKLHLPG*CHSPASASRV AGTTGTRH
9634	23535	A	9705	352	2	CNSRSDFFQLMMNCFRLWAVSPRVECS/ GVITAHCNLNPDSVDPTSTS*VAGTT GHTP\HTWLIIIIIIVAGIFLFLFFLFS FFGRDGVSPCCPSWQTSEFRQSACL SLPKCWDY
9635	23536	A	9706	6	351	TWNSRPRRPLGGQGGRIQDWPKLHGKTR SL/LKKLQKLARRGRASLWSQVLKRLRL TWVDCSLGG*GCSQP*SH/IHCSPAW
9636	23537	A	9707	76	359	CFLFVCLDFVIFLAYFCN*YLFPPFLISH TFFFLLKKGLIFAPGVNLRDQNKFYFTL FDVFFNIYYC*IFFIF/CLVLLFFIFFF FFYCFVMRFIVL
9637	23538	A	9708	342	3	GEELLLMDEQSKWFLE\TPGENATNIVD LTTKDLEYSISVVDKAAAGFERIGSN*N STIELKTVN/SVPHAR*IFCKRLQSVWQ TSLLPILRN\LP*SPHPLVSAMLIQQS STLK
9638	23539	A	9709	211	350	RQDIALLPRL*SGTITH/CDPQLSGS SEPPTSASLVAGTTGACHYV
9639	23540	A	9710	253	3	VKCFSRHMLIRRSATGGKKHIEKGTLI MSFWVYVSQSEH/NLCNHAY\SHIKK VWLGTVDVYNPSTLGGQGGRI*GQEF E
9640	23541	A	9711	80	324	LITLTMASMCSNERKSHTSLTSNQKLEM SKPTEEGMLKAKTS*KLGLFHQT/SQLV KTKKKFLEEIKSTTPLNAPLMRK*NSL

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9641	23542	A	9712	246	3	QLAKHGLLFFLFFEMGSH*LRLECSL\TALLSKISAHCNLNLPGP\SDPPTSASQVAGTTGACLLAQLIFKNFVVTGSHYVA
9642	23543	A	9713	2	359	AAASTTIKEQDMLKFYFLFYFFETESHPTQVGVQWCNLCSLQPPPP\GPSDSPAWVTEQDSVSKE*KRKKLIKINVYLQVTHP*HSPQHIIVRLSVLN*LNEKINRRVTKSSSKEKDR
9643	23544	A	9714	278	53	KLFRGLNNHRKFQTRCGGLFFFLFIYF*DGA/YALSLECSGTIMAHHSLDILGSSHPPISASLAA\GVVRTCSPSC
9644	23545	A	9715	166	402	TLSLKKNENISRWWHVVPVSGVWKAEAR*SLVPRSLRL\HCTPAWA
9645	23546	A	9716	168	1	VDCIIMRRSIAKSPRRKCRGTISARCKLRLSG\SGHSPASAS*EAGVTGVGHDP
9646	23547	A	9717	1	553	TSIRLFFLLSIFFFSRARNRILFKIYCNQVRAKGRGGGWTGCRGHNTMTWPGPQLLLSWGRGMKRQDQGSWGGREGEDTGCI PPPPGSTSRPWTSPSPWPLRLHLFSASGPPGSSSCSP*LFPLTDSQVGRCSGPDNPPYHLMKVQPLPALLLPLLKPHRFPPLGQ\PDPPSSPPSP
9647	23548	A	9718	13	364	PENR*RNPLTTLTNHSLIYLPSTPS\GISA**NFGSLGACILQITTLGLFLAMHYSPIRLQLAFSSIAHITRDVNYG*IIRYLHANGASIFFICLFLHIGRGLYYSPLYSQT*NIGIILLAT
9648	23549	A	9719	82	351	GEALEPELMPALSH/HAATLLAPLPTTFFVGTKTIVGQAQW/HQAL*SQHFERP RRVDYLHLFSRNGQNPSTKNTRISWAWRVPVIPA
9649	23550	A	9720	179	365	FSLFLASLKAQIIDSKPFFSNTLENI*KYEVINFFLYI\IKLHFMNLTSLCFYCHSVCTILL
9650	23551	A	9721	2	320	PIPPGNESSPPTAQEDMQAANKH/IRRYSTSLAIRET/QL/KTTTREPYPITMAT TETSANTTCWREYGESGSCYCWVGCKTLR PLCKTVWQFLKKPSM*LAYDPAITLF
9651	23552	A	9722	1	344	PLPTQNWPPQQSFLHYVLLPAVSVLWS SFFFFFWKQILLPLPRLEG/NGQNSG*WKFPLPGPSLFCPSFQTSNGYGPQQAR AIFWKFKIKTGFGHVTREGLNFLTSGSAPLGS
9652	23553	A	9723	156	3	VTEAYFILFYFETESHVS*WHDLGSLKS PPPG\SSNSPASASQVAGTTGALH
9653	23554	A	9724	76	337	YLSIYLSIYLAIVVSIYLPYHPSISIYVSSIYSINHLPLYFYFTHLSSTHSSIYLLSISILSINYLSSISLSIYLSI*LSIYDSSIHLIHLSHLYIYLI*YLSIYLSIYLAIVVSI\TIYLSIHLSSMYHLFILSIIYLCIIFLPIY/LSTHSSIYLSISILSINY/HTSIYLSIYLFVY/HLYIYHPT
9654	23555	A	9725	249	436	ELAG*IQDHP/GQHHKTLSQLQIKNLAR RGRHL*SELFRLRQEDHLTPGVRCSE L*SHHSTP
9655	23556	A	9726	177	3	HLN**FSNLIFFETESPSVT\RGIISAH RNRLPGSSDSPTSASRVAGTTDT
9656	23557	A	9727	272	233	RKNQRIYQIARKRLNEMARISPLRSMII



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LNVSGLNFPPLKRCRLAEWTEKKK\DPIT CCL/QKTHFTG/KDIYRLKIKGWKKIFH ANGSQ*Q
9657	23558	A	9728	368	380	RKGQRISSEIAIKRLNKMARISPLISIII LNVSGLNFPPLKRYRRAEWTEKKK\DPIT CCL/QKTHFTG/KDIYRLKIKGWKKIFH TNGSQ*RR
9658	23559	A	9729	294	2	KGNLSPKKKKNLKNFKVTPQNFGLKDQK TQGKPTLKVSQNKQKPKFK*NLKGKRPL KLFPPKKKKLNPSRSWFYBKKKK\INKLD GTLVRQINKKRKNQ
9659	23560	A	9730	7	284	SQGLGRLRRENYL*FETESHVARTGVQ WRNLSSLQSPPPG\SSNPASASQVPVI T
9660	23561	A	9731	1	322	RSLKKKKRREKKGKNQPGQHGKTLFLPK TPKI*KIKKIYPG/RGGTHLNSQLLRNL RKENHLNSGGKGCNDPKLGHCIPAQMTK TPFKKKGGAKQNGKLLQLIYGIK
9661	23562	A	9732	168	2	GFYRKSLSLSVWICFKDEFFFEVMSR SVA*AGVQWHDLGSMRPPPPG\SGDCPA
9662	23563	A	9733	43	317	LKLQPRDTHCIWLSTTSFFIYFFFEFES CSVAQA*MQWHDLGSLQPPSPG\SGDSP ASASCTGMHHHTWLMKCINSFDVPMPL GLGLNSHI
9663	23564	A	9734	8	296	NVVSACSLNGLVKGRSLCLTLNQIL*MI TLTERFLKAERGQKLGLLHQT/QVVN /AKEIFLNEVSSATPVYEGIIKRLNSLI ATMEKACVVWIEDQT
9664	23565	A	9735	3	300	TRPSNSPAALSKCSSRRKT/R/TCLTLN QKLEMIKLSKEGILKAERGQKLGLLHQT A/QVVN/AKEKFLKEVRSATPVYEGIIR KQNSLIANMEKA*VVWIEDQ
9665	23566	A	9736	352	1	PFFYLLNFPTFFKGPPLIHFFLESFLEN FGFQGAFFKLQNFFAFLSLLNGPFLN PFFYKFPINC\KFLGQNTFYCPYLGFF* RSFFFFFFFETESRPVA\RLCSCGAIS AHCKLG
9666	23567	A	9737	130	3	KIFFFFFFFFFLRQSLSVAQAGVQWC/N* LGSLQPPAGLKRFLV
9667	23568	A	9738	167	3	ISRSVFCFFFEETESCSTVQV*EQWRNIG SRRPQPP\GSSNYCASACRVAREFTGLV
9668	23569	A	9739	140	419	INVKYLSRHFFKGNIQSPNKHRAIREI QIS\*TDNNKCW*GCGEVQYFIHCCMCE MVHSLWKIVW*LLTGL/HIELSDDPAIL LGGIPPEEMKT
9669	23570	A	9740	93	371	KLCNGYYQESKREPTERN*IFANHKTG CISKTYKELQLNNKNS/NPTQKWAKDL D ISPQTMKQTAKNQVKRCSTSLVIREMQI YTKSIPLHH
9670	23571	A	9741	1	288	GTRDHLRSGVRDQ\PGQHGETRSLKIQ N*GCGHGGSCLSQ\LTWRLRQVNCLS
9671	23572	A	9742	296	563	FIKHLNSYMLGQNLATKLSEICKLPFYI EK*IQAGYGGTCL*SQLLRRLRHDNCLN LGGGGCSEPKI\HCCTPAWATDGGSVSK KKKSR
9672	23573	A	9743	32	400	DALVPHWSSYSPICLDLNLVGIYLFSDR VSLVPRLECSDAIMAQHSDDLPRLR*S SHLSLPRNWLMFVILVETGFCHVA*DGR

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						KLIGSSNPALA/FLKC/WRNMRKSQL* PLLLGLLSADHSD
9673	23574	A	9744	60	356	HSEVDSIIIPILQGRKQISEVRPQRMCE REGGLFISETLFLCPAPSCS/HFLTPA Q*SYF*KNVSWLGAVGDTCPNSTLGGRG GWI\RGQEIKTILANMV
9674	23575	A	9745	2	446	PMVKNKHVKRCSASLVIRAEQIKTIMRSH CTPNS*M*KTDNTKSW/*GCGATGTPIH C/WMKYKMVQPLWKKAAQQL/KHIHLPI DPINLLLGIS*EK*NHLC/YKKTYVRI TAALF
9675	23576	A	9746	257	1	VWLRLSFPSFLLPILSPSSQGDLVCCFL MVF*RDGVSLPIIPAGVQWLDRSSLP/P SPGSSSPPASAS*VAGTTGMHLHAEFYA SC
9676	23577	A	9747	148	3	IKLCEQFHK*TIHVLNHK/L/WPGMVAH AYNPSTLGGRGWIT*GQEFDS
9677	23578	A	9748	769	1	YPQLFKIAKKKKSNVPIKSIMVSQYGH *ENKKWVLNKHGATLQ/BGKGNFGDTFK VTLKDKIAVAVKTRQERLPQELKLFLL EAKILKQYNHPSNVKSGVHTQRRPIYV IKELVPGGDFLSFORKKNELKLVKFS DADSGWCISKKCIHRDLAVRNCL/VGE NNVLKISDFGMSRQEDGGVYSSSDLKQI PIKWTAPALNYGRYHSESDARSFGILL WETFGLG\VCP*PGMTNQPPQEQVERRY WMSVSWQC
9678	23579	A	9749	607	986	SFSSSSSPEFISYGCDDLPMRDPHFVIT HPAFNLPFLALGMFFSLFSPSPLFYF LPPPPRPPC*HSPP\PPPLTNSLFVFL PPPPGVSPSPNTSPPHLPVPRPPSP TSTHLSSPPPPSPH
9679	23580	A	9750	313	339	AR*GLSCSG*S*TPGFMQSSCLNLPKCW DYRC/RATVPSLCFVF
9680	23581	A	9751	213	453	NLAVNVDEINLFFFPLFLIVTLASKFCS /HLLVGR*FIQSCHYLFIFDTERSV T\RAEMSATVLAHYNLCPLGSPDSSA
9681	23582	A	9752	368	3	PLSSPRLPFLFDPSYIFLISISSIRFL SPPCYFLCVFLSISWGFSLVSQDGSDDL SS*SAFLGLPKCWDYRL*PPHPAWRELS FFFS/SFFYLR*GSLSPSLECSGMIIGH CSLDILVSSARA
9682	23583	A	9753	2	335	ARAGFSGGDWNVGMQSTASGLSLFHCPI S*GELFIILYILLKCYITL*IN*LMFGS FYFRDLQHFRLP/TSIVGKKRPGTVAHA YNPNTLRGRGGWITQGGQEFETTLANMVK
9683	23584	A	9754	467	120	SQLFGRPRQTDHLKSGV*DQPG/QHCET PSPLKIQKLAGRGWV/CAPIGPRLGRP R*ENGLNSGGEVCSEPRSRHCTPAWVRE RDCLKNQNKTKSGVLFPSPHQCFILISNT SRNLL
9684	23585	A	9755	137	368	DGVYLWTHRPYCGLGSLNFGSVIIVLP* VKAYGWMVLTSGLDAIQPLADPECSF/G QLRELRCMDLHVDPEDFRLLGK
9685	23586	A	9756	172	267	SKSGNKPNDYHLMNGSVRWICIRTV*QLL KRLTTELPGPAVAFGLGVYAREMKAYVH MKTYSLOQMCT*IFIAALFGIVKKWK*A K*LSPDEWISK/M/WCIRTVEYLTIRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9686	23587	A	9757	56	318	QFWGFSFFFFFCFIDTETCSVSQAGVQ WHNQSWLTA\ P*SDPPAS\AS*VAETTG MCHHDQLIFFFFKQALCPRGWSAMAQSQ LTSSS
9687	23588	A	9758	179	1	KDTRVSRGNTQDTLKP PPPG\SSDSPT SAS*VARIIGVHHNTWLIFCILVEMRFH PRA
9688	23589	A	9759	219	208	NFCNFQMPPLYQKILFWVRVSLSPRLEC SGTIITYCSL/RTPKPK*SS*LSLGVQG CSKL
9689	23590	A	9760	133	371	AMAYQLYRNTTLGNSLQESLDELIQ\LR NRVNFGRSLNTRYFCDNVRTFVLNDVEF REVTELI*VDKVKIVSL\DGKQTGF
9690	23591	A	9761	813	3	CGEGWAAGQDQSRMGSLPVPFRAGRL GSLFPAFQVYCSCGTQRSSSQSWHKTE RSLPGNNPAPQDS/ASAPKYQTPGPVLG VQSPLNQQSCHTALSPEASSSAFFHTTP ATLLHQARTLSLTQGSRPITTPVLLKMP A*RPRESRH\GR*EWTKRSQARSQEAIN ARPRKALGLSDPAPSLHPGSLEDSPKFS LGAPKAPPLPASSPTAQETQQSHISQOP TATGFLGARLCPSPQHCQRGGFPQVTP LLLLGEWGVGEHSFPDVLV
9691	23592	A	9762	96	377	RYHTNMAAQIPESDQIKQTGFHHVQGAG LELLTS\FKEFLGTYNKLTET*FLDCAK DFTTRERKSEETTLSEHCLPKYSTMT\H RISLT\FTDNHI
9692	23593	A	9763	164	399	TDEELLLRDEQ/RKWFLKIESTAGADAV NIVEMTTGDLE*CINLVDKVAARLERTE TNFE/RCSTVRQ/MLSKSIACCTE
9693	23594	A	9764	225	25	KCKITMNST*IE/TVFKDYEHLYVCKL KNLEKTDKVLTIHNFRLRNQ*EPEVLTR AKMYKIYNDIE
9694	23595	A	9765	128	218	FFKDLDPDCF PKWSHCF TLL LAVYEGFTF ST*LVIREMQIKTP\I*YHFSNRMVIM KKSININKCWQGRGESKALIH C**ECKTV *PLWKT VWQILKKLIIG
9695	23596	A	9766	194	551	KNFFFLMEF/SVLLPRLECNGVISAH RLRLPLSSYSPASSSQVAGDYRACTTTA G*ILYF**RQGFHHVQGAGLELPTSGDP PASASQSAGITGVSHCPQLKKSILHETP KGLTGVT
9696	23597	A	9767	238	3	SFLWKLCPRGAPACLRCLSA\LLGGVS* SGYMGVRDPLEEAVCPFSELEHHAERTT ALFRAVPQGCLSLQKLSAFCSC
9697	23598	A	9768	343	1	RGAAHSRGDCVRFTGFCAPIVNLNHPKP LFPFFV*KSPIERSLLGPPLKRSKNRF PFLR/VPRFFKNHPEFFPKIFLFPFFF FFEMESHSLA\RLSHGAILAHCNLSL PGSC
9698	23599	A	9769	191	2	FRINH*TSH/LRGQKKKKKTNSKAIGRK QITKIRA*LNETOPPESIQRINET*S*F SGKIKLI
9699	23600	A	9770	165	2	GKPPNCFYILNFKKKKQGDVFNRT/WLG VVAHACNASTLGSQGGWIT*AQECKTS
9700	23601	A	9771	97	912	VILSTGCSGGLPGWQSVLHHSLTRCPF SFFLSSPTPEME/FSLLLTRLECNGEIS AHCNLLLLGSSNSPASASGVAGNTGI/C

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						GLHAC*AS*FLYFHSVETGFHHVGSGLG LELLTSDD\RPASASQGAGITGVTPRV* PLNSFSRHGLSCFFKETRVLSCCPSWT* TPGLK*SSCLNS*/C*GYRHTPAHPAQ DMVFIFITY/CPFFVFPL/VYIPRFLF LRWSFTLIVQAGVQWRNLGSLQPPPG\H KQSETPSQI*INKY*LLN*LTFFFSIK
9701	23602	A	9772	3	363	HELRSSANEHVFASTFGPTILGLPGVLL IILYPLLIRTSIYLISN\RL\VTQQ* LIKLTSKLMTIHNSIGRS*SLILGLI IIATTNLLGLLPYSFTPTTQLSINLAM AIP\*AGAV
9702	23603	A	9773	38	385	YLIILDSPEKGLICGCLCNCMHSSLLDH LNL*SS*MCLYANIHIYVAISCIYFI* F*SI/YIFII*YFHYSIAYVYIY/IYIY MYTHAHIMCI
9703	23604	A	9774	13	1350	DRVSLLLRLLECNCSISAHNRNLGLGSS DYPASASQVAGTIGVHHTRPTFALFLV ETGFHHVGQAGLELPTSGDPPPL\ASQS AGITGVSHCTWPHLSTTGKILSSGTICP GIWQQRWWAFLIL\SLPWL*LWHPCLSS IMCLSLFFFLCQ/RCKPLISD
9704	23605	A	9775	376	1	KYFELMYTPVIAICLFNSEVFLNK*QFF NLTSSSGIQNLNRLIISNEVESIIKSLP TVKNLGPDGIAATF\TYKEQLTLILKLF QKHEEARILSNLTSETITLILRKQPK KVPNEHTVKILV
9705	23606	A	9776	192	2	NVYQPPPVFLYPPGVAGGV*PF*SPPVF RVK/LGF*GSLFFFFFFFETKRSVTRL ECSGVILA
9706	23607	A	9777	77	350	WLRKFGSRNSGKLTLYLVVYLOTSEFF FFFKIGV*LSPTLECRGPIWVN*NLCFP G*RDFTLTS*VL\GPRVILEFGFLEKT GFSHVPQL
9707	23608	A	9778	133	325	PRWVRFPYLGDCPTPRVSEMLGLQGVVPS SSPFFVCFT*SCSVAQGVQ/WWCDLG SLQPLPLG
9708	23609	A	9779	145	362	RLAFGSCSTCFPLT*TVLYYLI*FNIFF VFEMESLSVS\RLECSGAISAHCNLCTP AWTTERVDAANSRSMN
9709	23610	A	9780	260	1	QKQNEKKRKKIFRNKIQRDYNEQ*YG /NKLDNPEDMNKF*ETRYT*/PNLHQEE IGMLNRPVTNKVL*LVIKIPLTKKSPEP DGFV
9710	23611	A	9781	230	1	SSDSKTGSSVVLVACRFFFFLETGSGSV TQAEVQWHDHSSLQPPPPQPPK*/PGTT GA*STLAS*NAEITGVSHHAR
9711	23612	A	9782	20	322	SOHFGNPKGNPKIFRNLEINFFRLRNAD HMIISTDAQKVFDDKIQLFII*TS*QT* TERIFLNLIKAS*KKPTANIILNG*RLN I\FPKTGETKHIC
9712	23613	A	9783	158	379	LVKIIICNSFQYISFFFFFLETKFCFFP QVEVQGGNFG*LNLPPLGNLHFS\ASAS REPEIPGPPHPG*ILVF
9713	23614	A	9785	54	312	KVDKSTKIGRNQSKMAKNSKNQNASPP KDHNSSPARKQNWTEDELDELTEVGFR WVITNSSKLKEHV*PN/GKETKNLEKRL DQ

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9714	23615	A	9786	13	613	PGAGWARQHGGV* DQPGQH\KRPSLLK IEKLAGHGGRCLLSPAIGGGLKQGESLE TGGRDCSEPRCLCHC\MPAWGNRNKTL SQ/QNKTR
9715	23616	A	9787	794	164	PSFLFCFFFLRWSLTLSPLSCSCVTSP HCNLQLPGLSHSPATVS*VAGTIGTCHY TKLS*FF\FDDSL*APFLGVVDTEYYP DPPSSKGLLPHSGQHGQQHPPAISRAWL SC*VLPHLRS/STSLGQP/RIW*LSKVE V*RGFTFSPTONTPTNNNCIAPGRVD* SLID*LQWCDHSSLPQTPVLK\HPPT LASQSAGITGISHHTRPD
9716	23617	A	9788	256	380	YIFRQAKTQGLPPCALFREAVGENTP*V FAC/PKNVLFYVHP*LPF*I*YQLKRI F*NYEGMVT/FVFRFLFETRSHLSRLE CSGTITTHCSLELVGSTNSSISAS*VDG NTGVRHNASC
9717	23618	A	9789	22	226	TKINSKGNKELNVRAKTIKLEENIDRN LCDLGLGNCFLD*YCIL*TKINSKGNKE LNVRAKTIKLEENIDRNLCDLGLGNCFL DMTPNAQTTKGR\IDKLDFIKI*NFWD DT
9718	23619	A	9790	288	2	QVWQE*AETESAIHCWWERKAIQLL*KM RWQFLKMTNV\ELPYGSAIPLVGIHGRE LER*ST*NIMFTAPLFVIGK/T*NLFKW PSPYEQITKMHC
9719	23620	A	9791	142	361	PPGEGKRVFPTTEPSRIPSKAKSVSQG DTCTPMFTAALFTIARMWNRSKCPSFEE *IKMRCITT/MECYSA
9720	23621	A	9792	305	346	TYEYTDYGGIL* LITFYDHAVLIIFL ICFLFL/YALFLTTLTTLTKTTGGDAQE IETV*TLPGIILGLIALPSLRRLYITD DAPDASLTIKSIGHQWY*TYEYTDYGG ILNS
9721	23622	A	9793	2	317	SRDRPRVRDR*LFSTNHKDIGTRYLLFF A*AGVLGTALSLLIRAEIGQPGNLLGND HIYYVIVTALAFVIIFFIDLPILI\SSF G\SVYVLLILGVPCTAVFLHSS
9722	23623	A	9794	384	1182	RIGKIKG/LCFLFV*WFLKFFFKMEFL LPRLECNKI\HCNLLLMGSSNSPTSASQ VAGITGMC*F\VFLIEMRFFHVQAGLK LLTLGD/PPRPPKVLGI
9723	23624	A	9795	205	1	GLQIKCTMRYHFAPTKMAITYFFLKKGK G\NNKCW*GS/GTEIGILIHCCWECGMV QLLWKTADAWADAW
9724	23625	A	9796	307	348	QSARL*EAVCPFSDQLRTGRRTALFKA VRQGHLSLQRLLSF\VCLYPAPRGAY RGRQASLSCGGLHPVRASRLCLPKQAW AMVGAPTASLPCCSSIHCASNQRDS VGYPDSSP
9725	23626	A	9797	193	381	ILLI*THILLSMISSPFFETGSHSS/V SRLECSGTASAHCSLDLPSSGGSP TSAF*VAGTTGA
9726	23627	A	9799	153	359	FGTYMCFADSYQLSYLFFVVGTF SWLEEEGV*WCICGSLQPPPRVK*/ FLPSLSLLSSWDYRCAPSC
9727	23628	A	9800	2	396	ARAARAARELEELIKIFFFFFFFWGQIL ALMPKGGQGGILTYPNPPLPG*NNFPG

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						LTPPRTGINGLGPGRVNFQIFKKKGGF PPGARGV*NPGRGTPPPGFPKGR\DKA PHFGPL*TFEKVPRPPNFPQ
9728	23629	A	9801	256	347	LYILLNSLK*LVEKLR*NVVLASLIIR YKVTTKRF**FSKPAQSEELQLLTSAPG LNF*RYIIISFFFWIQSFALVA*VGQWQC DQGSPPQLPPGFKRFS/CRSWDYRHEPP R
9729	23630	A	9802	109	401	HLRRPCPTPPFALRTSGDQPLSPEARPD SGLLHSPPLTSPRGLNGQCPPRGSTLNFN P*ASIPASPPSGQPQASQEPVASEH PPDT*GDPAQPPP\RPQDFWGPATVPRS QAGQWPSPLPSDFSKGAQWPVPTR/PP PSTSTQSRWT
9730	23631	A	9803	371	2	PGFPLFSFPEGNGPSKRQTD*IRCLF* DGKVWECSPPKKKKKTKRKKAVIF/CV PVQTKCIVVEGGEETLVGDV*V*P*\GS FKHVVAMFPEK/DCLCTLYEASFKTKE RRVDGFVCRVGT
9731	23632	A	9804	188	1	FLFFFFSET*SQSVTHAGVQGLEQSLPP G\SGNSRASASQVAGITSRRKHSWIIFFV FFVETG
9732	23633	A	9805	112	383	VFINIRVFRILFTFSFFFKRGFNLSPRVK CNG*TKGHCIPLDLPGRV*SFPFSLTNW DYRCAPPKPNKFFF/SFETGSHSVTQA
9733	23634	A	9806	599	237	FRDRSLTLRLHCHCVITAHCSLKLGLG SSELPPQASPLSSWDYRHSPPCLANFLFF VETRSHY/ASRNSLGSSNPT*A/FPKCW DWQV*ATAPSLAYWFSEAKLILRLAL KVSDENICTNF
9734	23635	A	9807	168	2	PQQDVFFFLETGSYSVTKAEVQWCDHG SVQL*PPG\STDPPTSASQEATGTHRA
9735	23636	A	9808	225	3	GPLGYLPPYFPQPLISRG*NPSDFLKIS RVFYGT/HYKFEFLFLFFETESRSVA\ RLECSGVISAHCKLCLPGS
9736	23637	A	9809	541	3	RQLTGINSRRQFQPMNSYVIPYMMDM IILKTKKSNNKYWQGCETELLIHCLWE CKMVQLVWKT*QFLNRSDIEFPHDPGI PPL/GYKRKKMKTCLPKKLCVLVEP/RM FTAALFEVAK**KQ/PQTPITR*INIMW RIYTMYYSAIPRKTPLIHPIA*LDTES II*TEKIQSQETTY
9737	23638	A	9810	213	1	FLCVDFVPCNFALKLALVGLFVCLLFG SVTQAGVQWCNL\GSL*PPPPGLSDLPT SAF*VAGTTGVSHH
9738	23639	A	9811	54	388	PARPLPRQ/WDERPNQPTKKKKRGRN LPTKKKTQNYSHQNPVAQRNPGKTNQK KPKTNPKKKKGGAL*KKTQRPKQTGGR K*KISPKNKGGK*NPCGKLEKNPFSGGE K
9739	23640	A	9812	429	24	RSKGAFFPICPCRSSKFSVLQQRQVRIV FQHPGLGESVAR/CRYSQLLGRLRQ*SH LNWGGRGSSSEPRSCHCIPAWATRASSIF CNFQASSVEVRRSARKKLFSIDLKRHNT INWRVSGLLLVDSYFGRLATPVRTQ
9740	23641	A	9813	149	350	CHFPCFHTTL/CE*EPGEDVTGPIGTKF FPAPGRTDGHTHTHTHTHTHTSDPH HLCVWNTLIHFV

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9741	23642	A	9814	66	401	PENKKTIVYRKPTIATIFNCRNLNALPLK LETRP*YLLY*LFNIMLEVLASVVRQEK EINLSIFT*DIVIK/MKIPKNLENKLLK LLSPFSKITGYKISIQKLTSSFLYYGTV
9742	23643	A	9815	82	1	APPARFFFFF*EKFSFPPEVQRG VFCPCNT/CFP*G*KIFL\KPLKKVGF WPPPPGPKNFYF*KKGFPPWARGFFI PTPFVPLHPFKKGVKRG*APPPARFF FFFFFL*GRVSLCHPGWNA
9743	23644	A	9816	256	2	QHFP*LPIPHIPIQT*QHFPQTRSPFQG PPLCQKPFSSPWGSKVVFILLSFFFFF* DRVSLCHPGWNAVM*SQLTAASNTW\VK *SSHLSLLSS*DYRCVLS
9744	23645	A	9817	53	411	TIYCSNYVNVFVSOHFRSLYS*KNCGLC L*FHLFVLQS*NFMQFHM*FCLKI*VDP IITFEV*FTYI*FF*TYSSVSFTDAYNF VKPHR/VYRGP GAVAHICNPSTLGGQGG WIT*GQEFK
9745	23646	A	9818	100	417	DEHSEKQDEPLQRPRLPFPPTPPSS LLLLNHIGQESGLTHVRLASCLNRGFC FDMKERLCLLPMLECRGMISDHCSLI/R PG*DKPPASAYQVGETTGTTHRA
9746	23647	A	9819	136	2	IYMGMPGAVAHACNPSTLGGQGG/WWI T*GQEFKTRLANMVKPC
9747	23648	A	9820	257	426	IVPGLFLGTGSCSFTHAGVQ*SNCSVQ S*TPGP\SDPPASASRVAGTTGAHHKAW L
9748	23649	A	9821	151	416	LHKLCLMVMESEGTAKTPSLSPIFNSVGL ILLLLLEYSIDSLC*SVLCCYKEIPEAG* FIKKRGL/WLGVVAHACHLSTLGGRGW ITRSGN
9749	23650	A	9822	50	513	RGDPVRVRPRVRIIKLSEEGMWKAEIGRK LDLLHHTISQVNSKEFLKEMKSATSV NTRMIRE*NSLIADMEKVLVV*DOTSHN IFLVQNIKSKGIGLFKLMRAKRDEES/ AEGKLDASKGRFVRLK/EKRSHLHNMKV QDEASVDIETTASYLKV
9750	23651	A	9823	48	406	LIIVVYTLTRWIGHSAVSYPPLRPYS LRHNEIRPINNPTMASKSSERKSLS LTFHLKIKMIKLSEEGVSKAKTG*KLGL L/R/QTVSQVNVAMKKYLKEIKSATPVN T*MIRKQNNL
9751	23652	A	9824	143	444	WNKKNKNELADMILWCGDKTIFMRKL TRDETKYGIPLALRGHSHFVRDGI\N LDGQVDLS\G*WDGTLHLWDLTSGSTTR RFVNK/TKDVLADFS
9752	23653	A	9825	297	2	HRSPKTKETIIASIKKKTMITKDLNRQF SKQDKHLTSEYMKRCPTS/LREM*AKTI MRYHLTPIRRAPIKNKNK/NKSKCW*GC GETEILVHCW*ECKMVP
9753	23654	A	9826	175	400	GGKGGKNFSLKGGEKTNLGFGRKPIF GGGTNGANPPPKIKSGKEKNF*VFPP FFKKNFFFP*NL*FLGGWPHLSPPQK* V/CFPKIPKLVSFSPPLREKFFPPLPP* NLGPPGF/SFWGPPLFFFFFFFF*RDKF SFYHPGWKAVIAAHFSLELLGSSNPPTS
9754	23655	A	9827	64	622	MFSFFFLFDLILNHLFFCFV*MFSFFLED

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LILNHLFFCFVIRQQFSFLFF/ISFFFS FFHCNVNTPELCDFSVCIHSDNSFRFLH LF/NF*HMTLCISELR*TLKQSCSYTK IC**FYSVQLSFLTILY**CKS*QALSI ALQNEFLSV\QYHKNNMYITLTIEFSRN KFLSVTFLLFSIFSHNFGISASISIFIL HVYIKNNPIGFVK
9755	23656	A	9828	298	1	MRNCLTDDERKWFPEMASTPGEDAVNTV EMTAKDLE/Y**YINLVDKAASDFEMID SNFERCSTV/NKMLSNTACYRENFHER *GQSVQQTFRVVGERV
9756	23657	A	9829	361	1	FLTGTQWGK/DSPFNTWC*DH/WNIHRN LDLYLIPYIKINLKQLTGPNLRAKTIKL PEQNIGENLCDL*LSRERYSTKSITRIR KL/DTLGFIKIKNKCISKDTIRKR*ATD WEKIFANHVLKG
9757	23658	A	9830	402	2	RFHHRFSFVLFGPFAKVAFPIGAKNFIS NHYWAGVFPFWEKKNKIDSFLPPFSKNP ILGELKA*F*NFLF*GFQIFF*SLFFCP FGGK*IPGVFSFFFFFLVFFEIGSHSVP \RLKCSGTITAHCSLDLGLSSN
9758	23659	A	9831	2749	3215	FCQ*IKMYVMCICIYNFRVYLCTIYTYL HTHTFTHTHKHTPTQIPEKDS/QCSLSD LKCHSL
9759	23660	A	9832	3	386	KLRIGQLNLSAMAACK*SERKS/R/THL TLNQKLEMIKLSEEGMLKAVIGQKLGLL YQ/TSQVNAKEELLKDIKSATPVTAM IGKQNSLIVDLEKV*VV*IEDQ/TSHNI SLSQSLIQN
9760	23661	A	9833	1	370	RRCRWPPDPSTRTVGRQIGKLVTHRPTVF QERGCPPLTRQAGSHHGGGAFAQVISP TKSISPCGRGGSRL*SQHFGPRMQVDHL R/LGVQDQ/RWPICGQYGETPA\LLKLP KISWAWWLPVIPA
9761	23662	A	9834	125	409	GQENRETWKIVHLV*VLYT*HIKRLNCF SHFI*CYQPTASQAHVHDSNDSSTHV\ N*NSRWPGTVAHACNPSILEG*GGWIT* GQEFETSLANM
9762	23663	A	9835	223	1	PKPQKMGTF*PPMEGS*MGPPHWEKMGP FLKKKEGHPFFFFFFFEMESRSVT\RLC SGA/TISAHCNLCPLGSSNS
9763	23664	A	9836	377	515	FILFLRQVLTLPLRLEYSGAIVAHCSL\ AF*G*SDPPASASRV
9764	23665	A	9837	274	1	AGEWHDQICVFKIPLMKNLHGCARVGQE SWKERNQOV*DRQKQNLSDS*IQT*R/ M/WPGTVAHAYN/PSTLGGQGEWIT*GQ EFETSLANMVK
9765	23666	A	9838	553	114	GAGVKTHPGHKGKTLFFFKFFQKLPGV GGKTLPSPLSRGLGRENSFHPGGKGSNK QSSPPSPFG/WGKKGGGLPFQKKKKKEK RKKGKKNVAPSEPPLKYSN/WQATWG* RKLLNDTMRVQPTKSRMQKILQDRGPVN GIFTKTGRL
9766	23667	A	9839	36	434	LPFPQCVTEFIIVLISWCYIREDACKNL KHVAITIINVCIYICVVCVPSTLYVYMY MLP/HLSDTLTLN*VTLVEMLSFQCL MFWYHGHI*K*HELDVVAHACNPSTMGG QGGWIT*COEYKTSANMVKPR



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9767	23668	A	9840	268	1	RFPFFFCPLTLFWAPGVVFSNFLGVRA PQPP*IFFPI*KKPSPLIFFFFFEKES RSVS\RLEYSGTISAHCKLCVSGSQHSP ASAS
9768	23669	A	9841	463	86	LYMHFISGLFLLFCWSI/WSVLCQYKN CFDDKVYGLDYGNTSQVFT*NSKLIKLY TLTMYSFLCINQTTIKPSEMIQATKANI DK*NYMKLENFCTAKETVNMKMRQLKKW EKVFSIHIPQEVNI
9769	23670	A	9842	37	400	VHSPPPKFWSLYVSVLKFPFCSLYFKFL ALYSIFLQMCQHLLV*AFF*KRGLNSV T\RLECRGAISPNCNLCL/SGSSDNWAS LPRKAEAGNSFT/CR*SQVAGNPISIS TRLNQRKTPFES
9770	23671	A	9843	42	407	NCLSFLITFFFFFLFENKVSFCPQG*G/ RGGPFWPHGTLPPRG*GNPP*LPGRGE *RGAPPPGYFWLFGKKRGFPL\GQGGG KPPALKEPPPLGPPKGG\NYKRNP PPP GNFF*LPYQVV
9771	23672	A	9844	113	379	LGPVVATSLRGRFLGYQLQSKKH*NYP TVR*GCGEMRTSVHCW*ECKTA*PL*KT VWQFLKKLNTGLPFDAETPL/LAETPKE LKA
9772	23673	A	9845	284	528	PLPKTMEIMLDKKQIQITFLFKFKMGHK IAETTRNINKAFGPGTANE\KCTAQWWF KKFCKA*E\SLEDKEA*\GHPSEVDTN
9773	23674	A	9846	888	1295	LEQGCNLFHKKHS*LGEVFFVCFRRSF TLVAQAGVKWRDLGSL/HKLPSSLPS SWDYRPLPRLA/NFFVFLVEMGF\TVL ARMVSI*PRDPPTSASQSAGITGVSHR AGPVAGILMFCRWNI SNKPKGAVFKKK
9774	23675	A	9847	88	387	AYRMKIIDRISLSLYTAALWVTLFLFLF LFFFFKTEFCFAPQAGGQ/WGQFKLMDP NPPPPG*K\DFLVSHPRDLGIKGAPPQC GQNFVFYKEKGGWLLTAT
9775	23676	A	9848	298	438	KIPRGAPNFPGGGKIFSPPLGGPIKTPR GALEKKTLE*VRGPWPGFVKKESPRPKK LG*QIFWPPGKKPNPPMGG/SLDPPPL ILSRPDP*KKKKKKKKKKGGGPLKNP PGGPKFPRGGKNFFPPFRGAYKNTPGGS *EKNPFLGGGKKRKQP
9776	23677	A	9849	251	498	ATIKKMESKKFW*RHGEIGTLIHCYWEF KMOV*PFWKTV*QFLK/D/LNMGLPFDSA FQLPDICLGLKTYVHTENCTQMFMAAL F
9777	23678	A	9850	478	37	ESRNKSHLWSINFQKGLR*LNRGKQPL NK*CRHNSISTCKRMKLDPLYLTPYIKI\ KSKWTKDLNVRAKTIKSLEENIEVNLHD LG*GNDFLDMTPKAQTTK*NID*LDIIK I*NFCGSKDTINKVRRQSTE*EKIFANH VADKLE
9778	23679	A	9851	2	378	RLEGLFLCALFCSIAICMFFFFFFFF*K KRGPFQGGDPGGNFRQLDPLPGIKQ FWGP\PPRKAGTGGGPPPGANLGFWGK KRVPHGGQKGFKP/RNPRGSPRPGPPKG GVAFVFRPKPPGLEQ
9779	23680	A	9852	229	3	FGPYKIFFKKKGAPCPLENPPVF\HQKL GLGFFFFSFFFF*DGVSFLFLRLKCSAA

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						LLAHYKFLLPG*SDSAASAS
9780	23681	A	9853	108	420	GPRVCVRLSLRDDSLLATEDSLAHTEG DPVTASSHSQAPSLSVHPGAALGVVWG TGAIAGTPEPQKPPQLTPGGRPA\PIAP GLTWEPPSHPPPPQ*RSPPPPP
9781	23682	A	9854	2	256	FFIFPLRYYIYCARFQFLSPILYLK*K MD**RRVFQEKWEQAYFFVEV\SPMCLI CNQTLVSKEYN*RCHYETNHGENFD*F TEKMHDENLHLTTTROP
9782	23683	A	9855	323	3	I IQMANKHRKRH\QSQ**VRVMQKKIIM IHRYIPQWLKTSKSDMIKCCSGYGTTEI FTHYLWECKLLHLLWRMVWL\ILLKFKT DTPHDPAPLLGTYPAECMHMPRA
9783	23684	A	9856	28	385	DGVTQAGTQWGSKFTAA*TA*YQGSTPN AWSFFSPPPVLTTPPPQKK/YPPPKKK KIPPPKKK
9784	23685	A	9857	436	518	AANRLNIYRHLIYDKD/EHYRIVGKDD LFNKWCWNWI/ASNKEKNLDSYLIPHT K/LNSR*IIQLDVKD*IIKLEDNLYLH DLGDRQKFLGRI/PVFTIKKKIGKFDPM LKLSTFVHQTPC*RLNSA
9785	23686	A	9858	153	492	RLAGSDPGVADVSQVLRQEKSPCPSWK AVSQAESSSSSAGVSLVLERLLADWMRP IPIKEENKL\SQSTDNLNFIQKHCHRN TQNSV*PGGVGPPGTCGPFRRQSSP
9786	23687	A	9859	2	419	TTGKLQVSHKSTYSHFSSKPTHTTNKD MKRYSPL/AIREMQSKTTG/MRYHFTP KYG\NNKCWLGCGETETLIYGW*ECKMV QPLWKAVWHFLK*LNIES/PIY**NYS* YISYSWRKTCITIYDPVILLGGIYPREV KTH
9787	23688	A	9860	88	419	TFFFFFFGFWFLKTKPLFVPLFEGGPI LG*WNPPPRD*KNFS/GPNPPGGGE*RA QPPPPGYFLFFKKK\GVSPWGGGSKPP TPGNPPPGPPKIRVIRGGPPPGGRKHF
9788	23689	A	9861	301	401	KRA*GGQEPKVCFFYNRKVGNSEPPK KFKKGRRAAFFGLRANKRGLFVKKGKKI WVGKVGEPIT/DPFKEFGGR\LPEKDG LV
9789	23690	A	9862	220	415	KIMGGAQIFRGGGGFFFFLEGWEKNFPG VSFRRKFFFGGVFLPPPP*HKKNYFSS QRQYISLGGGGRKTPPKKNFLKDTPK LFFSHPSKKKNPPPPRKIWAAPMIF*I PPPIIFFFFFFFFFFFFFFFFFFKN*P/S FFFNFKKPIFKTFLSPPKVFPPPKKK KKNPPISYRRWPLAI
9790	23691	A	9863	116	366	GQEFETSPAMFCFETESCSIA*AVVQWH DLSSLQPLPPG\SGDSPASASRAAGELL EPRIIRLQSVETITPLHSSLGNRVRHL
9791	23692	A	9864	619	295	FFFEMEFSLLLPRLECNCAISAHNRRL PGSSDSPASAGGLL*SQVAGITRLRHHD *LILY/FLVEMRFHRVG*AGLELLTSGD PPSSASQGAGITGMSHAGHYGKIF
9792	23693	A	9865	12	432	IADRRLLFTNHKDIGTLYLLFGA*AGVL STALLIRAELEGQPGNLLGNDHIYNGI GTAHAFGIILVIVIPITIGGFGN*LVTL IIGAPDMAFPRINNISFGLLPSTLLLLL TSAILEARAGTC*TVYPCLA\GGYSHLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						A
9793	23694	A	9866	30	380	LFSTNRRGIGPLYLLFGA*SGVLGPALT LLI*AELGQPGYLLGDDHTYNDIDTAHA FVIILFIVIPIIIGGFGD*LVPLIIGAP DMAFPRIN/NISF*LLPASLLLLLASGI REGRSK
9794	23695	A	9867	256	395	EVLKSEKSFETVCIINNKC/WPGMVAH ACNPMTLGGRGGRIT*GQEF
9795	23696	A	9868	458	2	PKKRFFSQKPPRGFYSAPLKGNKNIFFPP PVNFGDPKDFKGPPLFFFFFFFPP RFFFFFLEKG*KF*NNFFT*NMVFFYIS /CSKKFPFQFVLTPIPF*KVPKPVWFFW DFPIFFKKIFFFFFFCDRVSLCHPGWSA VARSLTASPRV
9796	23697	A	9869	144	425	IPLCSRIYSFGPC*FSLISSSSCLSPFL SIPLCVLS**T*YLFYISMREIYKTR TKGIYPGAQRNSLYTH\FSIEVQSTIKA ERFWPGAVARACNPSTLGGRGGQITWGQ EFE
9797	23698	A	9870	138	401	DLRLKLNLSKNIIRLQGTVESSVLTIKE MQIKAKVRYNLI PVKIKR/SGNDRWW*G CGERGTLRIC**ECKLVQPLKWTVWSFL KKKKK
9798	23699	A	9871	179	441	PSGKGGIKGP PPPPKKIFGNFFFLKKK GVPPGPPGPKPRPLETPPNPPKGGY GGGP\WPPPPIP*FFKGPFKKKGPPWTN RGNP
9799	23700	A	9872	57	435	FTQMRKNLKNNSGNMKK*GSITPLKDHS NFPAPVDPNQNMFEIPGKEFKK/SDY*V TQGDTRERCKPT*VLKTILDMDEKCSKE MDILMKNQSELLEKKDTFRELQNAMEFS NNRLDQVEERITELE
9800	23701	A	9873	228	443	FSSKFILISVFLFLFLETGSCSVAQAGV QL*DYSSLQPSQG\SGNPPISASQIAT TAGACLHALLIFVFFV
9801	23702	A	9874	349	2	KKPKKKNFLPPKNFGFFSPFSP*KFFFF LKGFNFFRGFPNFPKKKFFSKNSQL VFFLPPLKKKIF/CFPTPVKFGP/SQRF FLKGPPLFFFFFLLDRVWLCYPGWSA VARSRIS
9802	23703	A	9875	405	2	KKASRMENVRKKKLEMIKLSEEGMLKA NIGQKLSLLAKQQVNAKENLLKEIRSA IPLNTQMIRMQNSLIADMENIL/VVWI/ EDPTNYNIPLSQSLIQSNALT\FNSMKT ERGEEAA*EKFDAISG*FMTFKERS
9803	23704	A	9876	355	394	THPYYSHQEYQSP*P/LTGALSALLKTS GLAM*GHFHSITLLILGLLTNTLTIYQ* WRDVTR*SAYQGHHTPPVQKGLRYGIIL FITSEVFFFAGLF*AFYHSSLAPTPQLG GHWPTGITPLNPLEDPLNTSVLLASG VSIT
9804	23705	A	9877	47	85	TIYIHCIVRIYACEVCVCAYIHICGVP AHLTEQNL\KPARTQSPAPQKNPELPV DLVSI SL DREAQDVELNHRYLGNTCRTD VLPKVNTLCRL/NFFPCLPILEELQEL P*LENIPLPFPIDYIYTMRAYICV
9805	23706	A	9878	2	389	GRGQFPPEFFYFFWGGS LVPSTPNKKKP LGEVLGGWSNRAPKGWGGGFPPIILAF

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						KPKGPFPGPKFVLKFSNVPPLLFFPKMRG PLPKGGGFLPFFFFFFETKRSVTPGVQ WCNFGSL*PPP\TGSSNS
9806	23707	A	9879	351	1	FLGPSKNFNPFPQKWPFAPFPKSHRAR VNEIFS/RLSVINF*GLTKPQRLFFSLL NFSS\PIPPFQFPSRLIKEIRFSTLTP ENSKIKKPLFFF*FFFF*DRVTLCCPGW SAVVQSR
9807	23708	A	9880	123	387	SFLWLKLRPSGAPTCMRCLA\LLGGVSQ LGYTGVRDPLEEAVCPFSELQRHAGKTT ALFRAVRQGCFFFAFY*IELFPCY/CSG RVGG
9808	23709	A	9881	341	659	SFLGRVQWLHACKSQHFGRRLRQVDHLRS GV*DLPGQHDETLSSLKMPK/QKLARHG GMCL*SQLRLRLRQENHLNLGGRGCNEL RSQHCTPAWATEQDSISKTKTKK
9809	23710	A	9882	216	1	PKFFFWLRLDSQIFKPGFGPQGFF/GGFG NPQGGKKPGFWGLG*KKKGFFFFFFF LRDGISFCCPGWSIQW
9810	23711	A	9883	2	244	GRVGAVGRREGENFIKDELPPPPPEGK QQNLCKFLTGFSLPCQDKKP\CFFV*KK KKKKKKKKKKKKKKKKKEKGGGGA
9811	23712	A	9884	310	2	IFLQTLFPNTFENSLSYCIIFSEYSFT **KQ\TNFILSSILLYI*PSGSYISNL *Y*ELFSQNLQYHFLWI*KKWGLGAVA HTYNPSTLGGQGRWIAWSPG
9812	23713	A	9885	242	358	KTVWLYMNI*MANNHME*CSLPLVIREM *IKTPVTVH\TVGMAAI*NKK*NITR/C W*ACRETAVLVYCWFYFTQPL*KTVWL YMNIE/IPCDPAIPLLMYLKE*RPGTV AHTCNPR
9813	23714	A	9886	360	2	LLKLGFPPWAKKGKKRLWVEGPLGKPP GGFCQKLFFSPGGGPKGFSPIIILPKG *PFVWGPFFREVF*KKRFKLKKKFRPTFS /Y/LFFFFFFESHVSVA\RMECSGAILAH CNLCRLGSSD
9814	23715	A	9887	236	347	IKGFFFF*TESHSVT\RECTST/SAHC NLCLPGSSNSP
9815	23716	A	9888	310	3	NFFFFFFETGSCSVTQARVQWSDQ/GSLQ PRSPGL\SDPPTSAS*VAGNLKFLSGLC SSL*SLEIS*DTKKSQVQITDDLCTTVV LCLFFEMESHVVQAGVQWH
9816	23717	A	9889	119	391	APAYWNPHARDSPPFFF*TNFPFPQVG GQWPNSGSPQAPPPG/SPPP/YASASK ISGAPGAPPPPGPNFFSFSSPTFFSR DGVSPYEP
9817	23718	A	9890	195	3	DGVSLILLPRLECNLTILTHCCLSPV/SW DYRRLP*RL/V*FFLFLVEMGFHHVAQA GLELLTSGDHP
9818	23719	A	9891	3	378	RDGERNMLALGTASAKALYSLALSLPR LECSGTIISSHSLNPP/GLKWSSCLSSST SSWDFRPAPPHLAKKTQQ/HATFF*EG ESPYVAQAGFKLLASSPPAFSLPKCWD YKL\DRHAW
9819	23720	A	9892	231	1	PKPFFPKFFSP*N*KPFFQISPAKIQKI RVYQS\HKFFSFFFFFFHGVSLLLPRLE CNGTISAQCNLCLSGSSDSP
9820	23721	A	9893	2	347	APARQENVVCVYVCMVCVIVLHRHC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EVLCFYKMLGKKRSIYAY*LVY*YIYIH MCVYIYI/YIYV/YMYIYTYVCIYTH
9821	23722	A	9894	28	382	TAHLEAGATGYRTFLLPAIGLLCLPWVL DDGAGQTAQ*SMLLDHAMLLAHRAHEL I/DTYYEFETYIYPKDQKYSFLHDSQTS FCFSDSIATPSNMEETQQKSNLELLRIS LLLIESW
9822	23723	A	9895	93	386	FWKIISHYFYFYFSCSILISPSDLPTIC ICMFHLLKLCQSSEFLHLLFVWLVFET QSHSIKQPECS*LSAA/CHLPGSSDPP
9823	23724	A	9896	174	1	TLDWGP RKKNPFFFFFETR SRSVTEAGV Q*HNHGPLQPQAG\SSDSPTSASQADA W
9824	23725	A	9897	251	386	LQRLECSGTI/SAHCNLCLLGSSNPLAS AS*IAGTTGTLTGDDVDT
9825	23726	A	9898	127	393	GHMGTLTGSPATLSILALFFWGGRISTQ LDGINKS\FSLFLYFLRHCSLSRLLE*S GAIITYCRLELLGSGDTPASASQETGTA GTCHT
9826	23727	A	9899	3	334	KLRIGQLNTSAMAAC*KSERKS/R/THL TLNQKLEMIKLREEGLKAVIGQKLGLL YQ/TSQFVNAKEELLKDIKSATPVTA*M IGKQNSLNCLEKSCVVLIQDQTG/HNI FLS
9827	23728	A	9900	356	1	GRKPFSHLPKATLLPMGPVLGGRALMG PDSRPGVPVPSCLVLLTPLAPLPLTARE SLCPCPPS*TPQPSVNP/H/GKLARRSP CVVSGRQSLP*AEIVPLHAPPALGDRDE TPSQKKKK
9828	23729	A	9901	118	343	IPYAKEKKKQENVLRFIHVNLCISNWF FETGSHFVTQG*VHWCNLSLQ/PNLQ GSGDPPTSASRAAGATGVQH
9829	23730	A	9902	321	50	SLRTRV*RPPSAPG*NPFCLKPQKIFQG GG\ESPLSQILKRVQENSYNLGGKGFN *PKLPPCPLTWATKKTSPPKKKKKKNYR TWETSVS
9830	23731	A	9903	317	8	NCYDPNSGIVIPLLGILPKSTK\T*VRT KTCT*MLIVALCIIITKKWK*SKCLSTDK QVNKI*YIHIMEYYSPIKGRKY*HTLQH /WMNLENIS*KRLDIKKPHII
9831	23732	A	9904	287	3	RGALNGRGGPRGVKSPGFAPFKLQKPP GTFLNPK\QFPFFPNPPF*KKGAFFHFF LPLF*SFRWTEFYSVT\KLECGAISAH CNLCLSCSSDSRA
9832	23733	A	9905	2	406	PRVRTSSRSRATALFFFFFFFVFFWGKG EIWAPPLKNC/IPPEKFCYFGGAPGAG LPPPPGVIFFSLCRVVKKKKKKGAPPGG VLGKKKKTFFTPKGGTFLTLLGGF*KKSL FGKKTLLWVGGLLLKNFF*EKFR
9833	23734	A	9906	1	296	IWVGATECIFKNNPTIWHQETHFTCKD TYRLKV/KGWKKIHTHTNGNQK*AGI AIVISDKTDFKSKTIKR*KGHY/IMTNG SIQQGDILDWYKSNCSF
9834	23735	A	9907	474	41	FMEYLTLSFIHVLLQ*FIHCFVHLFIHS FFYALMKSLIQ*FIHLYSCF/ICIDLLI SSCIYSFIYALVKSLANSLTHSFIHTFL Q*FVHLFTPLLCISFTHSSIH*PSHSLT FIQLHLFFHALVSGFIWFSFIYLFCKINV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FLIDK
9835	23736	A	9908	286	84	LKPPPPFFFFFQANFLCFIRD/GFHHVG QDGLPLLTS*SASHGLPKCWDSCRCEALR PASPLISGPHQTI
9836	23737	A	9909	316	63	DQLLVRSIGFEALMSPIFFQMEF/SLS LPKLECNAGISAHRNFCLLGSSDPPASA AV*/PMANLLKLCASVSYCIELVLNELH WIK
9837	23738	A	9910	370	461	F*F*FLFSETESHVSA\QLECSAMISGR CNLRLLGSGDSPATREAGAESLEPRRQ SEPGLCHCTAAW
9838	23739	A	9911	294	28	PGKNSTVQKEPGKWFCEMKFTPGENAVN IV*PTTKDLEY/WINI/DKTVAGCERTD SNFERSSTMGMKL\SNSIAWYTEIFRGR KSQLMGI
9839	23740	A	9912	307	463	CKL*TLSNNDVIVGSLIVT/TCTTLVGV LIMGD/RLCMCGEKEYLGNLGTFLSIL
9840	23741	A	9913	377	28	REMLTVKPLAPSFRRWSRAYRAIFFITP TWVSKSGKVTGPLFFLHIFFGP/CPGL PIFFFIKTGTRFFFGWFFFERVSLCC PG*MECNAGISAHHKLRLPGSRYPASA SEFHR
9841	23742	A	9914	384	725	HLTAIRMTVIKDTENSKCERGC\KTLMH SCWEYERVQPLWKTRW*F/LQQVE/LPS PCDPSIP/LLRMPK*LNTD/CKRMC/C IPTSIAALFPVTK/SWKQ
9842	23743	A	9915	187	3	QPHKHLGLDNIYIFFEIGFCSVAQTGVQ *RDHGSLQPRPP\GSRDEPTSGSRVAGR PRQENG
9843	23744	A	9916	15	167	DGVSLSLPRLECNGAILAHCNLR/LPGL K*FSCLRLPSSWDYRLPPHPAHV
9844	23745	A	9917	345	477	YCSRTSLPL/TLKKGSA*PGAVAHAYNP SILGGRGRWIT*GQEFK
9845	23746	A	9918	460	42	HQRPKVDKTTKMGEKRSRKTGNSKNQSA S/APPKERSSSPAMEQSWTENDFDELRLQ EGFR*SNYSELKEEVTRTHGKEVKNLEKK LDEWLTRI/SNAEKSLRDLMEITPKA*Q LPPERTNLSS*FNQLEERVSVMEDEINK MK
9846	23747	A	9919	282	21	AAGYLQPSSEFWLHSLGSRRGLPISVFPV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RGRQAWLSCDGYHPVRPSRLCLPTQA
9851	23752	A	9924	254	3	PGGFYFPGFLPPPLGFPKGL*RLWPPC PATFFFLYQISKFPFFFGKYQKNFFFF FFFFPESKRSRVT\RLCNGAISAHYNL
9852	23753	A	9925	309	1	YTPTIMLLGIYSNELKTNVHMKT*I*MF TATLFLIAETWKQPRCSSLSEWI/QQLW YIQT I/EYYSVVRNIK/LMKTW/MKLK YILQSEKTQSEKTTYI*FQLYDI
9853	23754	A	9926	237	2	RWNFNFTQLILKCIFLRTKFFS*VSK*N FKYFLGFWFFFLRQGLTPVT\RLCSG TISAQCNLRLPGSTDFSASASQE
9854	23755	A	9927	244	1	KPQCLWRK*D*WHNTQKLDVEKGKPLIH YWWERKLV*PLWKTVWRMLR/NLKIIELP YDPVPIPLWGNYSKEMK*LCQREDSRA
9855	23756	A	9928	2	644	IVQVDQKIRLNIHCLQETHFKCKYTYRL KVMR*R*VYHVNIHQEKALVAIDGAYFR ARKITRDKERHY/IMIMGSMLOKD
9856	23757	A	9929	1	364	GTSGTRPINNTTVFSKCSSERKT/R/TH LTLNQKLEMIKLSGGGISKTDMG*NLGL LHQTVSQVNTKEMFLKEIKSATPLNT* MIRHQNSLIAAIGKVLVWIDQ/TQHNT LLSQRLIWNKALT
9857	23758	A	9930	88	374	ILKACGPCPCGNPHPWGPL*GQCGGLGPNP SKSPPHPHPRGDPTWGGTPIGDYGPKP KLPHGAGLPKKPCSSGGQNN/PKISGP
9858	23759	A	9931	384	2	LCSPRFFYRKIWGGGQGSRLPPPPFWKP GKDCFS PGVLDPPGEQRGAPCFP*KKI RWG*GAAPVVPPPEG*/VGRAPLTPKI PAPVSFGCSPALPGEGQSETPFFLKKKK KEKSEAMI PPPPGPRA
9859	23760	A	9932	32	359	IFFFLFFF/C*KGGPPVPVQAGGQGPKT PPWPPIWAKTKPLSKKKKKKKGAGPP PPFKGGPPPLKKGEGPLLKRKFLKKNNG ENFKKKKIWAGGGGNPREPPPPGGAR
9860	23761	A	9933	138	1	TGFFCCC*SFALVAKGGVQWCDLGLSLQP PPPG\SSDSPTYASCSC
9861	23762	A	9934	103	355	LAGQACCS*STSANRCVNH\PGYANGR CDTITCILVFIRNSWLITP IALITMFCY HVG*VRPQEQAPGNRVSLSDLL\PPVT C
9862	23763	A	9935	29	363	AWSHNAFLLEFFFKRELAFVQGERENN FVSLKPPPPG*SPFSAPNPPKGGNKGPP PPQLIFFYF*/GEKGFSPYNPEGPKPP TLGKPGLF*NTKKICPQPRGLKKGQHI W
9863	23764	A	9936	173	363	PKKRPIISLKRAFNSNPGD*QKFLKRGL PPMGSQFKRGNYPYDNLEKLCPPGGNK GSG/YHYGL
9864	23765	A	9937	360	3	NQKMRKNQSSKTGICKNQSACPPPKERS SSLAMEQSWMENVFDELREBGSR**NYS ELKEEVRTHGKEVKNLEK/NLDEWLSRI S/N*EKSLKDLMEKPKAQELHGECPSL SSQFNQLARA
9865	23766	A	9938	194	370	VSNFFFFFETEFCSFAQVGAQQGNFR*L KAPPP\NCCLFPT*ASRVGTTGTCHHS WLI
9866	23767	A	9939	426	1	SQEFKVAVS YDLTMHNSNSETLSQKE KTKQTKTKQKKT*EGRKHIKRCPTPLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IREIQIQTTVRYHFTHIRI/VLLPQKQNKWCRCRVEKLPVLR*WECETVQPLWITVWW/FLKILNIKLPFDLATPVVCIYQMEFSC
9867	23768	A	9940	255	16	RVIYNIYIMYILCIYTPSRLLVEIGFHHVGQDGLDLTS*SIRLSLPK\CWDYRYEPPCVNIYYLHIYLIYMSDGVKY
9868	23769	A	9941	206	355	FLQCHTAIKNCRG/WPGAVAHTCNPSTLGG*GGRII*GQEFKTSLTNMVEP
9869	23770	A	9942	3	402	HEELNPRSATSSPALVHVHTIAHVTFABEGCFQHDFFCSQPENRHIPLVFTTASKVRNIFYLLCRGRGILRFFLVCLKIDPAIPLMGIYPK\KSLYHKDTYIHMFLAAEFTVAKIRYQSKCPSTDD*IKKICV
9870	23771	A	9943	79	328	CIKILLKFLCLFCLPCCINFFLRQSCSVARAGVQW\SLQP*PPRLKHTPTSAS*SAETRGTTHHAHLIFSYNFL*R*VSHVA
9871	23772	A	9944	321	414	VPSWAG\PVAHACNPSTLGGRGGRIT*GQEFE
9872	23773	A	9945	142	480	QEAKSFDSDSTTMEVMDKKQIRVIFLFEFK\MGRKAAETTCNIENAFAPGAAND*QMRWWLEKFKCGEESLEDEECGRPSEVDDQLRAIIEADPLTTIQEVAKELSIDH
9873	23774	A	9946	191	3	FFLPRGGGDSVFKKPKKKNFGPKIFPPCPGFPPLAT/INFPQIFFFFFFF*DGVS LCHPGWNAV
9874	23775	A	9947	451	461	K*INK*KVKGW/RKEHHANINQKKVDVTFISDNMNFRRKNKITGDREGRIYIIKQPIHQENIAILNVYVPNNRVAKYVK*KLI ELKKEIHKFTILVGDFNTILSTIDRTTR*KVS
9875	23776	A	9948	186	405	NHTLAISLF*PYKP*AILKLGIRKERRLVC*RDICALMFITELVTAAKLWNQPKCPSTDK/WKMWYICTMEYYS
9876	23777	A	9949	18	412	PEFRITITLPEKKNLL*LTN*VSKFSGYNINI*TSVAFF\YSNNKISSETGKIVPFTILSNRMKYLGM/TLTKNMKDLHTENYKMLRKENEYQMGNMGSWILKINIVKISILHKVIYRVKFLSNFNAILLKK
9877	23778	A	9950	1	396	LAFDGRAERLKTGFHRTQDGLLELLTS*SVRLGLLKCWDYWREP/PVPGGLWD
9878	23779	A	9951	307	405	GIRVRR*PQGLRPPNPDALVFKKMWPPPTN\PRGWGGKGWEPPQGPQDPPQAAPGFLPETWRGPWNSLPTRGAWPPNSNLPPWPPAPSRHPAQRAPGPSTAAPPPGGGGEWDPPGRV
9879	23780	A	9952	2	402	YGRPKEGGSLRFVVLTFPGPKGETPFFLKTQKITGGGGGGP*FPLPRVRQENSFYSRGGGFN*PKRAPCALTGKKQKFFLKKKKNTPOKPKKLPQCRIQY*TQK/SSSLFMGGTPGKRQ
9880	23781	A	9953	249	1070	SSFISRFYFICIYLFETRSHSVTKARVQCCDYN*LQPQPPGAQEILPLQPP*SAG\ITGVAINTPQLIFYFFVE/SGGSTHVAPRLALNSWAQNIAL/RLPKVLYFTF
9881	23782	A	9954	75	396	GFKGRKRGLEPLPLNQLKTLNLSEKGLSKANTGQKLGLL/RPVSQVVPNGKFLRE



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TKSAF/PIEK*VI*KQNSLIPDMEEVLG V/WKTKKYSHNIPGLSLTQKRVLTLF
9882	23783	A	9955	181	458	RLWNDGLYNIFDLKLQ/SIHV*SLLLLF ILEPESHVS\RLECSGAVTTCSSLNIP GWSDSPQAFQVAGTTGVCNPAWVPSAF L
9883	23784	A	9956	67	430	LAPRLIYSPKFWQSFMSVRQIQVQSLA IGNFHNPRLPILICHCYAFHRILLFQMV RNFILYSISISANKQESKCILKYILLYI NLRNWLGTVAHAYN/PSTLGV*GGRIS* AHEFETSQGN
9884	23785	A	9957	77	422	LPLALWASCRPQLCLDTDFIHGPPTSGA ASQFLCFQTMQPPTCSSRLYNL*PALV LDHTTSNVVCFRSP/SFFLLPLPLPPA PLP\FFFFFFFDRVLLCHPGWSAVARFQ LTAAS
9885	23786	A	9958	3	422	LHSSLVTEQDSISKKKKKKKIFLGGTKK GGPSLGGFFFGPPGPFKIVKKRGALIG FPPFCPKKKPKPLFFPKPLGKPPRKKG F*IGEPWKT/EGPGFPKLNLFVFFSPWG GNFLFPPQKPGGKVKILLQPKKPPGK G
9886	23787	A	9959	370	2	PFSSWVANFREGDGEKCSVLQGI RFCMF CRYINVTPLVHFPPFISKGTSTFFPLYFF SPEVM/HFP*LPY*FGWALLSRF*/MSL L*LFFSKFFFPSTFFF*RFHSSPRLK CNGAISAHCNLCPL
9887	23788	A	9960	256	2	AWEETAPLHSHCLGNQARPWNHRHAP\ P*LIVFVFSVETGFHHVAQAVLELLASS DPPTRFNLLSSWDYRGLSPQPMRSKSAQ EG
9888	23789	A	9961	269	3	HRQACGQVRSPIQCWWACKIAQPSLQIV RSSLKGI*SPYDPVIPLELVIYPRELKT \SLHTKTCT*RFTAALFIARRWKQLKC PSIDE
9889	23790	A	9962	268	324	SGTSLH/WIFS*VGIETMWLKVDPQTK KISLRSAAIAIKYFLTQATASIIIRRAI LFNNRLSEQSSITNTNQYSSLIIMAI AIKVGMAPHF*VPEVTQGSPTVSGLLV L
9890	23791	A	9963	341	2	ITFLPTKIIRQSNFKTGKRKTDSDNLR HFKREDTQMANKYM*FI*KMQI\KTTMR YYFISKRTTISRKTSNIQC*DTWSPGTF INCLLECKMVRLLWKMTWQFLTEVHIHL VY
9891	23792	A	9964	250	2	YHPVNLYFKYISPIDV*FGCFIYIFDYP LCSCFSLHPLVYLQ*L/LFFFFFFEASHC VARLECSGVVSAHCNLRPLGSSDSPAS
9892	23793	A	9965	3	334	RTLRRHHIWLIDPSFE*HLSCFHLIAVN SAAINIPC/HSYV*THF*YS*MYRGRTA GSYAT/SMLNLLRNCSTLLHRNCTF*PF YH/WE*VPISPQSCQKLDFFIFLIIAIS EG
9893	23794	A	9966	179	352	NQE*TEILNRPMNSNQIESVIKYLPTKRS HRPHRFTAELYQTY\ILLKLFQKVEGEG LL
9894	23795	A	9967	2	350	THPSINSFIHVFIHASMNSLIHLPTHSF SIYLFTKSFIHLFIHFFSFLFLRPSFT

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						PVAIYSFIHPFTYSSIH*FIYPCVYSCTDEETHSFTHAFIQHLFIH*II/IFIYSFISFLFF
9895	23796	A	9968	228	558	CHQLRQELAIFTSFVILQLFSGHLDVYM QAWAQRDPDKYEYDNK*FIEIKKI IQFTL ISKRMK/YVGINLTR*VKDLHNENYKTL MKEIEEDTSEWKDISCSWNGRINSVKT
9896	23797	A	9969	196	2	DRKVFFRPLFTIFGLKKKIFPLFWFFPS /IRGRG*IFFFFFFFFETESPSRLECS ETISCHCTP
9897	23798	A	9970	245	1	TQCDMCFVIYTHIYISHICYMVIYIYHT RHTGILFTPKREKNSNTCTCATKDNP/ CMTLC*/HKRQTHHTHTHTHTHTHT
9898	23799	A	9971	163	380	NHRRQKKNGR/HNGNKYKTVTKMINSNP PITRNNLVNGLKTPIKRQLSDSIKKQ YPSIYCL*KT/YLKYKD
9899	23800	A	9972	328	1	AKCGFLKKLNIELFNSIPGHSCKT*TM FAAALYIISKYKQSPSCSNDE*MNEIW HILTIIGYSAVKKISWG\RWMNLENIARL SGRQRGHILQDSVDMKSPE*AIPO
9900	23801	A	9973	200	3	MASKCSSERKSHR/SITHNQKLEMIKLS EKGMSKAKIG*KLGLFCQ\VIHVVTAKG KFLKEIKSATP
9901	23802	A	9974	111	517	NLEQPLIKRTIANKPIKKINTTILITIT NVNGLNLT/LTK/RQRWSD*IFKNQDPTMI /C*KKN/HCKYKDTNTLKI*KNIYDA NMLTQIKKKAGVAILI/DKIDFRA/TDI TRAKEGHFIMIKGSVHQEYVVTILNLSAH AS
9902	23803	A	9975	342	3	FLATKKIFFFPVFPPQGPVPLVAPFF WAFGGGPPKWAPKKKFFGPRGPPFENFF F*GFFFFFFKTGGFFFLRFSKKVFFFFFFF SETESCSVA\RLECSGTISAYCNLCLPG SR
9903	23804	A	9976	13	326	ILDHSNRPSSTLKTNPAGKDVEQKQFL /LCCW*ECKIVNYLGR*L/WQFLTKLNL L*PYDPEILLGLIYQKELKTCIHTVACT *MFIEALFVIAKT*KQPRYSSVG
9904	23805	A	9977	74	396	LAPRTQPLPCSPAPLRQCHTQSLLPFFL LRLIFYFFCFKLTTRAHSAQAQAQ*RDH GSLQT*TPTLACTPASA/VARTTGTHHH AWLIVFFL/IEKVSHSLVCDKT
9905	23806	A	9978	287	2	QPHNSSYTQIFTPKIIKTTPPNLKQNN TTPIKKKTQ*FP/PSTNP/SYPSTHPPT HLFIYPLIHISPPSPTHPRIHPPTYLS IHPSTHPSIHPPSR
9906	23807	A	9979	97	332	GNNDLFLYFFFFLETGSHSVAQARVQWC DHSSL*PQPPGSSGPPISTC/RLGLQAC MCHHAWLIFNFFCKGRSLFGLLR
9907	23808	A	9980	168	2	STWLRWDYKTFEFTSKS/WPGTVALTY NPYTLGGQGRHIT*GQEFKTSANLVKS
9908	23809	A	9981	267	1	LKRERR*RRAN/SKTSRRKEIKIRAEI TATENRKPIEK/SNKING*FFEKTDK/I DNPLERLRKKERD*ITKVRNGREDIL*N NDLIKVKKD
9909	23810	A	9982	230	412	CHIYLC/D*PIDGIV*CHIYIYFGHKHT HTYTHHTHTHTHTPTC*VSKILLKKRR TCSVCA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9910	23811	A	9983	229	415	SYVFCHIRFCPLDSLKEIVA/SQVQWC VSVVSTT*VAEAGGSLEPRSLRPDWASQ RDPISK
9911	23812	A	9984	2	288	RGYDSTSSAYTVGHFT*EDKATITRLSG KENVKHAGGETLRRLLDVYP*TORIIDS VGNLNSA\SAMM\GPPRLPKVLGLQAWT TMPGP*KYIHIFF
9912	23813	A	9985	246	3	FLLDYQYCALCCHCFLEFNCGHFNIL LGGVKHTKFPKYS*KFVS/LWDAVAHS CNSSTLSGLGWITRGQEFETSLANMVK
9913	23814	A	9986	342	1	FLNFGLTGFFPKGPPKPLGLRDGALPLD PPQFLGVFKRGAFLLGTQ*FHF\LEGFK FWFWEPKAFFFF/CCETISAHCNCLP GSSDASASASWIAGITGAHHYARLSRRL RQQN
9914	23815	A	9987	330	1	NRPLNNLVMASKCSSERKGYTSFVLSRK /LRKMIKLEESMLTVTG*KLGLLCQT /VQVNTKEKFLMEIKSATPGNKGTVTKS NLTADREKV*VIWIKNKNHKLPLSQ
9915	23816	A	9988	209	2	IKGSHFPVLI*YRKIIIFGGVKGGGF YSY\LFFFFEKGYHSVTQLKCSGMILAP CNLCLPGS*DSPTS
9916	23817	A	9989	256	357	QHRWMNTEMLNYLC*IIVVHF/HTHTHT HTHTHTHTHTHT
9917	23818	A	9990	263	1	IQIRVFENSHLWPSYVHPHGHSYLFCS L**AFFRH\G*FVLSVHFLKIFLNLKKI FFETG\SHSVAQACSGMISAHCNCLLG SSDR
9918	23819	A	9991	3	368	SLDPRRSRLHLAKIVPPRSSLGDRARPC LLKKLELFFETGFCCVAPGVRWC SHGP LQPRIPG\SSNPLTSAT*VAG\IAGMCY HTQLQLAF
9919	23820	A	9992	294	391	SGTVAHACNSSTLGGRGGWIT*GQ/ESQ TSLTNM
9920	23821	A	9993	317	3	TDKELLRLRDEQRKCFVEMEFSPGKHAMS NVDMTKDLEYSINLVDKAAVELERADSN FERSSTLGKMLSNSISCYKEIFLERKSQ LM*QIPLLLM/FKKLPQPP*PSA
9921	23822	A	9994	193	395	IFWITCCSSLSVLAASPTFMLWRQLLS LNLNMN*QDHSLSQSLIQSKSATLFSVT AERGEDSAEEKLEASRWFMRFKERSCL HNIKVQGEAARTDR/EAAASYPENLR/V KDEGGYTK*RIFVVDIAFCWKTMPST FIAREKSI PGFKVSKDRMTARCGRSL
9922	23823	A	9995	82	420	SFLWKLCPRGAAAYVRCVSA\LLEDVSO LGYTGVRDPIEEAVSPFSELKRCRETT AVFTAVRQGHLSLQK\FLLPFVQLCPAH RGGV*RQ*ALLCCGGLSPVQAPLPLCLP TQ
9923	23824	A	9996	376	1	CGRTDAPASTSPYAMTVRFLRPPQCVL DGLHNCPARAPQEONSLGEVDKRGPREQ TR\PATAPPRPLGSPSWICPGDW**CR NSLQGFSLAASVARGRDWALAGLPATVS ARFQEQQKMTV
9924	23825	A	9997	495	982	VQKFLRPNLAPKKHQKRLAPNSLQGRLR SLPSPTVWCTMAPPTGVLSSLLLVTTIA VCLWRMHSWQKNHW*ASFKKTHD*TGLA EP\SCARKQCSSEGRYSNAVISPNLETT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RIMRVSHTFPVVDCTAACCDLSSCDLAW /WFEGRCYLVSCPHKENCEPKKMG
9925	23826	A	9998	401	341	IASKCSTERV/SRSHTLKQKLERFKL*EKGM/SKNEIGQK*ALLYQ/VSQVNAKE KFLKEIKVD\LHAQMIRK*NSLTADVKK VLVVKIDQTL/PLGHSVIQSKALTLFSS MKAQ*GEEAA*EKS
9926	23827	A	9999	30	393	DTTILKLRQLIIGAVATKHWSEKSLTS LNLNQKLGITIKLTEEGMLKAKKGQKRG LSCQTVGQVMN/SKEKFLKEIKHAIPGNT *MISK*NSL/IADMEKVLVG/WSKVIF *DOTSHNIP*SQN
9927	23828	A	10000	133	1420	BQRRLPVTGPVASLQTLCCFLPRRGCSH G*ESAATHPPGPELVLLLQGH*AGYLG /DFG/PRTATGSPG/PAGVQPGCLVPQ LSRAAAAG*PDPT**GAIFSYHCKALRA TAARHCPPGC*WPG/PAGSPPGTSRPLS HPSSPSPPWTVGVSSFLNLVLCP*ASDA QGHACYPGVPALAGQGHDSAGGRLGDP GHHWQQAALHG/DQGPFGHQAAGTQPS AQGLGC*ATHPGEGG*VGYQGLPAG*GR SHPRFPVTRPMGRSCPYATVRPGPGSQ GQTPPGLV\PRGEAGQNPCCAAPGLSCI QEVTGRWWW*GKKPLGHYPCCGAVRCPS S*PHPDTFMFGTGREGLPPTSPVGVGTG QMS\EGSRPCEWTLTMSFPWGE*SPRASC AMLHFCPSRVGGYHGCPLHHMGPOST AGQAGQPHTLDIKAS
9928	23829	A	10001	1818	6682	IKFPEAEEEEIQEVLVLLFRVAEEKENP SRVGNQREYENQVVLYSICNQLRYRNN L/RHVKKDERGYEEELNYSRDHMLLYP YRLLDIMVKGFSITPFSYTGIMENIMN SGHNFTAADCLRLLGIGRNQYIDLMIQC RSSKKFFRRKTAGDLLPIKPVEIAIEAW WVQAGYITEDDIKICTWPEKCATDKTV DSGPQLSGSLDYNVHSLYKKGFTYLDV PMSDDSCIAVAPLEGFVMNRVL/NFDYF ETLLYKIFVSVDEHTNVAELANVLEIDL SLVKNVSMYCRGLGFAHKKGQVINLDQL HSSWKNVPSINRLKSTLDP*KMLLSWGG GESRRPVQEASSATDTDTNSQEDPADTA SVRSLSLSAGHTKHIAFLFDSTLTAFML MGNLSPVQSTGEGEAQRYFDHALTLRNT ILFLRENKDLVAQTAQPDQPNYGFPLDL LRCESLLGLDPATCSRVLNKNYTLVSM APLTNEIRPVSSCTPQHIGPAIPEVSSV WFKLYIYHVTGQGPPSLLLSKGTRLRKL PDIFQSY\DRLLITSSG\HDPGVVPTSH VLTMLNDALTHSAVLIQGHGLHGIGETV HVPFPFDETELQEDSC\NMGVHKALQIL RNRVDLQHLGCVTMLNASSQLANRKL S DASDERGKPDLAGSDV\NGSTESFEMV IEEATIDSATKQTSAGTTEADWVPLELC FGIPFLFSELNRKVYRKIATHGL\*EKR AFKNLLHSSRKLSLQVLNFVHSFQEGAS TLDIHTPEPSFSSLLSQSSFADMGVPLPA KKNF/SLKIVSY
9929	23830	A	10002	439	1135	MAVDFYNFVTKLVVTTGYLRISFLAYKF

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						FSFPFLDLSL/LLSPRLCSGVIPASLQ PLLPGFKRFL/CLSLPSS*GYRRAPPC PALLYF*VETGFHHVQGAGLELLTSGKL TRLGLPKCWDYR
9930	23831	A	10003	216	572	LTIVSIFTAKQSVTLPIICMLEMRKWL NDTSAF/PII*KVLFPKIFFFFFF*KG LFCPPGGREGAQFGLTKPSPSGLKEIFL PNPPGGWKQRRVPPFAGYFCFFIKRRVS LLWRGLPN
9931	23832	A	10004	3	354	YSNNPKDRKGETGINEKTNNKMVDLSSY TSVITLNF*ML*/D/KIN*KFKVSP*KK PTLCCLLETYFKYGIGGLKVKRWKKI*H ANTIGKKTLVAILITKQTSLS*YPNKE EHYILIKE
9932	23833	A	10005	187	455	ASTHYSLGVRICIYIPGCIHPGEKSQKC NTCGKNSTQKPELVN/HR*LKGHRCKM* NEGGKTFTRVQSL/ACHKRVYTERKSYK C
9933	23834	A	10006	134	456	IWNPLPLGKPCAWKQVTSDLISPDALFIN AAIHSLSFFFFFFFETKFLFVPQVGGPWH NLN*LKLPPKL\SDFLVA*VSKKVGIT GPPHHPGVLVWGFKKKGGSPMLPR
9934	23835	A	10007	210	451	CYYTIQTTEQPANDSMLGIKPHVSIITL NVNNLNTPPKRLGVADWIK/TQDPAFCC LQETSLTCNRTHRFRKVG*/WKKIYH
9935	23836	A	10008	169	462	YPCWVDMAKNTSYNKCWQGCGEIRILPH CRWEYKMASPLWK/SQFLNK*NMELP*D LPIPLLDIDPKWKGTGVQTKTCR/RMFI AALFPTSRS
9936	23837	A	10009	490	724	EMPP*FMEKNFLAPGGVTPPGVNTRV NPKTAFDPKRSSSPFLEKSQKPGLIBGL THLKTLLINPLKKDESGEIPVLF
9937	23838	A	10010	306	588	KQFIRAFIEMSWLTPVIPVLWDTKADG SGIRDQPSQHGETPSLLKIEKLAGHGGA GL*/SQLLERLRQENHLNPGGGGCSEPR SCYCIAAWVTE
9938	23839	A	10011	473	53	ISLGQDSTDISTINIPMAFKLSSKRKS HMSFSLNQ/L/EMIRLS/EEAC*KPRS QKLGLLSQS*PSCSKFLKETKSATPVN TQMI*K*NSLITNK\LKEVLMVWIKDQI KHTISLRQSVI*CKALPLFNSMKAERGE ESAKC
9939	23840	A	10012	184	455	FWLSLIKKPLSSVTQKKINRET\ILLTT KKKKKDCNFLEGGLLIGGSVCRLVYRHY ATLYSVFCVDSSKSERGSVDPTQVFVET *DKCFDY
9940	23841	A	10013	203	453	KEELYISRERKSSTSLLNQSQK*LIKL SEQAMPNANIGDRLKARPLSPNSHLIKT KQKFLKEV/KCATP
9941	23842	A	10014	237	483	TLIRYIILQGLFSYIPFFFFETESRSVA QAGVQW*DLGSLVPGSRHSPSSASQVAG TTGFHY/HAWLIFCLFCATGS
9942	23843	A	10015	157	875	DDPVRGRGEESAMPSGGRNRNSVSSSWV GSMAGITTEAVKRKIQVLQHQADDAEE *AEHLQ*EAEGKRWAWEQAEAEVASVNG RIQLVEEELDCAQECLATALQKLEEAGK AADESERDTKVIEIWALKD/E/EKMELO EIQLKEAKHIADEADGKYEEVACKLVII

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EGDMGCTEERAEAEASRC*EMDEQIRLM DQNLKCLSAEEKYSQKEA*CEKERKIL TDNLNKSPMR
9943	23844	A	10016	579	30	CGISTKKNKWMIKQNSSELSTCVHNQIT LHKIAMATQWG\KNSFFNK*C/W/BN*V ST/CKKIKLSPSVTCTI*KQYLKWKVYL NIKI*QTS*IS\NGGKYDIGLGTNFFLQ KTKNLMSFS*L*NQMHKEQIEKWDYIK LQNFCTSKKEFGVMSPKKW/DEIFEN HIFDRS*FSQYINNV*NTKSE
9944	23845	A	10017	44	228	EFVCRVRGLWW\CVVLASQLLWEAEAGG SLEPKSLRLQ*AMIM\DTTPPW
9945	23846	A	10018	471	40	PGEGRFQQTFRPPFLPPWPGKGGPFKK PKKKKRKEMIKLS*KPRQANQ*LGLLCQ /TSQVVNAKEKFLKEIKNATPVNTQVR KLNSLIADIETVLVVGTEQTSNIPFG QSPIQINILAVFHSMAKQSKATEEKF EARS
9946	23847	A	10019	217	486	KKIS*PVYLSLYLSIYLSVCLSVYYLSI YLSIYLSIYLCIYLSITIIYYLSIYLPV YLSINLLSI/CLSPIYLLTYHLSSYLLS YLPTYLP
9947	23848	A	10020	327	1245	TENQQGVLAALAALSKIRMMPTRLKWF LNIDYTKFCEAFHVFKKKKKKINKNIKQL KMPLTKRIYLAFTYSTQ*QQNT\FFL SADETHGKIE/HVLGPKTRHNKFKR
9948	23849	A	10021	329	490	GESPTDNHCRSPKSQVEKVIYTFETES RSVTPAGV*WCNLGSLQPPPP/GTSD
9949	23850	A	10022	3	394	YRVLEVLGYMLNIRFVVLGCSSCGQAAQ FREGSRCTACRHPAHTLHAAKMSRRKV SSAKCR*RETPKKRSARWSAKPAP/QSE TKPKKAAGKDKSSTSS\FSSSSSLKAEK GGKEKQAEVADQETKDLSE
9950	23851	A	10023	448	477	SQVFETSLAS*MSKNIL/WAGTGAHTCN PSTLRGQGGQIT*SQVFETSLAS
9951	23852	A	10024	198	455	SLKTNRRREIPEDFHGQPCGKLVHSEKPR VRMGQTESKYASYLSFKVILRRGGVRA S/TRNLIMLFQTIEQFCLWFPE*GTLDL KDW
9952	23853	A	10025	469	26	PPRAVQPPFLPSSSLHTCVPLCRTVFSA TSRPDSLLPALQVSAKMSPVLS*SSLLLP SLGQGFPMASIAAPRL/PHRSLRSCVVA AHSRAELDRHEAFLQCSLGQWPRNDFLF SFFRDRVLLCHPGWSTAA*S*LTASNS GAQVMEFQ
9953	23854	A	10026	222	489	KKKKKKKKFCFIARVKSNGAISAPCNLC LSGSNYFPASTSLVSGNTGACPLARVNF FY*NL\FLVKMGFHHIGQESI
9954	23855	A	10027	313	2	QDWEISKLYSYCHS*VRRL/IFLKIRLS LYIILQHSNLNCNIIG*LQFESCYIKLAG DKIAFRFLTTLKTNHQLGLVAHAYNSSTL GGRDGWIT*GQEFKPSLANM
9955	23856	A	10028	49	388	TPKIRGVFPFKGWFLGVFGAFPPQKDI FYFPRTPMGTSLVSPGKKKKKEV*RVLY GLKKAKKIFVLKVKFSHKRGFFGEIQFK KLFWK/HLKRNPPPKKKR
9956	23857	A	10029	394	231	GRQIASAQEFKTSWGNMAKLCLFI*RDR VSPCCPSWS*IPELKQSACLSLPKY*DY

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						RC/RNTTPGL*HLLFRCLLIILPSYLF CKSFKLLYMDI
9957	23858	A	10030	265	2	HDNMRGSDYFPASNGLAVPFKRQVFTIA SNFLEKSPRLAFT*LVQD*ERKWAG\ P VAHTCNPSTLGGQGGWITRGQEFKTSIA NMPKP
9958	23859	A	10031	235	413	KAGKLFFFTETITFKKGKAGGGGSFLKP HLFGRPGGNNHRVRIL*KRGFYKMGRVV LKSPLCDSPPLASQKGGVSRKSPPPRP CPF*RLFP*KKAFRLFIPKKV**ALV/ SLFFIGEGKTLFFFF*DRALLCRPGWNA VAPSGKLSSCLSLLS*DYKHVPPCLA MF*KFF/CRN
9959	23860	A	10032	167	424	GREFDLRMGHMVKPPLSFFFFPSETMS LSVTQAGVQW*DITALSASWTPVISDSP VSASRVAG\IGTTGVRHHTQLIFL
9960	23861	A	10033	252	3	VEGCLSSGVQDQPEQHSSETPSLQKKIFF \*LAGHGSML*SQLGRLRWEDHSSPG G*SCSEP*SCHCSPAWE*DPISKKKK
9961	23862	A	10034	175	492	CPTCPFVWIPLCSEQPVQLYMVVHTHTH THHTHTHTHTHA/HLLFSLSFSFLRQG LSLSPTLWRSGLM/CGSTQSQSPRLKQF CSPRYSRG*GWRMA*/DPGGRGCSE
9962	23863	A	10035	200	448	LYLHLVQLSELDFTPLFRVFCPVLSL CLSF*FP*VCFVFLVSLGLF*GRVLLC RPGWSAVVQSQLTAD/SDFPVLKHSSCL
9963	23864	A	10036	229	463	MILGISKISFSLAITLANFPPTLNLFI LDTGSCSVAQADVQWHNQGSL*/SELLG SSDPPTSAS
9964	23865	A	10037	164	422	GLSSQLTDGHLALLRVGSEVGSREES EREEAGREREGERRDSRG*RREREEES GAREEREKKEKRER/ERDREEK
9965	23866	A	10038	1	490	PNQIQNAVLIMISFSCFVSVIFFKSEI YNGQPKFSFFFF*DESCSVAQAGVQ/W CG/LQSQQPRPPG\SSNP\PTSASGVAG ST
9966	23867	A	10039	255	446	FFLRQSCYVAQARVQ/YAIHRCSTLTQ LPALASSNPSALLAPRVAGTAGMQHHNQ L*YFFRIHS
9967	23868	A	10040	157	390	DHTCPPPSTADYRLS*FLYFLLLLFRRS LALPPMLECSGAISAHCTLCVQETRETD AAHFKAARTIRAPHPAQLTIAFQVQTHV YQDGH/DGSWWCDLRTHPPRS
9968	23869	A	10041	290	30	TLKKRKEFSSVLCPRGYIVLLLLVHQFL FFQTGSCSVTQAGMQ/W/CDQSSLPQ* T PG\SNNPVVSASQVAGPTGMHGFHTE YESRGPP
9969	23870	A	10042	190	929	NHRYISYLTRLVKIKNFANKSWLESLS TLKHS*/W*CK*V*SLWKTVWHYLVNL\ KDDLTFDPAIFFLMIYLIEMCAQVHPEI YARMFIAVLFEIFKHQ\NNPNKLWYIHT RESYKTIKIKE
9970	23871	A	10043	457	724	HFGRPRQVDCSSGVQDQPGQHGEVQSV LKL\KKLAGHGGAHL*SQLLWRLRHENH LNLGGRGCSEPRWCHFTPAWTTQDSV* NNNNNN
9971	23872	A	10044	111	429	KPDEDTTGRENYRPVFFTTNDANLSKIK CMYPCISVH/HVNMYGKIPMMFT*Y**

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						*LFLSFFFYEMESGSPRLECSGVISAHCNLSLPASSNPPPGFPR
9972	23873	A	10045	30	220	LGVLYKKNSVFNKCYNWDN*ISTWKRM\GLDPYLTPHTKINFKWIKDLNIITKTLICCSWMKTKA
9973	23874	A	10046	203	361	TYKLLVIFIVIDHF/LFSFLSFFFRDRV SFLLPRLCSGAISTHRNL*LPGSSD
9974	23875	A	10047	198	358	IQRKCFTEFFFEV*SCFVAQAEVQYCGSPG\SSNLPSASEVSKTIGVVILPS
9975	23876	A	10048	270	272	RKNQRFKTIARKRLNKMTRISPLISII LNVSGLNPLKRYRLAEWTKKKK\DP IICCL/QKTHFAG/RDIYRLKIKGWKKIFHTNGSQ*QRSEFF
9976	23877	A	10050	256	1	GVTTNLYFWKNFLNPPFLVKKCENCPI NKVFP*KPDLKKTLFFSKKKFCGV/HPT EKFFFFFESLALSPRLQCNGTILAHCNLR
9977	23878	A	10051	112	359	SKVSEPTENEVEHNLKV*SFILPLKQYSM**QKKNIH\ISFYKK*ELTWPGMV AHACNPGR LGTEAGRSPEGQEFETSLA
9978	23879	A	10052	346	2	RVSSYTLITLNLNRLNVALKRYRRNLGFFFLKKP*PN\ICCIQKTNLIYKSTYSLK VKGWKNH\HANGKKQAEVAI\LFISD KKDFKSKIVKRDKEGHVMTKGSIQQ*DRTIL
9979	23880	A	10053	376	6	TRPSQHPDFILLNKCLLFEATPFLVICYSGHRKLRPVAPP IIRGSKSQIIPMPPAVL PRWHLSCLSFRIPSSFF*LRLPRLCKSR /SAWGPVSPHLPQFLFFQAISFFFL*D GILLCHPGWSAVA
9980	23881	A	10054	102	347	FLSFFVDGKLCLEAKIWLAPAVFIVTRVLLLLSTL/RQVELRNILCSNVHIHFH LYFCIYLSAYILQTMSTLY*HL*YHSNV
9981	23882	A	10055	251	51	ISLVNWLFILENMKLDPLYSPYTKINIR /WQ*DLNVKNGTTKVLEEN*GTIYVMVG WKRPIACQQPKS
9982	23883	A	10056	169	342	SQKQYSTCQNVFCFVLFLETRSHLV\TT LECSGAIMAYCRLDLPGRHPPTSAS*VDG
9983	23884	A	10057	1	586	AAARPAQGGKARPGLLLRRGRVVELRAGFLTAKGAFRWWLSQKHVKMSYPPQSRGCG GGMGAAGPPSLTVHQELCGAYS PDGTTEALPLASWPRARPSPAKAPAYDTAKLPAL ICGSRPPPGVNP GASSLKPGACVSEGA GPTGTLESAGSRPPTPLPPPV/CPCGPP ARADH*FCHVTPQCR*/PPRPS
9984	23885	A	10058	393	43	HARPGAECERPAEGEAAADAFSGRHACPHSLYCLR*RGFFVHKLHLNKA/RLIKRRKADNIKCWQRCGAPGTLMHG*WDYETM GLLEQTVFSFEIRSHCAAQAGVQRNNHGLQEF
9985	23886	A	10059	228	466	GLLHGPPITYDLPEPVSTPSLYHPPIVP*ASPLGPSAILTLPFHSPPPA\PLFSPP HSVLGSSGPRSLPT/SPTHLPTLTPH
9986	23887	A	10060	293	9	DILQFYTFSPIQ\CPVYILHL*YISLQRL*FHQKYLIGIYFIETWSCSVARLECSGRITPRCNLNFPGPTYPTTSASGVAGTTG VCDFLGLPWSR



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9987	23888	A	10061	199	428	TAYCRTLP LKKS NPTTISGS FFF FLETGP RSVPG* RAGG\DLMAHCSFDLP GSRDSP ASPRQVVGATGCPCHHPWLIFE
9988	23889	A	10062	191	2281	LQTRGKLFKYKEKGICTKLHRSEITIGK QWKEAVCPPTGQAQSQGLDPKSRREALR GGHGFVPGGGVCGHQEL*LHSDGLKAVH PAGSEPSDPGGVQAAACQDAATGGTPLQ PMPETARGC/TATASSREAGPGMDP/RE A/GPEAWQLGKARSSWGSSSTSGGPAWV FIRDTPSWWGIPGTVSPFAGPRCPPTTR PQWEQLGSGRPG*MQTTABETNAAPRAG QERTPSRGPSADPGVSQHVLSHRSCPK CERRSVPPNG\AGPTLWTELHPSDASVS ALTPL*GDVEVGPGY\CEGYIKPGRRTH QHNWLDLDRPAASRTCRKMLELPRV*F LLRLPELAETYSSTPPACAQRPRGTGGG /PPQRCVLMMSGSHQGGAS*KGRDAPSLG SGLERPREGGPGWLS/RQPSPHAVQPCF HMLCLGPAF*RGRGARGVPVVRASHFP FHGAAWWPGDHMSQP*WQMLSRPARGHR PSWQVRRQCTVLGALKPGLPDLKCPGPT AFLPG*GVS/EENGQIPNVSTQLYLQNL PLPREQN*RRFPRDLSSGGAGPGTG*CG GGGGHALSPTPSRRLRAHSDNSWAQPL CCWMPAASGC\PGIGCNGVPPVAAS*QA AA*TPPWSEGLPAG\*QPSAHCVRTRV PGGRIPHLAQAVPPDDRAFPNCQASGQ LLGVHSRPSLSAAGCRQFLAVSGIGCNG VPPVAAS
9989	23890	A	10063	65	453	ISREFLFLETKSLYIMLKGSIQQEDIIIF VNIYTLNTGAPRY/IK*ILLELKRQIES DTVIPEDDNTPLSALNRPSRQK/VDLIC TIEQMDLIDYRTFHTASEYLFSAHG SFSKKYYMLGHKICLETFLN
9990	23891	A	10064	100	466	LGILPLQSRPSGPGGQCTPTLPFWVSLP LPVRGCFHLHCWCLPYSGALGSPCHTGL VCWHIPCF*CCGVSP*R\SCLEVHLYTH THTHTHTHTRFVLM*MRTPLRKGRQ VMRLCGGGGRA
9991	23892	A	10065	226	377	GLAGSPCTISGSVSFCSGCTY\RGHGIMF ICNDCKVFRFCKSK*NCFKEHNP
9992	23893	A	10066	292	458	KVSSICLKMSFLFLFFRTGSHCH*KVS SICLKMSFLFLFFRTGSH/SSPRLECS GMIIAHCSLKLLDSSDLTASAS*VAG
9993	23894	A	10067	252	36	TGFNPLHFYYYYYYY\FESKCSHAQ AGVQCCDHGSLKPQP\SSSHPPTSAP* VAGSRNAHQANSTAWPMVS
9994	23895	A	10068	56	481	GILKNCHNLMIKLERMRSCVLMGEQRK/ WIY*DESTPGEDTVNTVEITINDLEYFI NLVEKTVA/GVETVDSNFERGPTVGKM\ IVCYREIFHEKKSPMQQL\YF*KFPQP LQPSAATTLVS*QPS\SKQDPLSARRLQ FTAGSD
9995	23896	A	10069	263	435	HFSFLSFFF*KTESHSVT/RVEGRGGIS VDCKLCRPGSRDSFASASRVPGTKGISQ GRG
9996	23897	A	10070	116	474	RGAGAWGVSGRSSPPLSALPIQPPPHLS TPPPLETP/PPVLH*PLKDLGGWGALLA

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						Q*RLPG*HSPKKKKKKKAPRPPYK*GP PKTPVDPPDGPFLLDPPLFGWPPPP\VFLL PGERPPPL
9997	23898	A	10071	159	377	KSHMPLTLNQKLEMIKLSEE/GLMSTAE IGQKL/GLLLPNSQVNAKEKFLKEMKS TSPGNT*TIKWPGAVADA
9998	23899	A	10072	180	473	AIETQLLSRPLCLWPSGRFPDAQVANIR VRVAV*GNPLR*VGPAEPGEQRPSPWGF PSIS/WDISPTWSSASPPGLSADCKFT CHYRCRALVCLDCCG
9999	23900	A	10073	98	440	GQLNKLSGPYPENVGTYLPLVLIPLAQP VIYSTIFAGTLITALSSH*FFT*VGLEI NMLAFIPVLTCK\INPRSTEAALKYFLT QATASIILLIAILFNNILSGQKKKKKGR PF
10000	23901	A	10074	358	404	PCLYTYHLHNSNST*SLRLVSIIMEIVT SNLHRTVPHSYTPPTQLSINLVMATHLS AGAWIISYPSMIKNALVHFLPQGSPTPL IPILVVIETISLLIQ\PRPLAVRLTGN TAGHLLMHLIGSATLAISTINLASTLII FTILILLT
10001	23902	A	10076	3	419	KWRKKMWCLQKMEYYSS*KGKKLLSHVT IWMDEEVMLS/EIS/SVTEGQILFNST YV
10002	23903	A	10077	335	414	DKSPF/D*RFFLPNPNNGFLVKMPSPVK RLPFFFFIFPFSFFFFFETESRSVT\RLBC SGTGLAHCNLRPLGSRDS
10003	23904	A	10078	279	1	KDTQLPFTQFFETGSCSVPEAGVQWCD HSSLQPPPP\GSSGSSPLSL*VAGTIGM LIFKIFSRNPLNFFFFLRLWSLALSPDWS AVARSWFT
10004	23905	A	10079	397	3	KSSSLFQNLHLWANSSTYSHLIPTLGYIL NHGNQFDPTL/RDKM*NFECTIVCPHY ELPSLEQW/VSLGSLNYDTILPLDLFCK RQGWSEIPYAQDFMTLYQNLTICQT/P QNPPPPPKESSKVELDIIDDPH
10005	23906	A	10080	281	1	IFLGEWGPFFPPQKKSFFPKIPQWVEFT PPYRKKIFFFLPR*NWA/HPKIFFKRPP PFFFFFFFFFFFFGFKENCFILLPPKEHI TQAPAWGFAG
10006	23907	A	10081	207	35	QENRRC*RGRGES/GTLHGWRECQTQV PLWKTWQQLKRLNTEFFYDLAIIILLGE FH
10007	23908	A	10082	2	408	IAPLHSSLGDRARLRLKKKKKKGKIRPL LALFFKNQNPSPFKNSHSFYGALMEF\P PPHIPPFFWKVQPPPLFFFRGTLEFPGP IGTCKLQTLGSPG*WDPPCPLPHQSPGR GGLIPGRKGEDPPSFRGLPPPHF
10008	23909	A	10083	195	2	ECKQRPQLEMVSFRRRSHEPFFFTGPR SVAQAGMQWH/DLSSLKPPAPG\SGDLF TSAS*VAGTI
10009	23910	A	10084	219	1	RLKIKLLKIIITTTIDSGICSFKSKCL* H/LKIQNMWLDKLAHAYNPSTSGGRGRQ IT*GQEFKTSLGNMVKP
10010	23911	A	10085	364	413	KKKGGEKGPLLKKER*KTNGQFLVHTNF /RLPGLKYFF/CPPPPSKWGLRAPPPKP GDFFFFFFFFLVFLVETGFHHVQGAGLE LLTS*PIPLGFPKCWDYRRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10011	23912	A	10086	200	3	INFILLLLFIFVLLIFETGPCSIAQATVQ WRDHGTLQOPLGLKQAILP/ASAP*VP RITDVHHHARLN
10012	23913	A	10087	154	329	FSLSDFKTYKAAAGHRGSC*YQHFGKP \RRTDPLRPVQDQPDQRGETPSLLKKK KKK
10013	23914	A	10088	157	390	NSSSFFPPSCGAQ/KSEVKKSSGPHSSS SSG*RGE/CLPLLVSOGSWHFLAYGSLT PVSACVFT*PFSMSLCVYIQISVS
10014	23915	A	10089	305	1	KKKRAQSLPGQKGRGFSQPVTAGDRSF RPKIRKEALGLGLGLTDLCRTFPPTAT G*TFSSAPFPG\YPPV*PTKKKNTNLN *FTRIKIISRIFSGHEK
10015	23916	A	10090	329	2	RGFFQPLGFWDPGPIISNLGGPPKNLLK AEIMGYNFCVPPFPFPGGLPTTHFFPPR NPPF/CFPFTPSLGFSPNPPGFFFFF FFLSRVSLCHLGSVA*SWLSAAS
10016	23917	A	10091	84	408	EKKGENKLEFWGFLLLGLTIFIGGYRFKII FCLVGYFIFIYLFGE/FSLLLPL* NGTCSVHHNLPLPGASGSPASTSGEGGI TGMRRHPRLY*IYLGRWSFALVARAVMQ WHVLGSPQSPAWCKRFSCNLRRGWYY RHAPAPPSLLNIQKIIILGFWLAPVY
10017	23918	A	10092	184	359	FQINSSVTRRSFVLAAGVQWRDLGSP LLPPP\GSSDSPASAS*VAGITGLHVGL SHK
10018	23919	A	10093	298	386	KLCEK**ITPIRMAII*KKREGENS\KC W*GCGEIGTLVYCL*EYKMOVPLWKIVW QFLKILGIEL
10019	23920	A	10094	310	1	ICMNEMLYKQDFGRITTIIRKIVIFYFWI FN*FGH*IRIY*NLRYKTCML*RG**I NLPQRSFKNLRLKI**W/WPGTVAHAYN PNTSGGRGRIT*DREFETS
10020	23921	A	10095	40	407	EHTHTTACEPGGI*IRPVD*MVLISWL* HGTITCKMVTLGETGQKPGISLIIF FFG\TQSLFVPRNGVHCRGPISAR*KLC LPGPPLSPT*AS*VAETTACYCCTWFEN NFFLRRLPLHCY
10021	23922	A	10096	189	2	PPFFFFNLFFKKSFYEQGLALSPLKCR GIIIA/HCS/L*TPG/YK*SSCLSLP\S SWDDRCAPPRV
10022	23923	A	10097	260	401	DHLRSGVQD*LGQHGETSLLKVQKLDG RGGLQLIP\RRLMHENHLN
10023	23924	A	10098	187	464	WYMTRCGSLGPSSAAHESHPPPQQLMN P\PSPPSSAAHESHPPPQQLMNPTIPLL SS*IPSPSSAAHESPGRVGRPEFTGGAH GYLHLSPP
10024	23925	A	10099	397	1	FFGGAPCPPPRRKGKTPPPRRKLFPPFF PKKPPLPKKNC*NKNPLLGPKKKNRPP PGRFFKKGFF*NPPKAPLTNFWKKKKK \SPFFKGVFPPGEPKKPPPPFFFFF FFFFPTRPPRVRPRVRPRV
10025	23926	A	10100	253	3	NAINRNKMQ*TKTSEWKVYADHNATIKQ KQKRKCQVL/WRGCGETETLVACWWECQ MEQPAPVEN/W*HFLENIKIQLPYDPAI HE
10026	23927	A	10101	121	404	VLASVVSIFFFFFFWKGLIFSRLGGG G/LILG*LKPPLSLGPGFSCSLTLPGEWE

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						LKPPPPDPGFFFFF*GKTGFPRGGQEGLNFLTWEPPPLAL
10027	23928	A	10102	468	1829	IRDTYTQNPDKAKGYFSCIFFEIEETM SRKQNKQDSSGFI FDLQSN TVLAQGGAF ENMKEKINAVRAIVPNKSNNEI ILVLQH FDNCVDKTVQAFMEGSASEVLKEWTVTG KKKNKKKKKPKPAAEPSNGIPDSSKSV SIQEEQSAPSSSEKGGMNGYHVNGAINDT ESVDSLSEGLETLSDARELEDPEASML DMLDRTGSMQLONGVSDFETKSLTMHSIH NSQQPRNAAKSLSRPTTETQFSNMGMED V/RPRHQ*KS*VPIFEKSVKDLQRC TVS LARYRVVKEEMDASIKMKQAFAELET LINGSRKWALLAEMDKVKAEMEFLSR QKKAELLKMTHTVAVQMSQQQLVELRAD IKHFVSEKDYDEDLGRVARFTCDVETLK KSIDSFQGVSHPKNSYSTRSRCSSVTSV SLSRPSDASAASSSTCASPPSHTSANKK NFAPGVY
10028	23929	A	10103	254	2	KKKDFPLTPLGFGGLKIQLEFFFLQKKKN FYFPP*IFPKIFFFFFFWFGTQSCPVT\ RLECSDRIPAHYNLHLQSSSHSRASVSH E
10029	23930	A	10104	256	419	KVIELHTGR/CAVGQHVGRPRRVDCLSS GIGDQPEQHGEPHLY*KNAQSSQAWW
10030	23931	A	10105	153	439	TTVTSLCIYYTIYYFRLLSTHAYTHIY THIYV*KLTIKQPQAGPSEGF*KKEF** RRW/WVGTVAHTCNPSTLRCQGGWMT*G QEFETSLANMVKL
10031	23932	A	10106	424	157	SSHLGRPRWVDHLSPGVPDPWQHGETP SL/LKLAGGACL*SQLIGRM/RLSSGGR GCSEP*SHHCIPVWETEQDPI SKNKQTI FRMFKN
10032	23933	A	10107	213	3	NYKCPPTPNLNTLKALYFKKLILSPKA* AIKEKID*/IIKIKHFIYASNIINRMKRO LTEWKKIFANHVSDKG
10033	23934	A	10108	300	1	TPKQRGKKGSPREKPPFVNLPGLTFL/Y EV*FMNPLK*QKKKNFQGFFFFLICGT VYHQFTSK*ERGVPGTVAHTCNPSTLGG RGGWIT*DQEFETSLG
10034	23935	A	10109	120	421	KKIKKKKNHMIISIDAE*AFDKIQHR FMIKTLNKLGPGEKHI/KIMKAIYGRGG QDQGLHTAKK/EPLPLRENKISGKP
10035	23936	A	10110	102	418	TLVCVCVCVCVCVSLSVFLSLSLCLS QAGVQWCDHSSLQPRPSG\SGDSPTIAS VVGGITGVHCHIWPFTFYFLFLIRLKSML L**TSSEMALTKMGVHSHGLEFN
10036	23937	A	10111	382	2	VNNATMPSPKCSSTEKSHMSLTSNQKLEMI KLSEKGMKAKIGLKLGLLC/QVSQVNV AKKKF*REI*NPTPVNIR/DMQKVLV/V KTEDQTSNIPNLNQLIQNKSLTLFNSI KAERSEEA*EKCEDSRG
10037	23938	A	10112	61	427	ENTYVQVQCSIKEEYLQRRTLKYASLFQ KHICGSLAFLHLL*PKLYHSRNSAESDW IIQLFSVQPNVKEISKHKIGW*RGHACN /RQHFERPRKHDLRLGVRDHPQHQGET PSLLSLKIH
10038	23939	A	10113	71	399	NVLGKEARSVGWEAVRGQISRVS IQMKW

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						KGLIKGEKLMKESQACICIFYFFFFETE TNFIAQAGGQGHDLGFMEPPSPG\*SDS PA*APHEQNGL/TGMHNNRIVFV
10039	23940	A	10114	362	1	SKKKSWSGSHSGSKCHTSFLSYPTKEQKS YLSLFYKCNLQSLTFKELLDHFRPVCLP TIY*KNKWP/RDLPLKPSFKTLM\*NQT L/WPGVVAHACNPSILGGQGGWITRGQE LKTIKANTVK
10040	23941	A	10115	314	3	WRERRCGAHLMRCSANMAHDKPSRMLNL *KPKMAT/RNTDHDNFW*GHGETEILNH YWDYKIM*PLWKTII*QPKMFNIKLPY VSYIQLLGIYPRNLKINIHTKT
10041	23942	A	10116	44	394	PGFORVSQDGLDLTS*SAHLGLPKCWD YRHEPLRPAGIYSYPAVFLVSTYRASN IT*MLMTPKPTSG\YSPLLSFRFSSFSY LRDISAYMSLSCLKLVFKSKPIIFLSP LWLLV
10042	23943	A	10117	398	3	MESCCFMGIEFVLKEEVLEIGCRTM*IY LHY*SLHLRMVKMVTSLLCVFFHN*TF KKSSVFLYAGNKQL*I*ILKNYIYVMIP FTITSRNMKRNNLTGDKDMSTETYKTQ LKEITD\*NKWRDITTFMQN
10043	23944	A	10118	104	386	KVPVWATCGVKMHRLAGHGGWRLWTRL WRLRRDNRLSSGSRGA\AAEILPLCHCT PTWVTEHDSITYKY*KKGAPCWRASS*C TLSGHALFFFA
10044	23945	A	10119	258	401	YNYPFLTVMKEKIGAGMAAHACNPSTP GGRGG*\TRGQHLETSPTNMV
10045	23946	A	10120	310	384	GVFPFLTFLYGGIKGGPPPPRFFLF*FA FLFFFF/ETGSHSVAQANCSSVSASRS FHLPGPGDPPTSAS*VTGTTGICHHS
10046	23947	A	10121	245	479	TSSLYRKIQKRFYMLALEVLKICNTYF MNTERFPLKLFQFS/FRIISI*FFPFL FPKIYHYFLRDRV*LCHPGWSAV
10047	23948	A	10122	268	469	NSVFWLGVVAHA/W*VNPSTLGGRGWI TRGQLEETTPANILPP
10048	23949	A	10123	221	423	GOAGAVAHACNPALGRPRRDSLRPGV GDQPGQHSKTPSL/LKSDNF*KMGLGP WAWWLTPIIIPALW
10049	23950	A	10124	73	183	AGGGWALTNTVINPT\PPSTPFTPCLSY SCTISTASAFRFPG\STSTAVLTHVRIL KSTPDAPHPPLKIPRARRNIQRDHTLSS NLFYYNHQLNVTEELTYDILT*INPTAT IHAIHTMPLLLFLHNLNCISI
10050	23951	A	10125	342	2	PNLGPCPPPRGTGKGGPFFPSFHPST\IG PNFFSF*RP*FF*MLKSLGP/SPGTP IPKPPFFPGFKNYFSPPL\PKGPLLKPP RALFFFFFFNRHRLV\CPGWSPTAGLK RSSC
10051	23952	A	10126	85	442	KKVINIKCW*RVWRTGSLIHCSWG*KMM PHWRAVWQSFR/SLSMYLSYEPALPLPG SYPRALRTTCVCTHSRCFSLLELPQA/W NH
10052	23953	A	10127	180	484	KSFFFFSQSAQPIKVIPAP*NHFFGVK RSSCLSFLRKWGPWWPPPPPPPPPPFFL IFVEMRSHYAAQAGLKLASS\VPPPSG IPRTLD*SYPD
10053	23954	A	10128	376	1	WSPGAQLLFISCLYLNLSLHTGRTPAK

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						PP*GWTLQKTTPLSCPAP*LPPPLPSPL QQIDLKEKLVFTAPACSL/PHSPNSSPW PQRRWPSVS/P/PVAHPAAPRLPPPPVC ARPLWLPEAPLLGIPPH
10054	23955	A	10129	140	454	CLIRSSINSVHNNIYIHTSPDRHLGCFQ FLVVTKNAAVSRLAYVF*I*IPTYDHI HTHTPAGYIPRHGIAGSQLTNIFNFSS* LSSNSF\QVGCTSYFLFPSHI
10055	23956	A	10130	340	473	AGARHSVLPRPPLAGSSCPSS/CGGHC VALGVSCPGGCGRAACVPGCCCLLGLP SDVCVC/SVCWGGSMGSRLLGGWAAPGF* GNSREGPGNCSSGRKAGLAGGCLGPAAW EQAPDILCCGPGPHWLGAPAQVPLAPPL SPPPCLYGCLYSDRGDL
10056	23957	A	10131	280	2	DSLALLPRLEYNGVNVACHCKLKSSWIRR SSHLSLPKHLDIRSMH\LPGLEIF*YS YCK*CLLTSPYFEFLMNSLEDISSCFIP IRVMPKCRMK
10057	23958	A	10132	244	3	IISTDLISHSWTLYLISSLVYVFLKQHS LAVLPRLDSCGMIIAHC/KLQTPGLKR/ FL/CLSLPST*DYRHTPENRANFYYYF
10058	23959	A	10133	272	3	VGKPRVFPYRIAFNFRVTSILGPHIKK YHFQCRGKGKCHFF*KAPPPFF\FNETG FCSVPRLECSGTIIALCSLNLOGSCNSP TSVSQV
10059	23960	A	10134	217	3	FFRFRPLVSPALTELGQF/HFLTRGL*K KKPFPFLFFFFSETESCSIA\RLWGSGM ISAHCNLCPLGSSRTRG
10060	23961	A	10135	229	3	KNDYLCWQCGGRTTETQMLGCWDIK/LI QP/LWKI IWQFLLKLNMHLLCNPTLELL GIYP*EMNVYVHTQTCICTDAW
10061	23962	A	10136	84	352	RREFKTGLATWQNLVSTKKYKTTVRYHL TSTRMDI IKGR*QVCW/RKC/GDKGTL LDC/WMRMLVQPIWKIV*VWKFCRK*KL NLFFPPPPQ
10062	23963	A	10137	280	2	KCVVVPEERILREKSQHLGKIKQEGRLN AVVLIQPGQHGETLSLQKI/QLAGHGA PLRSQHLRRMRREDHLSPGVRSRSEP** LSLHWVTEQ
10063	23964	A	10138	2	386	HIOEKQLPNKDSTLNPYFLLISILKRKD EKIQMPSKHMKRCSTSLVIREMQIKIRS HPPH*VGKILKSANIKRW*MCRKRG\TL ITCW*TYK*TYKLVKTF*RIILQHPLLK THQSYYPAPHLKETQA
10064	23965	A	10139	229	1	TRSYHESLTILHTNHHLCSPFPQAATP *SRFPYSNRA\WLGSAHTYNPSTLGGGR GRRNA*GQEFKTSIGNLPK
10065	23966	A	10140	261	429	LSHLFHVALI*LGLVW/SFVVFVFFETGS LPRLECSGVITAHCSLDLLGLSLGPTSA F
10066	23967	A	10141	377	34	WVFGSSGPPPPGFKKFFSPPPPKKNPR GPPPPPIFFFFCKKGVSPLFLPPGGGP /HPFLSPPPPGVKPENFFDPGGGGFP*T KIFSRPPPPGGKQNFFLKKKKKKKEHQ IKR
10067	23968	A	10142	208	424	FFSLFMQTFHIHIFFYFFLAGGGGAGVD RVS/LLSPRLECRDTISVHCYIHLPGSK QFSCLSLLSN*NRYHAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10068	23969	A	10143	1	297	PTRSPQVSNLNHKSFIISFYLFIDLLSVC LSVSVYFETSLTLLPRLCSGAIITLHLS LLSS*GHRHAPPCQV\FFVETRFHNVSQ SGIELLSSSHLPPTA
10069	23970	A	10144	185	488	SGFPRGTELGAVCVVCVCACVCVCIK LGYI*NHKRIYI*LLYIYSTYYIFNLSL *LSVY\SYVNRNSM*DRSQSI*IFILPK LKTCLNTHTLKNTHEGG
10070	23971	A	10145	283	3	LGWPGRKADGSGKLTIDYGRLDKLVSP\ I*SAISDMASTTKAVLQAQRDQYSVLDL AHAFSSIR\NQSQFSFIRDSPQYATLP SEHLNSLDGQ
10071	23972	A	10146	146	380	CFLWDNFFFFIFTEKTGSCSIAQAGAGT Q/WVGIIISYCSLKLMSGRDPPTSLSCVA GTTGMPHHAQVIYFFIFL*ROGL
10072	23973	A	10147	275	3	IKGMLKAKTG*KLGLLCQ/TSQVENAKE EFLKEIKSATPVNT/RMIRKRNCLIAEM EKV*VTLLDQTGHNIPLSQSLPQSKCLT LFNSKKAER
10073	23974	A	10148	281	2	KIFLPQPPQEMVFGQFAPPGG*IFLVF* *KQPFPPPLGRFVFK/LPGGIPFFFFFFF FFFFFFETESHAI\RLCSGTISAHCHL RLSGSSDPTRP
10074	23975	A	10149	413	139	SLRVWPIFGLLOANKKKFFWILFLS/IR PLFFFSRERGGTPLFPFFFLRNP GKKS PPG*PPPPLKIQFPGKYFFTSRPAPFFP LFCQPPGKNLNYWGLPGFPKIFPPPPPL FFFFFF*DRVSLCRSGWSKVAR*LTWGK AFTTWVS
10075	23976	A	10150	100	431	GPRLTDHLRSGVPNHPGQHGETSFLLI/ HNYSGG*GRKIANRLNPKGGGCEPKSC HCTPSWGKKRNFVSKKKKKRE
10076	23977	A	10151	134	417	GLAAPLVG/WGKRNPFP*PFG*GEKTGW GPHPGKIFLKKKLLFFFFFF*KGGLSFPP GGRERAHFWLKKTPSRKKEILPPPPPR RGGGGPPPPPPFL
10077	23978	A	10152	403	2	LAFPILOEVPQCFCNLLHSLRMYSTGS KLFPLASPQPHSLLYHLTLARAPNILEE LQSPNTALLKYL*EAALKKKS*HITS SL*KVDLSFFLETKPRISA\RLKCSGTI SAHCSLRLGSPNSCATASQVAG
10078	23979	A	10153	382	297	GLN*ESWSGEKGT/LHCWWECKFVQPL WKMV*RL
10079	23980	A	10154	209	15	SSPKF*FFFLSPKKIPLPFF*PIFFFTK TP/HFFF/SFFFFVCVSGSHSVPRLECS GAITAHCSSTS
10080	23981	A	10155	153	422	RTSGKNGNRGQIILVTMTNWLFSFFFF PLKTGPHFVIQAGGQGRAHGSQA*IFG \SGDLLALVSLQAGTAGFHHHAQLSFFF KKTGLF
10081	23982	A	10156	257	3	RRLQNSKDCCLFFPLEAPRGATARCQPE LSCMRCLSA\LLGGVSQSGYMGVRDPHK EAV*PLAELKR*AGRSSAPFKA VRQGCL S
10082	23983	A	10157	37	386	DATFRINSGTAEGGLDRIEPLNDLQ*Y INLVGTAVRRPDRIESNFESSTVGKKLS NNIVCYRSFFCERESQLTQQTSMLYYFK KLPQLPQPSAITTLH/SRQDPPSARRLO

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						LGQ
10083	23984	A	10158	407	272	HKGGKREKRKKKKKKKKGGREKQGERRE/REKKGKREMKKNRYSKCTQ**LLSN
10084	23985	A	10159	248	478	VKVVRHRLLLDPSVEDPWKSLKGPLQP*/RL*IFFF*NSGLLCHPSWRVAQSRFTGVSTSQAILPSFSLPSSWDR
10085	23986	A	10160	458	129	GFSVLNRLEDEDLRQENLLMPAV*DQPGQHSKTPISTKNNMNPAGHGGVYP*SQLLRTVRPEDHLY/SNKPCSYLCAPAWATETLSLKNAFSCCSNHYGLSFQTSFHRILMF
10086	23987	A	10161	82	291	YSKTKSLFFAGHGGTCIYSQLFRQVQVRQEDHANPGV*GCS/DTMIMPMNSHCTPAWAA**DPVSKKKKK
10087	23988	A	10162	6	409	LRINILPEPISLSPLTAPAVFMPWTNYS SCDTFSLASMTLLPLHFLSTSLALPWSLFLAPSLFQISKHQLYLSPVLLTLSSCYFLNPCFRNHILMNLGRPRQANYLRSGV*DQPGQRGETPSL/LKNTKITWPPW
10088	23989	A	10163	249	415	APPECSLPLLVLVLLLLLLLLLFLRWEDHLGPGG*GCSEPKSYHCTSAWVTR\GDPVS
10089	23990	A	10164	1	405	RSEWRLRQPERQSETVKKKKKGGFFFSRGGGGGKIFGLMEPSPSGLGQFFLFTPLENGGYRPPPLGGPFFFFFKGGFPLCGPGGFEFPALGTPPLLFPKGLNFRGGPTPPARFFFFWGPVFSVFS PKN*NPPVFRGKNGKNRPPKKKKKPGRG\WGPPRKFNPFGNKRGVPRAGNSKPPGPQRGNPPFLKKKKKGPCKGGGR*PPFSRGVNKNCPKPEGEGSINPKIFPPPPPPREKKKKPFFFFLTVSLCRSGWRNLHSL
10090	23991	A	10165	175	404	AIKMWVIAQVPSQCLHGVGFYLP RSVCVKTP*NKRHRQGVVAHGCNPSTLGGRGWIT\RGQEFETSLTNMVKP
10091	23992	A	10166	317	2	PFKNSPLLLNEMTNHFEPTCNVNVNSPFLK*HKFLFF*EMESCSVT\RELECSVTIIAHCCCLKLLGTSNPPTSASWAPGMIIGMRHCPAPKVCSHASAHASAHAS
10092	23993	A	10167	325	2	KMGEKQGHFIKEETIRKANKHIERCSRLLAIEEM*IKATVTI/RKHQTKC*QG*RESGSLVHG**KHKIVHPLWKILSVSYKTKHSIIIIIGYSSVLLGTVLVHSGSDAW
10093	23994	A	10168	245	3	GEPFLFCFPIKKPKVFFCPYFNQAVFFLETHRGFFEFFFLF*KKKKKS/LGMVAHTYNPSTLGSRRGGQIA*AQEFKTI LGNMS
10094	23995	A	10169	164	1	MNKMSQYTFPYKN*QWGG\SVAHFYNPSTLGGQAMQIT*AKEFETSLSNMAKPC
10095	23996	A	10170	214	419	LS*PPPPFPFGKKFNRLRFYFKSKPGP/FMFVALFQKGGPFYQNI PPPVKLEPPFP TILRV SFFFL*DGVLWCHPGWNAVA*S QLTASSTSRVH
10096	23997	A	10171	168	1	WTWWLFPGF SITNNYCSHFSSSLHLAIW/LGTVAHACNPSTLGG*GARGQEFETSLT
10097	23998	A	10172	139	3	PAH/CES*PPGLKRSSVSLPSG*DYR/HTPPH\QLIFV FVVMGFHQPA/SA/FPKC*DYRS\DHKKWPT*HLK/SFHF I KK*N*LKRYLACSRWLWYLFCLIRCMV**NLDDL SILYLHLNKFQFLFIYLF FEMES



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10098	23999	A	10173	253	2	FPLKICNTLPPQIFSTQRGLLSLPFTTF LLSLILLRPFPPFF*TESHSVPECSGMI SAHCSLRLPGSSDSCASAS\QVAGKTCA R
10099	24000	A	10174	300	3	GRAFFFKGLVKWVFLTPNPIFLLKNFL KRVFFLAPSEKFVFFKNWPP*LSFLIFG EKNFFFFFFFFFSEMESCVA\RLECNMG ISAHCNICLPGSSDSP
10100	24001	A	10175	117	381	EILRYIVSIRIRRTNLKFOQEELRVNIK NNLSSLGNMVRPRL/ECSGVITAPTAVS APGFK*SSHPSLPSSWDHRRAPLHLGDF FLIETRSHHVQAQGVIFNVYSKFLLLK FKISPSDPYRNNISQDFLAIGPTNMVPL QPYIVLCACRTKNNKIIDLSEQSSRT
10101	24002	A	10176	194	412	TLKNLLLSLHCLSFVPTDLYQPERLSKP PRPAKKYKFLIL/WLGVVAHACNPSTLG GRGGWIT*AHEFDINLT
10102	24003	A	10177	100	339	VPVKSLLLCVCVCLLL*RI SDHLP TLY ANLG*CFFSYLVISYS\NSTYCLQRHL LAIQKQP/CSFLRQ/HLVGWLHKKKHTH THTHTHTHTKSNTHTHTHKSKDLTGTO NTEFLLK
10103	24004	A	10178	229	2	KEKYIKSKLHFEARHNGSHL*SQHFGRP RLMDCL\VQDQPGKCGENPYLQKNTKIS QAWWLVPVVPVYSHRASKTLS
10104	24005	A	10179	368	2	SGSSPSTSPQGRPDPLGLFSAKIVLGQL ATIPPLCLFLKIFHPLTLPLLLLGGE FNLSPQQQDSISLPWFLCYRGPTYKAF FYV*ASVPEKI\FFFFFF*DTVSLCHPG WTVAQSRLTA
10105	24006	A	10180	398	1	QNIMLYTINTYNFICQLKKKTIQWGENF FENKWC*ENWIFTCKRKNLHPYLIPYTK TNSKWISELNL\KSLKVNRCGNLHDFQF GNGFLGDTKSKTK/AKISKLEFIKIKNF CVLNDIIKKVKRQLIEWKKYLQ
10106	24007	A	10181	252	419	GARFKGSNFTSAGGQGITFFMGPPKLIS RPVF*HRGEGKTPGVTLNRLLEHPLFA
10107	24008	A	10182	101	380	FCWIYNSWLIGYLFPPFRTNLNLTAMCGG SCL*SQYFGRQRQADHLSPGVRDQPGQY GETPS/LTKISWAWWHVPVVPATQEA EV GGSLEPREVK
10108	24009	A	10183	2	377	PGQVDCFS SGVQDQPDQYGEILFLLKLQ KLGGHG/IR*EDHLSLGGQGCKEPRLY HCTPAWVTEQYLV SQKKKKKKK
10109	24010	A	10184	140	3	DGVL LSLPRLECNCAISAHRN\SPSCDS PASASQAGCCGTC*SQL
10110	24011	A	10185	364	3	SVCPPRLGGVSQSGDMGVRDPFEEAV*P LAELERCAGRSTAFFRAIR*AHL SLLK\ FTRNHPFPHVPCPRVMSR*FGLLPFFQR CPAQRGEIWRRLAAVALRSCGRLQVR TCWQLCLHR
10111	24012	A	10186	2	249	SVRLNKNKENTQIRNKKGDTINLTETKR IIKEYSEQLFANKLH/SLDEMKNFLER* NPLRPGAEAQRLVS*RFWRATAIDHMRP
10112	24013	A	10187	270	2	PWAQRGCVFKNQKIFFGFFEIPHLDP*P CVFQRPPS\F*VRLIFIGGGFKPFFFFF FEMKSCSVARLECSTISAHCNLRPLPGSS DSPASA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10113	24014	A	10188	428	28	PIFDKG/E*GN*WGKKSI*FNKWCWEKCI C/KKL RDSSLTSY/TRNLKWKIDLNVR TK/STKLLEENIDIV/IYDLGLGIGFLD MTLKARATK/AKIEKLDKIKIGNFYASK DPKKMKR*FIEFIEQGGKIFTNHVSDDTS I
10114	24015	A	10189	85	243	DRVS/LLSPRLECSGMISAHCSFDLP* SDPFTSVPKSSWNYRCPARKLSFT
10115	24016	A	10190	96	440	LQSNHINTLNVNRLSSSMKRFRLSDEIF \KKHGPALCCL*EMYYKDKGTCTLKIKG WKNIYHANANNKKT/GMVLLSGKIRLES N/TVIRVKEG*LVI/INGRLI/QEDLIL LFILNVYAP
10116	24017	A	10191	137	423	AKDLDRQFSKEDIHMTNRYMKT/SGRQ LIRETQIKTMRYPPLTPLDLRKSDDKS ***YEQKGTPAHC**ECKLVQPLQKII* TFPKLLKINL
10117	24018	A	10192	221	72	AKVK*VVVFFCFLFFF*DGVS/HVVVAQ ECSGAISAHCNLCPLGSSDSVRVG
10118	24019	A	10193	460	121	SDKTKYW*RCRAIKTLTHF*LKSKLVPL L*KTI*CYLAKLKIHIIVFDSAIP*DTY FR/E*FCICAPKTYSNMVIEALFVPAQ TSKKKNWK*LSCPQIVDNFLNIHLMKYH LE
10119	24020	A	10194	393	2	ATMPYQRLLLTAVHELESPE*MDQFLD TYNLPFRFNQEEIENLNSPIMSNEIQSVI KCLPFGPNPGPNFGFIEFYHTYKEE/LP ILL*LFQKIEG\ILPNSFHEVSITLIRK TDKDAT*ETHKPISLMNTDA
10120	24021	A	10195	3	353	EAAPMPVKFFQELLEPSGPPGLSMSCLD CNGYACFSVSLHQSANQSIDQ/SIYQSA IHLIIY/VSIIY*SI\YLL*SLI*PMY VPIYPLSCLSIYLSFMPLSCLSFNNLSI TRHGSML
10121	24022	A	10196	118	395	DFNAGLLPSYQVLSLYFCF*NGV\CHCT P/RLGDRPRLR/PPKKKKKTPPPPLGG SPPGGEPYTERPGVGP PPPPF EHPREN PGCFHPPPKAWP
10122	24023	A	10197	437	160	FGYPRVFPLPALLRGPGILFWGPNKKN YSSPARGSKICFFKRGPPFFFFFYFFF* QTESCFVAPVGVQWCDHGS LQPQPG\S SGPPPTS
10123	24024	A	10198	259	3	RQGNHVTHVYSSRLQLILSPASLAVFI QKIYVNLCTYIHIVNLYA*MCICVCICY TCIL\ICIYGLVAVAHYNTTTLGAKLG GS
10124	24025	A	10199	1	416	IISAHCNLFHPSSWDYSRTPPYPANFCI FSRDRVSPCWSGV*HHLQHSKMLSKK* NKIDMHGGMCL*S*LLK/RAE*DVLRQE NCLNPGGRGCGEPGSRHCTPAWATRAKT LSKASYASSSSSPKKKKKSPS
10125	24026	A	10200	369	3	TAPPPFFFCRDGLRTSLIIFPSRATPYS LVTSGSFLPAGAGGRGLSLEIRVLDLVQ DGCPCSQAWAAALGGPGWWAPFLCFFET ASCSVAQEGMQ*CNLGS LQPPSPG\SSD SPASVVLWTSK
10126	24027	A	10201	314	2	LHHRPEV*FTPSKLGVTGYMVSNISYP WRCRAHK*SQVLVSLRHKLFLPEMESG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SEVQL\DTNRCISANCNFCPLPGSSNSPT SAS*EAGTTDSRQPDADAW
10127	24028	A	10202	68	413	KIGILLKTH*PSIC/VSITNF*YNDTGE LKVKG*KNIYYANINQK/KAGMVMFVLD ETDFRAKK/DYQGH*IMEVSVHKE/E/ LVLLNLYASNKRVTXYMK*KDTDIKGEI DKSTTIVGDL
10128	24029	A	10203	351	1	PKFPPLNPAWGTTIKIFFKKKNHNWFS PRKEKALQKIHKKG/RLLAKEISFLGGF *TDYKTNPDSSQSI RTLGEEKKKIRPGTV AYAYNPSTFGG*GRWIT*GQELKTSLAN MVGRV
10129	24030	A	10204	2	392	FLEGVLLLLPRLECNGAIPAHNNLHLP PRFKRLSCLSLPSSWDHRHAPTRPANFV FLVETGFHHVGDGLDLTL*SPCLGLP KCWDYRH\DHHAQPSF
10130	24031	A	10205	264	2	PLSLSNLFPILNSILKIFFILK*L*IH GKLHKMYRKV/LV*TSPPSPQC*HLR*V *HNIQKKLMGLGAVAHASNPTLGGRG GWIT
10131	24032	A	10206	281	2	ISPPLFFLFSPPKIFFSQKHIFLGPPL FYPPPLFFSPPP\PHFLWGFRPVNEMP KIDPQTWAKNKDKGNFPFPFFILPPK KNIFFTKTYFFGPPPLPPPPFFSPPK KK/SYPFPLKKNSPNPPPS*K*AAISLP PPFFYFFFFFSSFFLENTWKMAW
10132	24033	A	10207	340	1	STKKLVQKLGEHTQCWQGCATGTLIHC RWECKLVQPLWK/SAWQILRQL*NFHML PYNPTIQLQGSYSRE\QHTCPYKDLYVA ALFTIAKNC*QAKFLSTGE*INKLWCIH ITE
10133	24034	A	10208	136	3	KNRGPPPRSGKFFPFLPLFFFFFF*DRV \YPSHPGWSAMVPSQLT
10134	24035	A	10209	327	2	INKKYYEQLYA*KFDNLDEIYQFPGRYN LPKLTQEKANNLNRPVSLRETKSTINNL PKRKVPDPDGFTGELYQTFFKEITP\F TEAKGILPNSFCEVTIIVRLFLLRQ
10135	24036	A	10210	89	485	EIVPLLRFPVIFIASPTTFYTYGFVSG EKSQYKKREKCLKDTLEQSRSLGMHST CGIALHPKREGQMCTLCACFY*FFLKES HSAARAGVQWHNLSSQLPP\PSSENS
10136	24037	A	10211	361	462	IQQIGSNTGNIPAMELALKRNSKNINRL AGWNGP*VFAC/PKNVLFYLHP*LFG*I *IYQLKITF*NYEGMV/FVFRFLFETR SLLSPRLCSGTITTHCSLELVGSINSS ISARAEFLQORGANL
10137	24038	A	10212	62	469	SLLWKLRSRGASTSLRCLSA\LLGDVSQ SGYTGVDRDPLEEAVCLLSELERGAGRTT ALFRAVRQGRSLLEKL\LLPFVQICPAP GGGIYR/GQ*ALLSCGGLCPV*AS*/M CLPC/EA*TRLLKPPPGS
10138	24039	A	10213	197	1	VVTQPNNEWCVTNKDSFQQRCTKKIKT/ WPGMVAYTCNPSTLGGRDGWIT*GQQFK TSLANMVKPH
10139	24040	A	10214	31	213	HASLDEGFHHVGDGLNLLTS*STCLGL PKCWDYRHEP/PAPNWWKKFLSSKAFKR *LGCY
10140	24041	A	10215	442	29	PTINPTMACKCLSKRKSHTSFTLNQKLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TIKLSEEGMLKAEAG*KLDHVH/QVSQI VNAKEKFLKEIKSATSLNI*MIRKQKRF IVNME/KKVLFWTTEDQTSNIPLSQSL IRKRP*LFNSLKAERSEEAPKLEASSG G
10141	24042	A	10216	195	533	LVWFVLRVITYGVAAKMSSGTTIIGRLSW GWRLLHF\KMAHL*GYWWEASVPLHMKLS SCHGTG\SLRVKDPRELRQKLQCFYDL VLEVITYWHFYCILFIRSKSLSPAHIQSK RI
10142	24043	A	10217	274	494	CVLKGLPFALPWFFFFF*DKVSPSPRLE CSVAI/SAHCSLNLGSSDPPASASQLA GPPGLRR
10143	24044	A	10218	142	480	VTIKIYLHPHDTTTPLRQGSRLKEILV SY*QKQVETRPESHVIFTVISTQPKKT TTRSGAVAHTCNPSTLGGREGQI/T/RG QEFETSMTNPVK
10144	24045	A	10219	163	464	AVYFSFWRVCEHDLASLYFENSGKRDNK FVFLVLQAQGPAPWRQGEVHKHLLPCVYH FAFVVLTPQPQSFF*DG/QSHSLAR/LE CGGVISAHCNLYLPGSSNS
10145	24046	A	10220	379	469	V*KVQM/WPGMVAHTCHPSTLGG*GGWI T*DQEFETSADVAKPC
10146	24047	A	10221	211	473	VTWLLLFSSIFRASSLSTDSVSYVIAFQ FYFYLFYFYLFIFETESCSVA*AGAQW CDLCSPPPPRGS\SEEPSTLQMTSGSS NL
10147	24048	A	10222	142	394	GVCQSLGSLCQLGGTGVRDQLEEAVCP LAELEPCAWRTLRLRLCCSLQSQAGIF /RFC*SYIHICFPQVLLSSEMGLSIR P
10148	24049	A	10224	77	396	KRKTKKSFWTSPSGFGLRPPIPKKKKFFN SRGKQGGFGRGSGSRGGGSGTSGRGGY MGKVFGMGQ*NFTGDQGLAKGGFVFL GRTTIGIKGALKRLFA/NEHDLR
10149	24050	A	10225	155	443	GQAREGLKSGFPFSPPGWPLILPGGV FSPKFFFFFFETRV/CAVAQAGVQNCNI DSSNSCASSS*IARITGAHHH\TELIFV F*ISPPSQ
10150	24051	A	10226	290	485	KRGEQPVQKKKFFFFFFETESCTVAQAG VQWHNLSSL*PPPPG\SSDSPAEFPR
10151	24052	A	10227	228	424	KLYQNLHDTLFGFELSHYEEVH*KMLKG SSWEFVMHSS/VSNKCILICSAXKKKKK KKKKKKKKKKKK
10152	24053	A	10228	269	454	DLFAASQGHQALLLELMATTLSTHTHT HTHTHTTPWSLF*SR/SALSVC
10153	24054	A	10229	255	1	FYIFSKFLYVWLVNVDLSDHICFCIQSV IISCFGVFYFYYY\FF*HQSCSVHTGV QWCDRSSMQPQLQGQNDPPTSASQVAGS A
10154	24055	A	10230	18	472	GPEEFGTRRERDRERERETRDRSRRER VRERER*/RQRERERERERERER
10155	24056	A	10231	52	361	WRKNYYFQIKITVYLENTKDFIQKLHTK CW*G*KEIGRAIHCWWECKM/VIQPVWK R/VWQFLRKLNMILLPHNPAVELLDIYPN ELKTHVCTKALYEAGRGGSRL
10156	24057	A	10232	3	402	APRLPLGGWISFSSPMGAMGLNRATGIM GSFFFFFFLKRKSPGLPQGEGRGQNLG*G

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NPGPRG*THFPG*TP*KAGNNGEGPPPR GNFGFLKKKGVPQKGQGSKP/RDRPGT PRLGPPKGLE*RGGPPPPAPQK
10157	24058	A	10233	48	470	PGRRFTTAGLGKQEPAAAGPRAPRPAQT PLKREAAARPSLRHLPEGA*APRSSARSP LLIPAAASLRSPRRRTCRRRLRHFGIITR PFQPGVRLPDSGPGLA/RWACAAVPAAS RALPALRRPL*RRPGHGAPSSKSHGHSR SP
10158	24059	A	10234	169	446	CPPGPAPSHLLEDRDDPQAGRQSSFYAG WDRWREKTLFLFLRQSLTSLPTTFFFF \FEAESHVTHSGMPCVISAH*NLRLPG SNNPPTSAS
10159	24060	A	10235	264	2	KLKPIFKMVFLKIMFMSYIMEVFFFIET GSRSVTQAGVRWHDLDLSQP*PP\GSSD PPTSVSQVGKWHKTWEAELAVSRDHATP RAKL
10160	24061	A	10236	306	3	SQDMVKSPKKKFP*LV*GLTEI*KIRAL VFNKKFFFFFPETGSGSCSVA\RLE CSGTIIAHCNLQLLGSSNPPASASRVIN SIKKLFANFIVSANPRPT
10161	24062	A	10237	20	469	QCGAIPRRGDHLRSGV*DQPGQHGETPS LLKIQLSRHDGH/CRRLSHKNGLNPPG RGCSELRSCHCTPAWATR\GNSVSKKKK S
10162	24063	A	10238	313	3	TRPRPTQGPPHSGGRACL CIFSPHGPPQ TRLSTPVSPSVRPLGFQVLLSARHGFL CQHGMF\PSLFTMSNITLWPGAVAHTCN PNTLGGRGGWIT*GQEFQTS
10163	24064	A	10239	274	49	KGNPFFVFETGSHSIAQDGVQWCNHSSL QP*PP\G\SSDPPTSASRVAGTTGVCP EDKLSHILRRCYAQVFMLAG
10164	24065	A	10240	144	454	VCKIKIYLVLLLEDYIN*FVKSSL*LK S*K/LIQMWAIISLPECLNSVCLGKV G*KRCSQQTVAHTCNPSTLGGRGMIP R
10165	24066	A	10241	289	178	FNYSIKNNTDGWVWVWCLLPVLPALWEV EAIESF/CSRDEIPLSCPGWSPVPLKLR FYCLNLP*CWYRQEAPHPAISIIFDA TVIELFS
10166	24067	A	10242	352	294	PBRTTKMVV*DQPGQHVEAVTLQKMQL VERGGKHPQSQLC/REDH*SMGGGCSE PRP*PCTPAWVTERDHVSKIK*NKIK
10167	24068	A	10243	293	1	VSLCRESSNSFIWQCPVVSILALCFQR EKKRLDLP/S*MVGK*EIPFLVPLFLP HWPLLLMK/YM*IFFGNRVSLCHPGWS AVAQSQLTAASVPRR
10168	24069	A	10244	218	3	LERHIPVRPIICDYKWVRF/HFLRPL HN*FLFSFFSFFFFFFTGSYSVT\RLE CSGTISAHCNLCVHLLL
10169	24070	A	10245	185	1	KKQPQQTKNPLNNVKKEKGQHFFFFLE T*SRSVAQAGVQWCDLGSLQPPPG\SS DPPPS
10170	24071	A	10246	2	265	AHKKKPAKHIAPISTFLYGETEARRSM PKAAQLKCGRAGIILFVFKTESCSVAQDAV LWCNHGSLQP*PPG\SSDPADSACRVAR TTSI
10171	24072	A	10247	2	430	EAGGREALDGCGLTGRESGVQRRRDSMG

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						CQGTAGRGTRAGKEGPWRPEHLSRRPPA SSVLLSWAHLAWVEGS*TGSLCDLEAP GPTLSPWCWSPELLQLHV/HHHTHTHT HTHS/HPNTHDTQSLCHQPSFSVS PRA RTVL
10172	24073	A	10248	201	16	TPPGGVFFLGGFFLFFFFETESCCVAQA GVQWCDLGSPPHPPASRRPGNRSSI/AAA *GYHFK
10173	24074	A	10249	167	2	GFDPFEGMLSYLEKEET/WPGTRAHTCN PSSLEG*GGWIT*GREFKTSLTNMEKP
10174	24075	A	10250	92	389	FQPGQHGEILSLYEIKKI*/ELAGCIDM CLWSY/LLRRLKQEDCSST*VQGCSEP* CLSCIPSWVTEQDPDSGRQI*KKKKISL GRRGGIFLFLKIWHVFFL
10175	24076	A	10251	221	415	KKKKRGGRFKGSNFTSPGWRGNIFFMGP PKLNSRAGV*QRRD/WEKPGGPQFNCFG SNPPFPFPGGK
10176	24077	A	10252	94	383	GKLNRCGIWLLGRCQRPASVSNALWLHR VAPREEEAGEAWAGTSLQLSCKSKITPN KIVY*KKNKT/WLGTVAHVCNPSTLGGR GGWII*GREFETSL
10177	24078	A	10253	249	2	YPTMIFKCSKRKSPTSLTNQKLEMMK LSEEGMSKAELS*KLGLLH/QVSQVVNA KEKFLKEIKSATPANTGMIRKRNGLIA
10178	24079	A	10254	132	414	NNTYFQGKIFILNSQVKGMLICCWBECK *VEPLWKAVWRFLK/DLEQNSKEYKL*T WNQPRYPVVDWIKMWWIYFMEYHA\A IKKNEIMFFAA
10179	24080	A	10255	359	3	YSLRHNIEMRPVSNPTRASCKSHERRSV ISLTNLNGKREI IQEASKEGTLKANKPKA KLFVPVRQVNAKEKFLKEAKSAAPLN\ RMIRKQNSLTADTEQV*VIWIEY*TSHS IPLSQSL
10180	24081	A	10256	283	2	SLQPWKLYVHVFLPKYATYPFGTLPKT HFFHKILPSKAGSDLNISIYAMTYSRHI TIFFETESHVTRLECSGAI\SAH*NLH LPGSSNSPATK
10181	24082	A	10257	216	386	PSKNPPPLINPFFFFETDSCSFA*AGVQ WRNLSSLQTPPP\GSNNSCASAS/RIAG I
10182	24083	A	10258	263	1	FSQWLILPSPLSYSFLFLRQGFALLPRL ECSGEITA\PSSAS*VAEITGACHAEF LNFFVEMEFHHVVQAALKPLGSSEPPTP ATK
10183	24084	A	10259	248	47	IPKSRVKRENRLNPGGKGCN*PRSPPCS PEWVAKQNSLSKK/NKVKIYQNLHTETQ TVHGDIRQEK
10184	24085	A	10260	159	2	KRDMSSLKLEY*KKE/RIWPGAVAHTYS LSTLGGREWIT*GQEFESLTMNVK
10185	24086	A	10261	190	405	ASLHMFMYFFFFFFFPKQIFFFVQAEHQ WGNLGKRNPPPPGLRDF\PASPPKEAGF RGCPH*PGLFLVF*GE
10186	24087	A	10262	39	293	PSSSTSRIYPEDTPLITQKYICKILFIV ALFIFPKHWKLCCKPHIG/E*IKLQCIY TWRYYYAVQKNEENLYQLMYNDYQEILV SD
10187	24088	A	10263	282	3	AFYNRFFLKIFFKRGPRGKEKKGGKKEK KKWGKKKKKKFFFFSPGQIFFLGGVFFF

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						FLFFFEAESRSVT*AGVQWCDQ\SSSQP RPPRLKPFQ
10188	24089	A	10264	196	376	KKGGGHIINFPPHKGYPGPEKKKFFFF FFEMESCSVA\RL*CSGMI/SQAHCNLC LPGSSN
10189	24090	A	10265	514	157	GLTSLFRLEYSGMMSL*P*LPG/FR*FS RLSLPSSWVFLMYVYHYAQQSFCIFFV ETGFHRVVQAGLKVLGLRQSAHLGLPBC W\DYRCEPL*LTCLICFTYGLR*RSKPP FFVDGIQLF
10190	24091	A	10266	57	378	RSRIW*DSVILCS*LVSV/VDQSYFY*V TEILEQIKLLGSKIMCFCILQLHFLCFL CGSFVGST\IFIFSRNIWLGTVAHACNP STLGGRGRWIT*DQEFETCLASMK
10191	24092	A	10267	1	212	LIQKDTNIYYIKEAL*IPNKHI/KKISS IVSHYKMQIKIMR/YHTRMAIIKRTDKC LYECRETRTLMHCW*GC
10192	24093	A	10268	3	399	MANKHIKIFSASLIRMEI*IRATMRE/H *FIPIKWLVLKSKRESNKCWQGCGRGTGI VIHFQRECKIVLLL*KTV*QFLKKLNIR LGAVAHSCNPSTLGCLRPRVQDQPGQHG KTLSSLLEIQKLAHWGLHLSPS
10193	24094	A	10269	190	386	FSPFLPLVTILECDKATCRRGKSFDFFL LGPSFYFFKLLL/FIFYF*ERVLLCGPG WSTVAQSWLTA
10194	24095	A	10270	166	327	KTNSKTAEVCPPLSVITLNINGLNSPIKR QR*TDF*NPI\ICCLQETHFRFKGTN
10195	24096	A	10271	180	1	IFFLFEVETCSVA*AGVQWNDLGSQQPP PP\GSSDFQLIFAFLVETGY*IMVPSSS CRT
10196	24097	A	10272	273	3	FLGLFSGNPLKANKPVCHLTLPILQRIF FFFESEFHS\VAQAGVQWCDLGLSKPPP PG\SSDFPGRRR*Q*AMITPLHSSRGDR VRLRLKKK
10197	24098	A	10273	399	27	YHFVPTRMAIIRKNN*CW*TCGEIGNL VYCWECK/LV*LLRKIVWQFLK/DVKQ NYHPVILLLSIYRI*FDCLFLCKSHVEM *LISGVRVGAWWEVIGSREWFLMSGFTI SSCHQDCEFSQDLIV
10198	24099	A	10274	275	462	KINLVQLDFFVEMESHSVTQAGVQWC HLSSPQPPPP/GSSGDSRASDS*VAGIT SVHQHAGL
10199	24100	A	10275	2	379	RGPGRGLGSGTCFHPGRGGEPIVYQHL F*FFGP\PENYILILPGFIISH/IVTY YSGKKEPFGYIGMA*AMISIGFLGFIV* AHHIFTVGIDVDTRAYFTPPYHTFEPEG YIISRRRRKTKGFLF
10200	24101	A	10276	2	407	FPSPSPSPFASVLSLSFHLPLPEHTW FIDGSPTKPNRHSQAKAGYAIVPSISII EATA/PAPFTTC*QAEIALTRALTIK GLCINIYTD/SHILHHHAVMG*K/GFLT TQGSSIIDVSLIETLLKAFLLPKEAGA
10201	24102	A	10277	203	545	FLWRGQSLALLRLLECSGSILL/AHCNL GPHRFKRFSLPQPPE*LSNW\DYRRLPP CPANFCTFSRDGFTTLGQAGLQLLTSSD LPTLASPKCW\DYRHEPLVHGLTFNRSF NFFF
10202	24103	A	10278	250	3	AKWFLEMKSTPGEDAANIEM/TKDLDY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DINLVDEAVAGFGRIDSNFERSCTVVKM VNSITCYRELFHERKSRMLCQM*LSYF
10203	24104	A	10279	333	3	SLILLFQSMNHTHVRTFIDQFCVCSN YSTDWLFPPLSPISLRTPYSLRYNIKIR PINHPTMAMASKCSSERESRISLTNLQK \LETIKL/SEEGMSKAQIG*KLGLLCH
10204	24105	A	10280	251	3	ITSKVIDSNPTTSITITLNLNGLNTSF*R QRLL/DWASSPK*DSIICYLQEMNFYK IFKKIGRRIYYANISQKKVGVAVLTPDK V
10205	24106	A	10281	22	226	TKINSKGNKELNVRAKTIKLEENIDRN LCDLGLGNCFLD*YCIL*TKINSKGNKE LNVRAKTIKLEENIDRNLCDLGLGNCFL LDMTNPNAQTTKGR\IDKLDFIKI*NFWL DT
10206	24107	A	10282	238	383	DAKRKVSSTEGDSEGVHERRSAHLSAK PCPAEVE/AKPQKAAEK*SSSE
10207	24108	A	10283	127	377	RIPGGSALGKEIRQCFVKGQAEIGKIE MSQPTQEREVVEGIGSQKAAQVDHLRS VQDQPGQYGETPTLLKIH*LAGHG/GRC L
10208	24109	A	10284	328	370	VGPGPGF*SSGRVSSCCPGWS\PSELK* SAHISLPKCWDYRCQPLRPATFFFKTAS HYVAQAKVQWCNYSSLQPGTLRLKCCIF KKIQVVQVV
10209	24110	A	10285	341	1	KVVCVLTAPLSGRFSVCLPFLGPPYFLQ HSDIEIKPINYPTVASKCSNERRSHTSL TLN*KLETIKLIEEGMSKAETGRKLSL L/QSVSQVNAKEKFLKEIRSITPVNT* MI
10210	24111	A	10286	199	329	LFFSFLNCLSPHRIEESY*KEIKSAPPI TPGIPRK*TSIAGKKNVFMWDKQTNH NIP/LSQSKTITLFSNMRATVEAEK L/ERGCFFMRFKERTHLHNIMKGPVVA HTCNPNTLGGQGRQIT
10211	24112	A	10287	358	387	YTNALLLYV*DQPGHLMGKDSL FNKWC* KNEYSHAKKKQNH\P*FSLYTKTNSKWS KDLNVRAPIKILEKK
10212	24113	A	10288	111	373	SAQCQPDQHGKTPTLLRIQKLAGPDGAC L*SQLLR\*GCGEPRSRHCTPAWAT/EG KTPSQKKKKK
10213	24114	A	10289	197	375	IRIGLCKFII*FLETKLHTVAKVECSSA ISAYGTLSLVDSGDSPASAS/RVVGTTG
10214	24115	A	10290	118	371	QCLLMMSPLGKT*MTGRRLRQENRLNPGG GGCGEPRSCNCTPAWATK\GNSASKNQ T\KNKQQQQN
10215	24116	A	10291	214	368	CGYHQKNKKTNPKNKSCWQGCIGETLM HYWKDHKV/Q/PL*TIVQQFLKTRI
10216	24117	A	10292	2	376	PFPLMAQRPTHLPVLSASSGTSLLMPST LLWLPWLYKAHAVPTVPLSKLFDHTKPY AVSKNNLGALSI*SY*VIPVPPRSRF/S FIRDKPTS
10217	24118	A	10293	1	379	NILHNLDFFKNTTLEPQSSRLQRAVIAP LHFSLGNIVRRCFKKSGWAQWLTVPVIS ALWEADVAGSLEFKSETTLGNMMPCLN FKKKKKKAFLFGAPGFFFFMGGKILFGI AAPF*SSGRVSSCCPGWS\PFEK*SGH ISLPKC*DYRCQPLRPATFFFKTASHYV



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQAKVQWCNYSSLQPGTLRLKCCIFKKI QVVQDI
10218	24119	A	10294	201	384	GEERLSVQCSAFK*LR*HINISLQTFFF LRRESHVA\RLECSGVISAHCNLCPLG SSDSPA
10219	24120	A	10295	161	400	VCVIESVKANHLVDEHALKSLSFHLSLL FGV*GVCVCVCVCVYMCF/CVCIYVC
10220	24121	A	10296	1	433	GEGGGGCSGWSGVETAGSRPAPGAEQDL LPAPALGRWQGLNSVCYPAPWQPNRRQP LALLCAAGLPGPQRLECSGMIHAHSLD LPGSGDPPMSAG\SIAGTTGTCHHAW\E FHHVAQGGLELLGPSDWPTVLGLQM*A TTPGH
10221	24122	A	10297	209	1	LTPELLYHHYTLTYFF*ESGSCSVAQARM QWCDLGLLQPKALG\SGDEPPASAS*DA* STGVDDYYSWHTCI
10222	24123	A	10298	225	1	RPGMPLSALPCTGHAPARQPHSAACSGP KCPWCQSPQPAVGWTV*VCPLPLSPCLC /FCVPQPPWHGGLPLPCPPV
10223	24124	A	10299	212	367	VTAGSGHMCYTWEERLEQSL*KTVWRF LK*LKVELRFDPAVPLL/SIYPED
10224	24125	A	10300	97	406	LHRCPTAWVTERGCKLTNNQNGQHNE GEACSSRPFTTIC/EEKIHLVCAITRED *RLAAETTANTTDIPIGSAYRILIKKLLK PSKLSTC/YVAKQLSPGQLQTK
10225	24126	A	10301	3	422	YRSSSKTFLIIRRGFIPSTFLLAHLST TLSTLSHFQKGWVKLFFFFFFKKGFPPW PGGGGGRAKP*F/HGNPPPPG*KNFAL PRQGGGKKG\GPPPPGQFWFFKKKGVS P WGGGAKTPELGNPPPGPKGGGITGGPP PP
10226	24127	A	10302	330	1421	RTKGRPLLLALPVLVLLFLHLAFFSAPP GPSSLSSTEDLKWTLLSPAQRKLPQPS LHRAGVRDLQWQGRAGBELTAAC/WPAP PRPETAVLLQGLPC/QEGRLLLES LN GF ALVVSAGETIFYASATIVDYLGFHQTDV MHQNIYDYIHVDDRQDFCRQLHWAMDPP QVVFQPPPLETGDDAILGRLLRAQEWG TGTPTYESAFLTRCFICVRCLLDSTSG FLTMQFQGKLKFLFGQKKKAPSGAMLPP RLSLFCIAAPVLLPSAAEMKMRSALLRA KPRADTAATAD/SKMRS*LTLSERLPN *FEIWDAAAPGTLPSPFFGAFDGGHIF CIHTRALRGSTRTRQCIAAALEGASFRN HVEL
10227	24128	A	10303	172	383	KIENKVVQGYBIEITLVYCWWECKMVQL LWKTTWVVLKILKLGPP*\DSIIPLLGI NQGTEIRFKRYSNT
10228	24129	A	10304	205	2	NEYPA*KTDFFLVGSLFIYFE*ASHPI T \RLECSGTIVTHCSLDLLGSCNPPASAS HVSGTAGAHHICI
10229	24130	A	10305	423	30	LLEGKLTNRKDIRTKTPSVRRHLHQSPKV DRTAKMGKKQSRKSGNSKNQSAYPKPKE HSSSPAMEQSWMENDELREEGFRQSS/M SKLKEEVRVNGK*VKTREKRLAKSLTRI TNAEKYLKDLMEKTSVLRPL
10230	24131	A	10306	211	387	IFFFF*IKACSVAGAGGQGRHLGSLQPP PPGKQDSC/SPSRGVGTGTGMYHAQFI

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						FFGF
10231	24132	A	10307	229	382	ERAVVQPG*HGET/PSLKKL*KLSRCGG MCLYSKLLRRLR*EDHLNPRSWG
10232	24133	A	10308	168	417	GSYCFVVRNLLIVKVMRSVHLLFIMLL YRGD*WYVTQYNFCILQKQEKLIYRIA /HVRNPSSLRGGG*IT*GREFKTSLAN
10233	24134	A	10309	253	402	KGGGGGVKTPARGNPPPGPPKGGKRG PPPTQKGF/CFFFKGTRPPGGKTGE RAKPNEIPAPGKKEFLPKPPEKGEIKG /PRPPGQINF*FLKKTGFKKGGGGGSKP RPGGTPPPGPGQGGKNGGGPPPPKGF FGGKKKKKNPPR
10234	24135	A	10310	182	400	LHVTMIIFWLYLIKNNLLNFTYF/CYIF SVATSTFKIVCV/WLGAVAHICCPHTLG G*DGWIT*GQEFKTRLANM
10235	24136	A	10311	371	400	FIWGN*ASNKHICKT\STSLAFRKIQV K\TTMRYLSPPTPIRMT/I/I*KSYSSK CW*GCEEIRSLIHCKMIQPI*KT/WQFP KIINIQLLYNPAIALGNRTG
10236	24137	A	10312	113	404	QRCGKIGTFTHCWWEYKMQPLWKTDWN LLQRLNIELPCDLAIPLLNLYPREMKTS IYICT*MFIAALFII/AKWRQP/KCSSA DE/IGKMWIHCIMK
10237	24138	A	10313	146	1	FLTQKFFFFFFETESRS*AVVQWLDLGS LQPPSP\GSSDSPASAF*VAG
10238	24139	A	10314	157	434	FFFSEIFFFGPGVFSPPFFIGPGIFF FCPLKKKILPPPRGKFFFKKGP/HPF FFFFFF*EGVSLLLPRLECNGAILAYCK IHLPGSSDL
10239	24140	A	10315	277	2	FFFTAFFLGVPGVFPFPRFFKPGPGFFF LGP*KKNFPPPRGK/IKFFFLKGPPSF FFFFFF*EGVSLLLPRLECNGAILAYCN LHLPGSSF
10240	24141	A	10316	1	388	KTITHEVITECIWLKVLVLLYFPNCMIY VRMHICVCVHISI*MDHIVSYKCIHI \LCIY
10241	24142	A	10317	134	399	LGLPGDTRGGGTIENPPFERALNSONG GK\NPLLGPKTRPLGWGLCSTPKFWEKP RVRVVDLN*TPCLEKRAPWLKAKKTPA FEIRI
10242	24143	A	10318	233	3	EFLLSLICAICL*CALQKQFSSCFCLAL IELLGSMLLFH/SSLETQPPFLQIFF /SFFPLFFGANYTYNKPFEYSLI
10243	24144	A	10319	221	8	CDQPKSPPLSGVQMGDILVVLVFFLFLF AF*R*GSHCVAQAGLELPSSDP/PQAT SQVAGTTGMHCTWLVF*F
10244	24145	A	10320	1	407	RSTPDPVYLGFSTGGCKTEKRAGCFFLW KLHTKGAPARCQPELSGMRC\R*PLGG V/SQSRMAVKDSLEEAGCPLSELKRCA GRYTGLFKGGRDLHLNLLRLCPQTLCP GALSQEDGSFIYKPLTGAAAFLSYM
10245	24146	A	10321	115	398	ADEELLLMNKQIKYLEMESTPGKDDVN TVEMTKESEYSI/NLKAVAGFERIDSNF ERLSAVGKML*NSITCYKEIFH/RKSQL MSQTSLSYFKLP
10246	24147	A	10322	137	454	FFSLYFQGGFFFFFLGKFFFSPPGKGI CPKPPFGPPPPPGKGFSPPPPGKAKKK GPPPPPP\GFLEF*KKPGGFLGGFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10247	24148	A	10323	246	372	LGGKIFFSPAGGKGGPQKPPFP ISTKSYQLW\LGGVAYACNSSTLGGRGK WIT*GQKFKTSMANM
10248	24149	A	10324	415	1	IWGAPRVFPPPPF*NPPPEKNFWGPKKK KKFPPPPG*KIFFFKGPPPLFFFFFFF SETESCSVT\RLGCSGGISAHCNLRPLPA SSNSPPPSLRMPSTPVLRLPHGDLLSPQ LSAWVLSWPFPLPSLLLPPDLDFIVQ
10249	24150	A	10325	3	559	GDGITGLSPTISKFLFFVFESISLSPRL GSSGAIMAHCSLTSRREPPCRSINFFVS VITLNVNLTNGKIGRMDFF*MM*YTIQ ICNLQNTNCRP/KDTNCFKMKRRKEIIH ANSNQKRAGVAILIPDKIDFKPKNVTER HRMLVRES/ISQEDVTIINTY
10250	24151	A	10326	24	387	NQGLGARNQKSQRVFLAGFFFFESSCS VAQAGVHW*DHSSV/PGSSAPPASATVV VGTGTVHNHPWLIF/VFPVETGSH
10251	24152	A	10327	145	396	CDYFGEMFSYLLLNLYLDDPAIPLLPY VPYENENTDSLKDMTDAHSSFIHNSPKL ETKCPGTDEWI*MTKKSDYCKHW*GYRV TGTLLEYEGECKIV*LLWGNV*LF\LLN TYLCDDPAIPLLPYPVE\MKTRIHSKT *PMPAAALFIAPNWK/PKCPGTDEWIN TL*HTHAVQYHVAVER
10252	24153	A	10328	94	639	ASISSSIKWDNISFLVGLGELNEIRNI CKAVNMKQALNKWKLILFVIENNVS SSNNFKIFYAYYIAKAVLLIITEHITLS IVLILKKQNNTRAVTKCW\RGGREKTL IWLVG*ECKLVQPLWRRVWRFLIKVKIE LPYDPT/ILGIYSKERKSVYRK\NICT PMF\VAALFTTAKTWKH
10253	24154	A	10329	143	3	SAWFFFQDRVLL*/SPRLECTVSISNHC NLRVPGSSKNYCLSLISIWDR
10254	24155	A	10330	153	389	RQGLTLFPGLVSNFWLPVLSHLLGLPKC WGYQCYHAWPS*CF*NRSI/WSGTVTHA YDPSTLGGQCKPIT*GQEFETSLA
10255	24156	A	10331	382	422	RYKLDL*KLNTLPYDPTVPLLGNYPKY *T*AF\SKTCT*MFIAAYSQPPKGRSKC SSPNE*INKMWPIYIMR/YYSIAIK
10256	24157	A	10332	194	1	CKRQCNKEDRNI/CSK**NPTILF*TTK RKG/WLVAVAHACNLSTLGG*GGRAS*A QEFKTSRANM
10257	24158	A	10333	348	1	NSGQSWIMYPLLKKGVGRVSPDPDIDVN SISMVWCGGRLFSNERFASLLTIKKKLA GHGGTCLQSLPLGLRLRREDRLSQGGQG/ C*GYSE*LCCRCIPAWAAEGDLWSWSPN SVAY
10258	24159	A	10334	388	2	IPGSPKRGPGEKKKTFHHYFLRAAPP LPRFIFFPKPNPLKGGGGFFPPPPKPL KTPRLRKKKKKENFCPWKKFFKKQTPQ RGRFFFFFFLQSFQFAVAGVQWCDLGS LQPSPP\G*SYHPARTRG
10259	24160	A	10335	3	396	LLRPPCSLRHNDIEIMPHDNPMIASKCS SKKSCISLTLSQLDVIKLSGKGMKLA KTGQNL/GLGHLYRTVRHAVNVKEKCLK EIKNAALLNTQMTRK*NSLIADTEKM*V V*IQE*AS/HSMPLRQNLIQNK
10260	24161	A	10336	165	442	GQMELLILARNFGILHLHFNLSIYRRLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FSIPRYLFIFTYLFIFTYFESVAHSD AQVECSGTIMALT*KKNASLP/ASAPRA AGATG
10261	24162	A	10337	33	430	TGSTHASANFCVSLVWVTQLISRSSGQGL ARLQLRCLPCCILFFSFFSLVIYRLHSY LRLPWRRICLQVPSGC*QNSFPCNFRIQ GSLLL*/MQQW
10262	24163	A	10338	284	3	SQHFGPRPRWVDHLRSGVDRDQPGQHGETL SRETP\SLKIQKLSGHGSACL*SQLFG RLRQENCLNPRGGGCSEWRQHQCPTV*V TEQDSVPKKK
10263	24164	A	10339	414	2	ERAGPFSRKIFFSPPLAKVKYFPFPPTP RARAHKRPIFSRYVKKERGNPDLFWFP FFPSLW*KQ*GPSLGRLFYFPV/SWGIFP SKP*GFPGPREKVFVFCFLG/LPPGPFGGP FFFFFFGDRVSLCHSRWSAVAQSOLTAR
10264	24165	A	10340	211	422	ASLGNGGRPSPSLAAALQFDL*LRAGIT FALFKAARQGDLSL*RLLLSF\VCLCPA PRGGAYRGRQAFLSWGGLHPDRASRLFC LPKQAWAMAGAPPPALLLPCSLISYCRA SNQODSGGIGPSEPSAGYKLLVPGFLLP AEK\RTIYGGVTRFFRGP
10265	24166	A	10341	116	432	SRQRMPSYHVQSGDRTKGEKPCANGN KCGSSILRSLHRKRFS*SLKALVWC GGACLEAQLRLRLRQEAHLSQGVPGCNE L*PGYCTPAWATEP\DSVSKK
10266	24167	A	10342	103	458	SLNVCVLTTLFSSCSPISLPLRGPPYSL RHRNIEIRPINNPTMASKSSKRKS*MS LTLNQKLE\MINLHEECMLKAKTG*NLG LLHQIVDQVNAKKKFLKKIKSAIPVNT QMRKQN
10267	24168	A	10343	53	408	SFQFFCSVFSPSLWFYLLLVFDDGDVQM GFWCGYPFCLLVFLLDTKTLSCRSVGVP CRVRCQCA\LLGGASQLG\SRGSGVRDP LEEAVCLLSDQLRAGRRTTLF*AVRQG HLSLQRL
10268	24169	A	10344	265	421	NNFPPSPPRGGGNPGPPPPRFFFFFLK NPGLPPF*VIYLL/YFTLTSPFCLWCYT ISVYCGGFVFFFSFFFFFEKKIFFFP RVEPKNRIPVYPKILFPG*NNFPPSPPR GGGNPGPPPPRFFFFFLKNPGL/HPF* KKGAKFPDLINPPWP
10269	24170	A	10345	207	420	WQKGCPTFMELGVVGPLYPCFLHLWIQ PTSHRKYIHL/WLGMVVHTCNPNTLGGQ GGWIN*GQEIETSLTD
10270	24171	A	10346	115	3	APRGAVKKR/RPWMGAATHVCKPSTLGG RGG*IT*GQEY
10271	24172	A	10347	41	421	FTFVSVCVHFKGIFLSFLSFFFETEVPG SPLGPKRGGGGNSGPWNPPPGLRGSP PPPPQRTGKGGPYPPPPGNFFFKFFRK RGV/PPL*HPGGPQSVT*GTPPPGPPKF WGAQSGGPVWGKNPLF
10272	24173	A	10348	228	1	SKQVKEKYDSFLHKIQKQAT*NRTFFRV TKKHVEITKK/WAGHWAHAYNASTLGGQ GGWITLQGEFETSLANMVKP
10273	24174	A	10349	405	1	GGFLKRGPPFFFLRQGLSLLPRLECSG MTVAHCSNILDSSNLSLRSDWDYSHQA QLIFLVSF*VLGSHSVAQAGVELLAS/P

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KCWDYRHEPL/WPSQSQNLNSFFLDGFS LLLSRLECNAAISAHCNLRLLGSS
10274	24175	A	10350	301	546	RHIFMNLDPFHNLVKTIIFHCRGKTLFLDI SNPYLKKQVSSSKPNCK/HLKEI*LFLE AKDYWLGVVPHAYNPSTLGGQGRSITG
10275	24176	A	10351	873	1258	FCYQCYFHLLHLLHHHRSPRLLEPPPG AALPPVPEGRIIPLPCSSGPRQTTPGPG KGRRHAPHRTPAASAASLPARRTLPAAPW*PLSFQNTTPGSA\PGGGNQPASGAG GNSRT
10276	24177	A	10352	184	576	GLSPLSHLKMAASSSEISEMKGVEESPK VPGEGPGHSEAETGPPQVLAVGPDQPEA PQPGPNTTAAAPVDSGPKAGLAPETTETP AG\PQKQPRPQTS*AOEGNQRPATAAPK THAQETVSKPEVSKEATAD
10277	24178	A	10353	110	384	VPGSPRKTRSPQQMERVLAPKTAKKGCP RPGDHRSLQNCRDTRARIKWADSVERP PWAG\PVAHACNPNTLGGRGWIT*GQK FKTSLVNM
10278	24179	A	10354	123	422	RKQIANDKSKLFIINKYLVNVELNSPIK /RERLAGWIRKEKHDPSCIHL*KTHLT\ KDTNSLKMEG*KKIYHANNY/QKKAGVA ILISDKIDFKFKKKVUREK
10279	24180	A	10355	36	426	PPEPQYSARVCVCVFYTECRGLAPKPE CRGAIIAHCLLNVLGSQ*SSNLRVWSS* DYTQLIFKLFVQTGSHCIAQAGFELL/S SKDPPTLA/FPKHWDYRH\DHHSW
10280	24181	A	10356	193	3	FQTRIFKISFFFFKEFLKFKKFFFIILI* ESRSIAQAGVQWRDLGSLQPPPP\GSSS PPASASLY
10281	24182	A	10357	205	377	SPVVFQPYRLTIPYQKC*LATVCI*VY *FFKLILYPAILLNSIIWINFTSDPL* FSSHITG*LSLIKNVWVGFGMLAHA*\N PSTLGG/RGGWIT*GQEFETSLANMVKP
10282	24183	A	10358	51	376	LCRPFQLCHGDRDMDWCPFPEELQDRCS CRSTSMRVAKGTTPCFLKVLQNIYTV* MFCRTFRKHGVVPLATRLV\IYKNSGPV TLQGRGTTYLSCHHGKAGRVCRATQHAA GVVVTKQRACI
10283	24184	A	10359	295	376	ASELTSSQSPGSLFENQKKGRCTAFLPC* KCNSEILVHCWWGCKM\WKIVW*FLKTL \RLELVYDPASPLLAIPRCI
10284	24185	A	10360	451	1	CQDIKTILRNEQEVLPISVTYKQVGVK SFVSRRLWSGCVLCYAFVTEASKTWHH FPYRSPGFWRSGRQFDS*PKSQADFR APQGPPTPPEPEGAERREPEIAPPPTADP SPKPT/HSPPRSGAPPSAPFPLGRAER GVG\PGQGRPRP
10285	24186	A	10361	2	776	FFFRLWSLALSPRLECSGAISAHCKLRL AGSRHSPASASRVAGTTGARYHARLI/L /YLFVETGFHHVSQDGLNLLTS*SACL GLPK\C\WIYRREPPRPAYFIFLRRSL ALSPRLECVQWCDLRSIQAVPPG\LHHS PASASLVAGTTGAHHHTRLVLIL\FYY FLRWSVTLSRLE\AGVQWHNLGSLQAP PPGFTPFSCLSLSSWDYRCPPCLANF LYF**RRGFTMLARMVIS*PRDPPPSA SQSAHDLFIVGQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10286	24187	A	10362	188	365	CPQLHTQSNLINMDASQRYQFELKIQAL/WAGTVAHACNPSTLGRSGWIT*GLEYSATSL
10287	24188	A	10363	146	1036	GWAVYQTLQAAWLGPRTESGVSFHGRFS LPHHPPQPTLHAWPAPPLQPEPCVPLRE DFMPESW*LPPSIPAEGVSF*ECDFSR RMMGKGSVPVTVAPPLGPAPEPFCVTAG CAPMHTPTHTQ\PPHCSIPLPKISFKSK HFY*LLFCKCLSSSVFSLPESILLFIV ESVCQPGERCLALNMGWDGKSGRRWAT KSQGVMDIAATQTPA/VFSPV/PATSCP AGVSGGK
10288	24189	A	10364	229	1	PLENAKSIYWGKGRLLKNNARLFTVA*S WNQPQFSLMVDWIKKK\MWRMYTTESCA AI*R/DEIVSCAGTWMELEAMY
10289	24190	A	10365	186	449	RFFFFFFPKFFWVFGKSPFFFFFFG/RLGI *EKDGGFFFFFFFFPEMASGSVA\RLC SGAVSAHCNLFPGSGSLPASAPRVA
10290	24191	A	10366	445	3	RVDNGVRGRYRGKRGRGR*TRWGWGHP QRWDQDRSRERPRETGRERAAGRRRETE AAETGRRRRERGRSDNRN/RGRPRERM IEAGRDAGRERR*ARQESWTEKKKTARQE EGDRD/RQGHQETRAHKGWGNND*GRQ AERSENRRMY
10291	24192	A	10367	1	491	NTAPFPPTSLESFAFVVAVQDRVS/LLSP GPECRGAI\LTHCC/LRTPG/FKPISHL S/LPS/SWDYRHVPPPLDNLILCRDNVS QSGKLLASSNPLTSAPFST/YDYRRET PGPRASP*TQMPCFMP/RS*SQP*TQI A/R*QSNWGSQ*VLNNRELAFGTMFFGQ RPKAFF
10292	24193	A	10368	572	40	LHSFRQHFSNTYPQCTPGTP*VTQSLAA RPAGLPEPTSASGGAGAVTPPPRTD\PP SVRWSGKKGLDPVLRGGAPRPSPANPAP APQGPAPRKGTECVPTASKTPRPGGRWE PAAPPHAHPGKDLQPPSTLVKECPEARC PRALTGDLPSSENGENRGLSAFQGGRRPA QKSGENCEN
10293	24194	A	10370	36	517	PFLFSDIDFLFSFYFLSFFFF*KRGLIL PP/GPEGQGNGK*WPLHPRG*REPPNL TPQTRGNKGNRQTGPVIFGILRKNGFPP FGQGGFKPPGLREPPGLALQRGNGNQ PYP/P/PKGFF*RTKRGEKSPQPPYNKP NKKFNPAPMEEFSSFKGRGPSLN
10294	24195	A	10371	60	403	DVEQPKLRSYPTLKCKPRSAILTICPWA LQYRSHGLIFGFSWGFLSFETESCSVSQ AGMQWCDHGSQT/PTDSTSQAQAIDPP ASAP\QAAGTTGACHHTCLIFVFL*RWG LAKP
10295	24196	A	10372	358	33	DSLGVPGAPLLSPGVTPHKQWFFRPTQ IKKLGFPPQIFFGFKV*KAPFFFWGFGN LKKKGKGGGGGGGGSEMASGSVA\RLCS GAISAHCNLFPGSSSLPTSAPRVA
10296	24197	A	10373	264	3	RQTSVSGSNDGKSWPPADIDTI\KYVIG NRLITTQQ*LIKLTSKQMITIHNTKGRT *SLILVSLIIFIATNLLGLLPHSFTPT THCI
10297	24198	A	10374	298	384	TLVI*KDGVHTTPHHQQHAYPGPKKEYML

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						HKAPLLHSVSRDPSPPFAQSSNCYNRSIK QEPVDPLTQAEPVPRDAGKMGKTPLEVSQNGGPS/HK*GQYSGDV
10298	24199	A	10375	84	518	IMKLRQKSRSSSLKIMRSKLQHTRAS/GTQLR/PMLGGNFIALN/AHIKKLGRQTQINLTSQLEKELEKQD/RNPKARGQEIT\K I*AEKLETET*KKEIQKIYEFVR/WFLE NINKP\PASRLIQRMIERNTIRNDKGNVTSAPPDV
10299	24200	A	10376	70	363	FHQKNLVPGLWVQLLGRRTLQSQHPPAP PPSSEPEVNPSEVQAD*LCCIFYDVK VRKCSTPQKKTRKRKKGCLF/CAPGQTR/CLC*KRGEKNLVGKT
10300	24201	A	10377	299	2	YPVAGRGNR*GCGAHLGVGGAAMPLGATISSVSLTISSLCAPRRGGLEPSLPAPHTPPPPPE/P*ASSPSRGEWHLVPPCMQ PGLPPLPPRLSPLV
10301	24202	A	10378	302	3	WPTVATTCSCKERSHSTLT*NQKLEGTQLSEEGMSKAEIGQKPGLCCHQT/VQVVNAKKLLKEIKNATPVNTQITRK\QNSLIADT\EKV*VIQIEDQTSHV
10302	24203	A	10379	125	375	NEYVFLEKSLKLAGRVGSCLLGRPRQVDHLSSGAQD*PGQRKTPSLQNIQKLSRHGGMCP/RLRWEDHLS/SRGG*GCSETRST
10303	24204	A	10380	458	3	ITISTISCKATSFERAPRASRPDPDEWVSQAGPAPLRGWEN*GTRRRDDWPEASLKDPRRSGEPEAPL/PLRLML*SRLPPPLRWRRPPPPDSHTPSPGNGKSPRVPTGSKDKRPEALPP*FAAGEPLEANVPVQHG GGSVRSRGSYLTAT
10304	24205	A	10381	327	2	LSAPKKFFQKSLFLGANFRSPFPGRPFTNRFSDLVNPLTKKIYFSHKSSNPPT FFFFFFFETGSNSVT*SGVEWRNHNSLRPESPG\SGDRP*V*HTTGAPYHTWL
10305	24206	A	10382	754	1	NTALETDTTFSGGGGGHQLCVRSRVSGG G*LIMPDLDHNHPLQQTSGRNQRLQGEVTDPSPGMSGGAQTGPKAPPRPPSALRHGSLQGGP*FAHLYCGTIPYPCYTAPLPR APPPTPTGH*CPGEA\PDDELPCVGCSP WPRPPGQAQAGRKH*FSGQRSSRDTTA CSPCSQSKQSPSRPPCVNDS/PGQGP GP KAPAGPPPALPEASLGSVHCSP*VGVMTPTRPGHFLVPGKVTLEQAPGGGASGGVP P
10306	24207	A	10383	39	433	SHDQTYTEELLFMDEQRKWFLLMESTP GEDAVNVVEITTKNLEYCINLVDSTVA/GVSNFERRSTVGQMLSNSIVCYGKIF/R *KR/SQSMWQTSLLF\NKLSQPP*PSTP TILISQQPSMWRQDPPSEERL
10307	24208	A	10384	283	1	NVFSCKPTSSCLISPDSPTPDRRFKADTYRNFMFPLRRHMTHTYMHTHVHVC TQLCLHLRPH/ITHGLSL/TCAPPVL*R PSFKPLHPTPV
10308	24209	A	10385	12	471	SPPWWTHGFRYWEPTPPRFSPVPHDALGQ FHTALFRLTRRFQLLSSCINISHTCLP PCLGLCVGGPLEPAVCWAR/CP*RGMV SGWKASPLG/CPPTLLPPC

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10309	24210	A	10386	287	1	SFCVRSRPAPTSGRTFFPAAPPFFPAAPP FPAATTPSTAEDGVPG*/G/PAPAANCSP HSSQRGSAAMGIPLPQAS/PPAPTAPP SP*SLPFFPPAPMY
10310	24211	A	10387	336	3	LIEGKLTNRKDIRSKTASVRHHQSPKV DKPTKMGRNQRKAENS\KIKSASSPPK ECSSSPATEESWMENDELREEGFR*LVI TNFSELKEKTGKLNPAALVCGRSEDQTT
10311	24212	A	10388	15	470	APSPDAMGR\FTEEDKATITSLRCKVNV EDAGGETLVRLQVVYPW*QRYFDSFGNL SSASAIMGNPKVKVHGKKELTSLVDAIK HLDDLKGTFAQLSELHCDKLHVDPENFK LLVNVLVTVLAIHFGKEFTPEVQAYLHK MVTVVANSLRYK
10312	24213	A	10389	3	438	QTQREPTMVLSPADKTNVKAAGKVGGAH AGEYGAEALERMFLAFPTTKTYFPFHD SHGSAQVKGHGKKVADALNNVAHVDDM PNTLSDLNDLHAHKLLVDPVNFKLLNHC LLETLDGHLSAEFTP\AVNASLEQFTAF EITWLT
10313	24214	A	10390	2	444	TMSFNTLAICLDCLCSTLQPTRSIPGY SSPLPGNPTPPMTSSSVPMSPNQEVK SPFLPDLKPNLNSLHSSPSGSGPCDEL LTFPVRDGVV/SGALPPAAQPGC
10314	24215	A	10391	405	3	KMILTCLALPAQHCPPSACPQTMQAPPL PLSIKGAASMSDKLPYKVADIGLATWGH KALDIVEN/EMPGLMGQELYSASRPLK GACIADCLQITVETAILIETLFSLGVOE QWSSCSIESTQEHAVAVFAEAGMP
10315	24216	A	10392	248	5	RINKVGGHGGNYEHLYVNKLETLQEMYK FLDIYNLPNLSLEEIE\NLNRPITSNKF ESVIKHFPPTKKISGLDGFTEAFLTN
10316	24217	A	10393	262	3	LPRDRQAGRSQGPVVPQAVGRARKMPF ISYQVYSKNFFEIEESCVTQAGVQWRNI SSMHPPPP\GSSDSPASASQAPGIPGAH HHA
10317	24218	A	10394	287	410	ALKGSSRILIMLGAWLTFVIPA/LWEAK AGRSSEVRS
10318	24219	A	10395	175	1	GGREVDDEIPLVRESTIFHIFFFFFETE SHSVAQAGGQWRDLGSLPSS\PPG\SCH SPA
10319	24220	A	10396	661	963	STLIAFIVISTLFLPLDMTEIYFSLDDE IVDTLGEAGFGKVVECIDHKAGGRHVAV KIVKNVDRYCEARSEIQVLEHLNNTDP NSTFRVCVQ\MLEWFEHH
10320	24221	A	10397	1	268	PQTHREATMGLSTADWTNVKAGWGKGA HAGEDGAEALERMFLSPTTKTYFPFHD LSHGSAQDKGHGKKVADALTN\AVAHVD DMRNAL
10321	24222	A	10398	33	302	SRGATLIYVDNENGEPTRVVAKDGLKL ESGPSIKALDGRSQVSTPRFGQTFDAPP ALPKATRKASGTVNRATEESV\KTRGHL VQHEP
10322	24223	A	10399	16	233	PTDYEFNTTTYRECGRRRPEFSTSLDLL SQPCRAVYM\VGKENDIPFELRIVDLIT GKSILGFGEPSQEGDR
10323	24224	A	10400	177	1	KLLDLGQPQSPALAACLEYSGAIAAM\C NLCLLGSSNPPTSASRIARITGVHHAEP



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						YA
10324	24225	A	10401	185	419	HVNKDTLESHLVWKLKSAALLGRKSESVT GPSCHPEPSDKTVEL/WQGAHAHACHLS TLGGQGGWITLAQEFETSLDNIV
10325	24226	A	10402	104	3	GIILIPKPGRDITTKEN/RPLIPIDAK ILNKILAN
10326	24227	A	10403	3	344	SQVMAVAGPAPGAGARPRDLQFLQRF QILKVLFPSSWSSQNALMFLTLLC/LTLL EQFGNYQVGLIPNQYVGLGNKDLEGFK TLTFLAVMLIVLNSTVRSFPLSVSLVLS SPV
10327	24228	A	10404	3	404	ARAQRRGDLSATGRNWSPLPPAGLPATV VLRHSGSLMAATCEISNIFSNYFSAMYR S\EDYTLASVPPAATFGADDLVLTLSNP QTSLEGTEKANWVG\EQSQFWPKTQGLD WISFQAEKNKYEASAIGPRWDK
10328	24229	A	10405	254	443	NQLSSIMVMFKKIRSFEEFNDPEKVYV SGDKVAG\RLIVEVCEDTRVKAVRILAC GVAKELRM
10329	24230	A	10406	26	461	GEVARRSCCGAMAGTALKRLMAEYKQLT LNPPEGIVAGPMNEENFFWEALIMGPE DTCFEFGVFPAILSFPLDYPLSPPKMRF TCEMFHPNIYPDGRVCISILHAPGD/DP HGLREQ\PERWSPVQSVKILLSVVSML AEPNDES
10330	24231	A	10407	1	463	QQAAKMAENSGRAGKSSG/T/PARGRGR C/PAEQVIAGFNRLRQEQRLASKAAEL EMELNEHSLVIDTLKEVDETRKCYRMVG GVLVERTVKEVLPALENNKEQIQKIET LTQQLQAKKELNEFREKHNIRLMGEDE KPAAKENSEGAGAKASSP
10331	24232	A	10408	180	446	KKAAASVSAASGSHLSNSFAEPSRSNGS MVRHSSSPYVRYPSPDKPFLNSDLRRSPS KPTLGYPESNSRAIFSA/KNLQD/KIR RLNL
10332	24233	A	10409	1	417	EAGLVTMEEIGILGEKAQDEIPALSVSR POTGLSFLGPEPEDLEDLYSRF/KKLQQ ELEFLEVQEEYIKDEQKNLKKEFLHAQE EVKRIQSIPLVIGQFLEAVDQNTAIVGS TTGSNYVYRILSTIDRELLKPNASVALY
10333	24234	A	10410	305	53	LEAQPHAPPLLGHHLPCWRIPSHLGT RPRAMRVQGESEEGVA/GQAPPLPWVHR GSLPLVRRRPAGKPTGGNAREEKGV VEG
10334	24235	A	10411	419	2	NNSRKFGNGTLKLVEVETIPLISEIPD KSELLLPQDKKHAPLPSAVPNPSA/CP DLRPHTTPASPV\PAKTVETRPAPQG PLPGPVRRPRGRFSVRAASPQTSGRPGA PRPPGPALREATDAPRAATPPIAALAGH S
10335	24236	A	10412	74	322	MDEMA'TTQISKDELDELIEFAKVDLSS NGFICDYELHELFMENMPLPGYKARET IQKLMLDGRNTDGKIS\YDEFAYVSM
10336	24237	A	10415	1	415	PQTHREPTMVVASADKTNVMAAWGKVG HAGEYGAEALERMFLTPFTTKTYFPHLD LSHGSAQVKGHGKMVADALTNAVAHVDD MPNALLYALSDLNAHKLWLD/VNFMLLS HCLLVTLVAHLDPDEFPAVHACLDKLL
10337	24238	A	10416	19	454	APSPNAMGHCTEEDKATITSLWGMVNV

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						DAGRETLGRLLVVYPWTQRFFDSFGN\LSSDSAIMGPNPKVKAHGKKVLTSLGYAIMHLDDLGKTFQAQLSELLCDKLHVDPENFKLLGNVLVTVLAIHFGIEFTPEVQASWPKKMANVA
10338	24239	A	10417	2	395	ALSSSQPSAPMHPFYTRAATMIGEIAAAVSFISKFLRTKGLTSEKQLQTFSSQLQE LLAHYKHHWFPEKPKCKSGYSMIGVNP\KMISLILQACIEGGI
10339	24240	A	10418	2	374	LSTPHAFGTGKWTFTISLLFLFSSAYSRGVFRDRAHKSEAHRKIDLGEEDFTALV VIAFAQHLQQWPFEDH\VLANDVTEFA TTCAADESSENCDSLHTLFGDLLCSRA TLDESHCVQDGRP
10340	24241	A	10419	48	347	DPKAQLPEPLRVLWQLTYAMAAGSR/TS LL/LAFALLCLPCFKAGPPNRPLSRLFD HAMLQAHRRTTAIDTYQEFENLYPKD/Q QYS/FLMTPTSSALDSIPTPS
10341	24242	A	10420	166	1	NFLKKPGPFQKFFQRLPLILITFFFFF\FETKPHSVSL\LECGGTVAHCNCLLPV
10342	24243	A	10421	2	251	LGCTQHRSQELVAAATSHQTCIQASEDV KBI/FARARNGKYRPLKISIEHQMLMIG SY/SSQPSDSDWDNDYDSFVLPLEDKQL CY
10343	24244	A	10422	251	1271	KEDLSRAPMSGTQSTITDRFPLKKPIR HGSILNRESPTDKKQKVERIASHDFTPT DSSSKKTKSSSEESRSEIYGLV\QRCVI IQDDNGFGLTVSGDNP\VFVQSVKEDG AAMRA\GVQTGDRIIKVNGTLVTHSNHL EVVKLIKSGSYVALTVQGRPPGSPQIPL ADSEVEPSVIGHMSPIMTSPHSPGASGN MERITSPVLMGEENNVVHNQKVEILRKM LQKEQERLQLLQEDYNRTPAQRLLKEIQ EAKKHIPQLQEQLSKATGSAQDGAVVTP SRPLGDTLTVSEAE'PDGDLGRDTCSS GDASRPSSDNADSPKSGPKERIYLEENP EEQKKG
10344	24245	A	10423	198	569	QRNMVGQRLVEPRRLKPGFINVKSNGD WEWHQGFLLVCFLLRWSLALSRLPCS GAISTHCNLCPLPGFKQFSCLSLPSSWDY RHAHCTQLIFVFLVEMG\FHHVGQAGQ GFFSLEKSLTII
10345	24246	A	10424	2	343	PQTQREPTMVLSPADGTNVYAAWGVGA HAGEYGAEALERMFLSFPTTKTYFPHFD LSHGSAQVKGHGKVS\DALTNVAHVD DMPNALSALSDLHAHKLVDVFNFKLLS HC
10346	24247	A	10425	31	342	RAAVMPREDRATWKSNYFLKIIQLDDY PKCFIVGADNEGSKQMQRMSLRGKAV VLMGKNTMMRKAI\RGHLENNPALEKLL PHIRGNVGFETIKEDLTEIR
10347	24248	A	10426	196	2	KNLTIISQTKKVICPNTFLVFPKRVFFF FFFETESRS/VSPRLECSA\SISAHYN LCLPGLSDSS
10348	24249	A	10427	1	405	RLECWLPPHAGLQGLGWVWVSCSVSTG PTMQALV\LLLCIGALLGHMSCQNPASP PEEGYDPDSTRALEDDEDPIDPENK LPEAGSNFGYDLYRLRAIMSPTSNVLLP

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						PLMVATDLWDLSEAAQQLTESII
10349	24250	A	10428	223	361	EGPTEENMAAKVPES/ICKFGLALAVAG/GPVNSALYNVDVGHRAVIFE
10350	24251	A	10430	3	359	LTQREPTMALSPGDMTNVKAANGKVCAGAGDYGAELERMFLYFPTT\KTYFPFHDLSHGFAQVKGHGKKVVDALTNAVAHVDDMPNALAALSDLHAHKLRVDPVNFKLSSHCLLVTLA
10351	24252	A	10431	273	1	NHKDGGKKQSGKTEKSKNQASPPPKERSSSPATEQSWTENDFDEFREEGFI\RQSNYSELKEEIRTHGKEVKNLKLLDDRITNAQK
10352	24253	A	10432	211	3	SFLWKFCLRGIPSHVSCQSA/LLGGASQLGYSGVRDPLEEAVCLFSDLKLHAGRTTTLFNAVRQCHLSLQ
10353	24254	A	10433	281	2	TNQEKKKGDENKIRSGKDDTTDNTVTIIRDYYG/HTYTNKLKN/LEEVDKFLDTY YLPRFNQREIENMNQPTISNEIESVIKSLQTKKSPGPMAS
10354	24255	A	10434	219	1	SFLWKLRLRGAPGCMRCQSA/LLGGVSHLGYSGVRDPLEEAVCPYSDNLNCAERTTTLFKAVREGCLSLQKF
10355	24256	A	10435	133	2	FPKPPGNFFFFETESHPVT\RLECSGAISAHCNHLPGSSDSPA
10356	24257	A	10436	248	376	KGGVFFFFFFETESCSITQTGAQWHT\YGSLLQPRPP
10357	24258	A	10437	250	1	KGTRKELTFIEQLLSAKYWAAGCMHYFRGSGKYSNGYPVFVFVIFSETESCS\VAQAGQWCDLVSLQPPPP\GSSDSPGASF
10358	24259	A	10438	354	2	KRGLKKNPFFNPRNMGEFLKLWGPNNPKKIFKNCKIFKMGLKKKVLGFYKNSKNLKRKGLNPFVIFFFFFFFFFFLETGSYSIA\RLKCSNSGTNTAHCSPELPGSRDLFDS TTQVAG
10359	24260	A	10439	126	1	GMVDCVCLFCFAIKEGREEREKERERKERERERQREKER/ERERDKERKREERK
10360	24261	A	10440	29	347	IQKPTADTKKFFKKLKYTTRENHLHNKEDRKEGKKEEKTQKHSSKSLINKTLNINGLKSPIKTHRAE/WNKNKDPMLYCIQETPFTYKDTLRL/RIQGWKKIFH
10361	24262	A	10442	405	1	IFFPHPPFFKKSFRLSPOVEIQGIFLGPWKLFPPGFNNFS/CPNLNNLGFKGLPPRPSYFFRIFCKKKGF/H/RVYPEGFPFLALGFFPLFPFKSWGFGDPPSWGPFPPFFFFVLVAEGLTSEGCRILIRGRWKNLVP
10362	24263	A	10443	122	372	LYNDPISYQVTLYRRVFWVLYSANWSLRWKNLFFSFFKMASDPVAQAGVQWCDLDSLQPP\GL\SDTPTLASQVSETTG
10363	24264	A	10444	171	3	RHPTMAGSSEMFLGSGFGCRITVFLFETESCSVT/RECSGAISAHCYLSLPGSSNLP
10364	24265	A	10445	173	3	CMNVVCFISIFILKINFILETESHSVSQAGVQW\LITVHCSSLKMGSSDPSSASQV
10365	24266	A	10446	187	329	SFLWKFCLRGVPGHVRCQSA/LLGVASQLGYSRVNPLEEAVCPFSDL
10366	24267	A	10447	27	226	YSYPVYLLHLIFLCWKCSLYFIYFVFEM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ESCSFAQAGMKWCDLQPLPPG\SSDSLAPASQVAGVDAA
10367	24268	A	10448	119	296	SPIHYILVITICFIHVILLIIIFSEVGS HSVAPAGV\SGAIIAHCHNKLGLGSSSP VSVS
10368	24269	A	10449	111	363	SLKKLVFFFSIYTHNFFPFDPTLKNST RHSLYLSLSLSLFLSHSV\SRLECGGTI IAHCSLNLPGSSDPHTMSQV\AGPTGS C
10369	24270	A	10450	218	1	QRFWGPDPNKVFNKLGSAFFLGRGKLF LEIWGGFFFFFLVFFLRQSHSIAQAGVQ WCD\LNSLQPLPPRFK
10370	24271	A	10451	179	3	GPFKLTFFFMGKFALGREKCHFFFE SCTVAPAGLQWRDLGSLQPPPP\GSSDS PAS
10371	24272	A	10452	71	232	SSPLSDLLFNIVLEVLAKDIMQVE/IK LILIGKDEVKWSLIVDKIILYVKNKSH
10372	24273	A	10453	153	3	ARGELYFLEIGGGFFFFFLVFFLRQSHS IAQAGVQWCD\LNSLQPLPPRFK
10373	24274	A	10454	338	221	MGFLHVGQASLKLTSICP\LGLPKCWD YRHEPPRPVIPS
10374	24275	A	10455	214	366	YNYKYLIHYYSYLFIFIF/NIIHYIF FILFFYLTSPIFLSYFFFFITLF
10375	24276	A	10456	155	2	DRVSLLLPRLECNAILAHCNLCLLGSR HS/PRVAGITVAHHHARLIFCIF
10376	24277	A	10457	870	1249	EGPRWADHLRPGVDHLQHQGETPSL QKIQKLARRGGTC/LCQSLLGRLSQEN CLNLGDGGCSEPRLHHCIPWTGDE\GDS PKKKKE
10377	24278	A	10458	222	404	KQRPGRQWLTPVIPKLWEAELGR\MLE ARTLRPAWAT
10378	24279	A	10459	122	362	LSEDQLNCYPQRLHHFIFLPVITRVQMS HYLCQQSCLFHFF/SFFFLYFEMESSV T\RLCTGMISAHSNLYLPGSSQSSG
10379	24280	A	10460	3	102	AASTLALSPRLECNAILAHCKLH/LPA FTPFSC
10380	24281	A	10461	133	339	KLKFKQGSKKPEIKANSDLALFYHNYI TRQCFTSYSNFFGDRVSLSPRLECNV ILAHCNL/RTPGFK
10381	24282	A	10462	3	193	ASNMMTELKSQIPILTNVGNLAPLKR HRVAGWINDPTICYLQETYFT/CKNNHR LTAK
10382	24283	A	10463	126	314	RLGGSTIKVQDLSSDRSKPGRFLYTSN SSYVRKGKRNKACFTERV/PVNDII
10383	24284	A	10464	1	332	KKNLFLSKDCLSSLFREFSKSPAILGPP RGWTPKTRFIGPKAFFFKGSLGRKY HFGLKPVP/CPPFLSKTRFLPGVPPFFF FFFETESHVA\RLCSG/AISAHCKLR L
10384	24285	A	10465	173	365	RFVCSTIKVLRDLSSDRSNPGRFLSLQI PP\LRKDKRNKAYFTK/RSPVNDIIST
10385	24286	A	10466	335	3	PFKKFYFKISTRALLEPVFFGKKIRVPP QRLSPIWAPLFKRGPPNSFQVNGVPLFF FFFFVRHGLALSSGVECSGTRLECSGAI /STAHCHLCHLDASHPPTSASWVARPTG T
10386	24287	A	10467	818	1008	VHTDVLADILKSINNAEKQT/RRCFLS \WLQGHCPFLTVMQHGCLGVELGGLPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PGDFCKRPR
10387	24288	A	10468	111	1	MVSFGRPRQADHKV\GVRDQPGQHGETP SLLKNIRI
10388	24289	A	10469	204	1	LWGPILKIFCQILKTICEGNFRGPTFFI FFEMESQSVTQARMQWCDLSSQLPLPP GS\SNSRASAS
10389	24290	A	10470	190	330	ERIKKQDLSICCLQVTHFTFKDSQRLKV KGWKK\IFHTNKNQKRIWT
10390	24291	A	10471	162	2	IKGPKRAPPAKNGRAFFFFFFFFETESC SCLQAAVQWHDLSPPQPTP\GSSDS
10391	24292	A	10472	120	3	SWGFFFFFF\EVESYSVAQVGVQWCDLG SLQAPHVMILVK
10392	24293	A	10473	298	1	RRALPCPANFLYFYFLSLLFFETEFHS \VAQAGVRWHELGLSLQTPPPG\SSDSPA SCEYSANYTGEYSANYTGEYSANYTGEY SVNYTGEYSVNYTGEY
10393	24294	A	10474	1	380	AVTGRAGSMVAPR\PLRLVLIFYQGLR SMAGNFWQSSHYLQRIIDKHDLLNERQK DLKVLSEEEYWKLRFFTKVIQALCEHL KLRQPGIATATAYFKRFYARHSLKSIDP VLMAPTVCCLASTAN
10394	24295	A	10475	289	2	TQGFPPINNSFYALYPKQKIPFFSDKLF RVKGFGKGPVFHYGVKDFKNKDGVFVFF FEMASGSVAQAGVQWRNLGSLQPPI\PG SSSLTTSAPRVAS
10395	24296	A	10476	138	402	ITGRAPPKPFPLKRGYLSGGLTNIGFSF SFSFFETESRSVTQAGVQWRNLGSRSWL EST/SPDSSNS/PAPASRVAAIT
10396	24297	A	10477	2	336	ARETNDTTQTRLLPANNTMRSDPYISI LTLNVNGLNTPIKR\KRVASWINKQGLM GCCLQETHLSSHETHNDTHKLKIKTWRK IYQANGKQKKARVV/ILISDKTDFKP
10397	24298	A	10478	51	250	RKVSFLFKKWCNTLTFICK\LSLDTYRF AKINFEWITDLNVREKT/IKLLKGNIKE NICDLGLGKDEF
10398	24299	A	10479	216	2	GFTRKALSGFKTGWFVFPNFSKLFFK KNFSERFFFFFFFEMESHVTR\RLCSG PISAHCNLHLPGSSLV
10399	24300	A	10480	191	3	FSTDGNVNCLVKYSIYIYIYFFFLIFF FEMKSCS/VSPRLECNGLSAHCKLCLP GSCHSPARA
10400	24301	A	10481	135	768	LGGQVLSCASQPVSLFPLFFFLISFLGC LLAFLSACFASTFSCVLGSPETSFSFCL HPPPKVLSSH\PPCSR/CPQPPKG/P PLPKHACPP
10401	24302	A	10482	126	333	MVVGQRYCVMCFVI\VLCLFLLV/VVWV FLW/CSVYIVWYGYAVLVIFFFFFFFF LLCFVCLFVWLLDRF
10402	24303	A	10483	240	2	ATEKNMGLGTSVRGLSGSNPSYGRVRER IGGGVCLWSQILLRG\LRWEDHLGLGG GGCSEPRSSHCTPTWVTEQDPVLV
10403	24304	A	10484	136	2	NRPSYIFSFETESHSAQAGVLWHDL SSLQPLPP\GSSDSPARA
10404	24305	A	10485	161	328	EKNFKPYGSCRHFLFYFETESRSVA\ RLECSGTISAHCNLRPLGSSN/SPAS
10405	24306	A	10486	193	347	ILFSFLLFIYFFETESCSVAQAGVQWHD HGSLRSRAPG\SYNAPALDSQGT
10406	24307	A	10487	114	2	GAVVQSEVQWRDSGSLQAPP\SRHSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASASQVAGLV
10407	24308	A	10488	314	49	IRRSTERSEPRYSMVCRQRQGGPCL\RSQLLGLRLRQEDHLSPTAGDCSEPRH\ LACTPAWATEQEPVLKKMSPTLFCFLW PLPCQ
10408	24309	A	10489	291	1	KSPPPPNRRGLTLRSRGQIGNGVSFYYE APVTDFI FFFQSLVLSAQAGLQWCNLSS LQLPPPG\SSDSPASASRVAPVSQGHAT APQPGRQTLSSC
10409	24310	A	10490	226	3	GSRCTMPRRRLAHAFPAARMKPKRVSS T EWATEEPPKRRSARLSAEPAPAKVETK/ PEKAAGKDKSSDKKVQTKLV
10410	24311	A	10491	2	153	ARGLVFFVYLVENTLCHVAQA AVKPLTS SEPP\LG LPKCWDYRREPPRPT
10411	24312	A	10492	123	342	THYLCLLRFFFLDRGFLLLRLDC/NAP ISPNNLRLRPASSDSPASASRVGTITVV NHYARLTLLFIFQNETLF
10412	24313	A	10493	194	2	IPGWPFKNFSLFPLFFFFFEMESCVAH AGV/GSSDFPASASQVAGTTSMRINAWL IFVFFSRN
10413	24314	A	10494	373	1156	KVQLKVYLFFFLRLSLALLPRLECSGTI LAHCNLPSPRFEQFSCSLPSSWNYRRP PPHHARLIFVL/SVETGFHHVQGAGLEL LTSGDPPASA/FPKCWDYRHE
10414	24315	A	10495	181	3	SFLWKFSLRGVPGVRVQCSA\LLGGASQ LGYSGLRDPLQEAVCPFSDLKLCAGRTT TLFK
10415	24316	A	10496	156	2	AASTTRLGDRDQPGQHSETPSLLKIQKL G\SGGGHLRLRQENCLNP\GGRGC
10416	24317	A	10497	157	300	IQSWFNILKSIHVTHHSNRLK/EVNHIV STDAEKAADKIQHPFLIKKQ
10417	24318	A	10498	3	289	LVKKMLTGSTLGKSYRHSFSSINQGHNA LRKAAG\PLPRKAGY\LQGFSPRYGL\ WDGKDLTIHQPDTRGSLVLSRISKGRP L/CSCPLGTECLSI
10418	24319	A	10499	138	1	WYGLIYLLLEMESCYVAQAGVQWHDLP S LQPPPP\NSSNSPASSC
10419	24320	A	10500	138	1	WEGLIYLLLEMESCSVAQAGVQWHDLGS LQPPPP\NSSNSPASSC
10420	24321	A	10501	200	343	LEAHSFLSFFIFIIIFDTSKHSVT\RL ECSAAISAHCSLLLPSSNS
10421	24322	A	10502	84	339	PRDGKRRDKQKQETGGEHYKSQLRGRIR QEDHVSPPGGRGCSEPRSRHCTPAWAT\E SNSVSKKS
10422	24323	A	10503	141	362	EWNCCVCC/CCCCCRCF
10423	24324	A	10504	198	320	TIKKQKNTGGLIFNSYILPPLFLEPGDL \RFLDVDNRVKLPV
10424	24325	A	10505	30	356	GYPNCNPILYMSTVGFTTSLLD FDIPL E HPILKVCPTHTRALRDLSSDRSNPGRIL STSNSSLY/EKDP RNKAYFTK/RPSVNDIIST
10425	24326	A	10506	16	375	KKFFKKKKKKI FFFPPFLKNFFFPKRVN FFGRGWPKSPPKKVFFKKFPGGFKKP PLKKKKIFFSPPVKMGPPKGFKKGPPP FFFFFFFFFFFFFFFFFFL/LCLIPR
10426	24327	A	10507	156	2	AASTTRLGDRDQPGQHSETPSLLKIQKL G\SGGGPLRLRQENRNLNP\GGRGC
10427	24328	A	10508	313	2	QSKWLLEESTLGEDAVNIVEMTKDLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YYRNLVDKAAAGFERIDSNFESSSTVAK ILSNCIVC/Y/REILHEGKSRPMWQTSL SYFKELPQTTQHSATITLTPRA
10428	24329	A	10509	325	1	ECAKEMNAETKRNIADATETQRIIRD YEHYNKMELEAMDKFLDTHNLPRLNHE ELENLNEPIMSNETETV/I/NSLPSKKN SGSEGFTAEFYQRYKTPILILKLFKK
10429	24330	A	10510	126	14	DSSGQVQWLKPIIPV/LWEPEAGRSPEV RSSRPACPTW
10430	24331	A	10511	435	769	PFKFPPLSHACDGGSLFCRLRLCESGVI T/AHCKPQLPG/SQSDFFASTSQELGP/ TGACHYTRLICCREEV\HVAQAGLELL CPKDPPTASQHARDYRH\GHPAQL
10431	24332	A	10512	147	412	RFVCSSTIKVLRDLSSDRSNPGRFLSTN SSLY/EKDKRNKAYFTK/RPSPVNE
10432	24333	A	10513	251	466	QTCPTGSPASLLELFNSIATQWELVRSL IAGNALKDEND\SAVKMLASLIMSYKAA AAEDYKADCPPRNPGP
10433	24334	A	10514	286	1	SFLRKFCLEGRVPSRVKQCSA\LLGGASQ LGYSQVRYPLEEAVCPFSHLHLHAGRTT TLFKAVRQEHLSLQRIILLPLVGRVGRPN DSRCDRVIGH
10434	24335	A	10515	28	428	RFVCSSTIKVLRDLSSDRSNPGRFLSTN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10435	24336	A	10516	263	2	IKKPADSESAGALILDFFASQTVRNSPL LLTSHSVCYFCYSSPNGLRQQLKIIFF FFLRQSCSV\SRLECSGMILAHCNLCLP GSNN
10436	24337	A	10517	62	292	PATLFSGVILPPTNSINAFSGSDSKSAH K/CEMLGTENFNFFTCHTHIAEHSNST HTHTHTHTQTHHTHTPLLFYE
10437	24338	A	10518	172	2	RGKKIFFPLEKGKNLVWWTALFFFFFE TDSHSV\TRLKCSGTILYHCSLCLPGSS DF
10438	24339	A	10519	42	194	ILVETF\CLRFVSLLENLVKMRFLKLKKK KKKKKKKKKKKKKKKKKKKKKK
10439	24340	A	10520	120	1	IFAKRWPIKFFPFFFFETVFHS\VAQ AGVQWCDLGSP
10440	24341	A	10521	202	375	SFLWKLHLSGVPGHVRCQSALTGG\ASQ LSYSGVTDITLEEAVCPFSDLKLRAGRTT TL
10441	24342	A	10522	272	402	PKIFYVTKAWNYYPYTITEYTCSF/IR KFFIHIEKYEDNKGSN
10442	24343	A	10523	147	439	LILYVNYISRKSTVYDSRHPCTYYLIPE KNCYKYHCNFLT/SSIPFPTSTPSR ASPKKKKKKKKKKKKKKKKKKARGG
10443	24344	A	10524	7	415	RFVCSSTIKVLRDLSSDRSNPGRFLSTN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10444	24345	A	10525	321	442	TSFSFLFF/LETEFHSA\RLCEGRGTI LVHCNCLCPGSSNS
10445	24346	A	10526	477	3	IEGKLPNRKDIHTKNPSVCRHHQRPKVD KTTKMGKKQSRKTGNSKNQSASPPPKER SSSPAMEQSWTEKDFDKLREEGFRGSIY SKL/REEIRTINGKEVKNFEKELDEWITR ITNAKKSLLKDLMEKAEAEQELRDECTSR AASANCVAVPQAFDRSHGVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10446	24347	A	10527	265	411	RFVCSTIKVLRDLSSDRSNPGRCLSTSN S/SPVRKDKRNKAYFTK/RPSPRN
10447	24348	A	10528	81	390	RFVCSTIKVLRDLSSDRSNPGRVLTSTN SSLY/EKDKRNKAYFTK/RPSPVNDII
10448	24349	A	10529	253	23	RIFLFYFHSFLRQGLARAEGQPHNHSSL QPPPPG\SGDPPASASRAARTTSAYHHI PLFFFRSYCVAQAKIINMLSL
10449	24350	A	10530	10	398	RFVCSTIKVLRDLSSNRNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSP
10450	24351	A	10531	289	423	RFVCSTSKVLRDLSSDRSPGRFLSTSN SSL/QRKDKRNKAYFTER
10451	24352	A	10532	152	401	PHCSIHSQVRIQANVHKHGRQRTYGSVI PHILPLHLVKKTFSLRDFHFSVSLKKNL VLTCLHLFL/GVTRPRNDFVSMMLLFT
10452	24353	A	10533	2	515	LDRISLLLPRLKCSGPVSAHRNLYLP/G FKRFCSLGLPSSWDYRRASPRVAKFVFL VDTGFHHVQGAGLKLLTSSDPPSLTY/P QCWDYRREPHLAAF
10453	24354	A	10534	469	566	PTKNTKISRWWCVPV/IWEAEARESLE PGKQRL
10454	24355	A	10535	354	47	KPKNLPGGGGPPFYSSFSKGGKIPLPWK AKVPINQILPLPPHPGGGKTPFPKKKK KKERKKKMATVQKGM/PHKYHKGKTGS YNVIQHAVGNAVNTNRTRGS
10455	24356	A	10536	1	409	TPKKRFFPKPKPGFFFFPPPKKKKKIFSP PEKFWPPQKNFKKAPPPFFFFFFF FFFFLKSNPPFFFF/SKNPILKPLPLPL FRVFPKKKKKKKDP
10456	24357	A	10537	204	435	TSGSLYKLLGMGDLGLGKTTIFKQGGHQ NSS\GWHPEATTG/VNWAFFKGLHWDPKA LAHLQLWNIAL/QER/FGKMTKACY
10457	24358	A	10538	208	382	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSLFER/DQRNKAFFPK/RPSPVNDIIS T
10458	24359	A	10539	63	409	GWRLTNFPVGKTPSTSGTGLLFIFLLLN LMGRLLKPSISMKREFRKQNRGQKC/EF MKKKKKKKKKKKKKKKKKKKIGGAF LKIFRGGPNFPGGEKIFFFLGGGIKSR GGGFG
10459	24360	A	10540	3	1322	RGYAWPNGALPASTVPCGFAACPGFELC SVNGRQAPAGSSGFLPPVPSLCPHTVCR ATFQCKEDSTCISLRFPWGSETHLLCP APIPSVPGVPCGTFTFQCEDRSCVKTLS ASPLPLLLCPPHLLPPSPDCGLQGPSSR IVGGAVSSEGEWPWQASLQVRGRHICGG ALIADRWWITAACHCFQEDSMASVLTWTV FLGKVWQNSRWPGEVSFKVSRLLLHPYH EEDSHDYDVALQLDHPVVRSAAVRPVC LPAR/SENREQGLQ/CSWITGWGALREG GPISNALQKVDVQLIPQDLCEAYRYQV TPRMLCAGYRKGGKDAC/QGESPG
10460	24361	A	10541	154	3	GVGNFFFFFLRWSLTLAQAGVQWRSLGS LQP/LTSGSLFRQFSCLSLPSTRP
10461	24362	A	10542	3	406	LMVLWTAHLPALAPGSRSTSLLLAF\ALL CLPWLQE\AGAVQTVPLSRLFDHAMLQA HHAHQLAIDTYQEFETYIPKDQKYSFL HDSHTSFCFSDSIPTPSNMEETQKCNL ELLRISLLLIKSRLEPVQVLTSMF



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10462	24363	A	10543	3	414	HSSAHAYGTYESSGKRKYLRPSRTAEL KKALKEKKNRLLQLQQRSKSVTSSSSSR DSSARDSSSEREETSTSSSSSDSDTDES SSSSSSSAYSTNSSSFSDSDSDSS\SR GRSTSTDSSADD/STNEESELE
10463	24364	A	10544	240	509	TFTSFIIGTPNLGEFCCKNNFGI/GKFR MKVACQIETLGILSFFETESRSVTRLK CGGAILAHCKL
10464	24365	A	10545	275	2	GCSRPFDTAIPLMGPYPPEKKLLFEKNK /DTCTCMFIAAHFPVAKMWIQPKCPSIN EWIKNPVTHIYIHTHTYMCIIYIYTHICV CVIHIYI
10465	24366	A	10546	233	2	WSWMAIQSVLPQTAFTELKNKYSQIQT PILFYFLKQSLPLSPSLECSGVIIAHCN /LQ/RPGSTTFPASASKVERTTGA
10466	24367	A	10547	2	420	KKKIPNRGGCLKRDTKAFLKTPPMLQRR TPPAFPKPGGFLPDNPLPPSKGNPPI YSWERFFPRFFKNIWAPVPKANLLSFFF FSIFWRTGSRYIAQAGLELLGSSYPFAS CLPESWDSRR\DHRRPTI
10467	24368	A	10548	190	1	AASTFFACVCFRLFFVVFETESPSVAQ AGLQWHSSSLQPPPNLG\SGNPALAS PVAGNC
10468	24369	A	10549	155	1	ARGEKYFLEIGGGFFFLLVFFLRQSHS IAQAGVQWCD\LNSMQPLPRVK
10469	24370	A	10550	223	392	RFVCSTIKVLRDLSSDRNPCRFLSTLN /SLAVRKDERYKAYFTK/RPDPVYDIIS T
10470	24371	A	10551	183	3	WQKLLFLFGTESCSVARVGVQRHLSSP KPPPP\GSSNS/PASASRVA\TGAHLHA RLIFVFL
10471	24372	A	10552	297	10	TDEELLCMEKRKWWF\DMASIPGEDTV NTDEMTKT/DLEYINLVDKVSAGFERT DTNF\ERSSTVSKMLSNSITCYRKI/F/ RERKSQQMWQTSFLSF
10472	24373	A	10553	509	3	LLTDRTLSCRSVGVPCSVRCQCA\LLEG ASQLG\SRGSGVRDPLEEAVCPFDLQL RTGRTTALFKAVRQGHLSLQRLLSF\V CLCPAPRGAYRGTAQLSCGGLHPVRA SRLCLPKQAWAMVGTPPP\TSLPPCSL ISDCCASSQRDS/VGVGPSKPGAGYNLV VRRF
10473	24374	A	10554	262	453	GWGILTANLLVFGGGLSISERIFFSPL ATGFCVSAQAGVQW\LIIAHCSLEFLGS SD
10474	24375	A	10555	112	372	KKKGGGPPFFFFFIFFLIRQRKAKLVVL AFNRRLRKPD/IFYAGVGKIVKKKYS GFFIELVTTCGKNYLMCALAVIDPRDSN IIRS
10475	24376	A	10556	50	358	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10476	24377	A	10557	203	350	QLHADKVS RFATHAECRGVIMAYFNLNL PH/FKRSSCLSLWSSWDYRHAP
10477	24378	A	10558	98	387	IQDIDLGRVYRYRDKKRAREKDSPPER EGEREIEKQKKER/ERKKERKKEST HQKE
10478	24379	A	10559	237	3	EVFFKNIFEIESCSVTQARAQQQDHGSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPPTPG\SSSPPTLASQSAVITGVNHHT' QSGLT'FQSPKQKALGKMCISSGG
10479	24380	A	10560	37	359	RLKCGGPVIA YCKLEILGSSNTPSTSW VAGTT/TCHHAQ
10480	24381	A	10561	170	3	RPFLLPWGGKKFQGV SFFFFFLVFFEI GSHSVP\RLKCSGTITAHCSLDLLGSSN
10481	24382	A	10562	1	388	LPEPLMVLRTANLVAMAPGSRRTLL\LA FALLCLPWLQEADAVQTEPLSMLYDHAM LQAHRAHQLDIDTYHELEETIYIPEDQKH SLLHDSQTSFCLSDSIATPFSNMEETHQK SNLEMVRI SLLLLIETWLE
10482	24383	A	10563	224	392	CVDPIKWFPLRTATROGCPLS\LFNIV LEVLATAIRQEKEIKDP/QIGKKEVK
10483	24384	A	10564	185	2	RYFGGPDSPQNGKT VFNPLFFFFFETRV\ HSCCPNESNGTISTHCNLCPLGSSNSPASQVA
10484	24385	A	10565	175	324	APGYGTKYRVLCKILLRLRLRHNHNLN PGGRGCSEPRSHHC/ITPAWVTE
10485	24386	A	10566	3	367	HELLWSTIKVLPYLRSDRSNPGGVISTS NSSLC/EKDKKNKAYFTK/RPSPVNDMI ST
10486	24387	A	10567	128	391	GETCEGVYGPQGGKQTKV FHSKRD EG PCSKTWDVGLGSSPQFIFLKKVRFFFFFF FETESHVTRLECSGTPGT/HCNLCYPG TS
10487	24388	A	10568	251	485	SFLWRFPLKGVPGHVRCQSA\LLGGASQ LGYSGVRDPLEDAVCLLSDCLKCAGR TT ALFKAVRQGHLSLQRFLLPLFSY
10488	24389	A	10569	176	3	FVPPILKKMGPFLLKKKEGK PFFFFFSEM ESRSVT\RLECSGA/TISAHCNLCPLGS SNS
10489	24390	A	10570	212	386	RFVCSTIKVLRDLSSDRSNPGRFLFTSN SSLY/EKDKRNKAFFTK/RPSPVNDIIS T
10490	24391	A	10571	134	489	SLFFLPSPRDRWSLTQSTEMPPSWKFPG REIRSPLLAMLHSLLLQPTAFLCPSS TL LLSLKPDLSLRTGSLFLSFFSFLYFEACS VA\RLKPSGTISAHCNLCPLSSSDSPAS AYIVSG
10491	24392	A	10572	1	470	GQSRGIPLLLTLDLEKPVSLLSVTNLY SKNSAQFSTILQTLSPATFTSPSPSIPL SSAYFFFFSDRV S/LLSPRQECGLNLG AHCRPQPFRFRFCLSPSS\SWGLTRR HHTTPGLIFCIF/SVEAGFHHVAQTGLE LLSLSNPPASA/FPKCWDHRR
10492	24393	A	10573	242	410	VMLRMQTYFSLHNP IFFFFETGSHFIA\ RLECSGMIPAHCNLCFPGSSNAPASASQ V
10493	24394	A	10574	236	1	ARTFFIHLKASCGDNATIGVLWHRATW CPSVLLDRDSLSEVCEILCIHAC/VMR IHEHTHTYIYANTHTHTHTHT
10494	24395	A	10575	241	35	RSSYLFI NFFVETRVAQPGKLCCSA WAGTPG\SSDPPTSSSQSAGIIGMSLNL FLOWLIIDQAGNTN
10495	24396	A	10576	294	72	FKNFKSLPFLSFLFFFLIGTRFCYVAQAG LK\SWPQGDPSALASRVAGTRGVHRHTQ LQVSFNYYKVLAMHSGSQL
10496	24397	A	10577	1200	1625	PDGWSYSSGHSWLPPEASNGRKAWS SCW

1189

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						V/EMPIKDLG/YRNLVDKAVPGCERVD FNFEISSTGWVWVLTTPAIPVL
10516	24417	A	10597	232	389	ILCWVFCFCCCCCFETEFLLVIQAGVHWC DLDSLQ/SPPPGSSDSPASAS
10517	24418	A	10598	463	154	MGQGKPRFFLFFHPPFYIFFFLKQGFSL PRVQGRAKKVPGTLASWGKILLPQPPR /RVRQENCLNPGGGGFSEPKIPPSFPAW GEKGSLLKNLKKKTKHIC
10518	24419	A	10599	208	38	LGPFGFFFTAPPPFFFTETESRSLAQV GVQWDLGSLQLPPPG\SSDSPGLSKKFL
10519	24420	A	10600	200	3	CQPELSCMRC\QSLGLGLSPSGGMEVR DPVEEAVCPALAEKRCAGRALLVRI CCS LQSQQAGTFK
10520	24421	A	10601	73	427	RVVCSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPGNDIIS T
10521	24422	A	10602	193	401	GEVSLSPRLECNGVISAHCNFR/LPGF KRFSFFFL
10522	24423	A	10603	181	395	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10523	24424	A	10604	384	10	PRRPGGECVHCLGDSLVTDRRYSGLRSS DQTLSGDPMBAVPWSNSLSCSHYRLKPA SGITWGCKQAGFFSFFLFFKMESHV\T RLECSGAISVPCNLCLPGPSNSPAPGGS LGPRSSRPPTT
10524	24425	A	10605	215	379	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSLC/EKDKRNKADFTK/RPSPVNDIIS T
10525	24426	A	10606	1	163	QTHREPAMVLSPADKTNVKAD\WGNVDA HAGEYGAELERMFLSFPTTKTYFPR
10526	24427	A	10608	283	2	TQKHGLIIRCPQETPFKNNDVGMQKVK RGEKSI MQIL/YFFFFFNS/HLSPRLE/ CSGAISAYCNRLRLSHSSDSPA/VDGTIG ACHHTQLIFLFLVE
10527	24428	A	10609	144	327	CSWSWFCGCVRVSTLIKKKNFFFEFR S\VAQAGVQGRDFGILKPPPPG\SSDSP ASASRV
10528	24429	A	10610	137	1	HKCPSTDEWDERV/WCMYTKKEYCSALTK EEIMSFSGKTWMELENIMI
10529	24430	A	10611	201	334	SFFWRFCRLRGVPSRVKQCA\LLGGASQ LGYSGVDRDPLEEAVCPF
10530	24431	A	10612	146	2	KTPLKKGLKRVPPFFFFFTETESCVTQAG VQWHNIGSLQVPPP\GSRHSP
10531	24432	A	10613	205	259	TTMPGLSFCTRTKSNKNLSFLTLDGSAR VDLFLYLLLFRTIFQNF/CGRDKVLLCC PGWSQTPELKQLICLDLPKYWDHRYEPL CLAYPFALGQNLTKI
10532	24433	A	10614	153	2	GVLMSDGVLSMLANLFFSFLFF/LFET QSHSI\SRMECSGVISAHCNLCLP
10533	24434	A	10615	213	8	KPFFFFPFFLFFFLRWGSHCVVSGY/C KGTIIVHCGLELLGSSCSPPAFQVSGIT GLCYCASIFIFEE
10534	24435	A	10616	146	1	ILTIRDYVWKITLFFFFEPKFHS/VLPR LECSGAISAHCNLCLPASSDS
10535	24436	A	10617	208	2	NNFWFSSSGKYQYFSSETESRSVTWGH DLYSLQPPPP\GSSDSPASASQVAGITG SCHHAQLILVFIVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10536	24437	A	10618	120	2	SFFFFFFETEFERSVAQAGVQWHDLSLQPPPG\SSDSPSL
10537	24438	A	10619	162	1	SFHWKLRRLRGAPGCMRCHSA\LLGGVSQ LGYSGFWHPLEEAVCPFSDLTLCAG
10538	24439	A	10620	193	419	TFFFFFFETESRSVAQAGVQWRDLGSLH/S QPGQQSETP
10539	24440	A	10621	313	460	KPGLWRGTRSQKQVLFEPESHVA\KLECGGTISAHCNFCPLRSSDFSA
10540	24441	A	10622	243	505	PTGCPKQEQVQAMLRPVVFFVFETQFN S/VPRVECSGTISAHCNLRFPGRSDSPA LASRVAGICRR/CATTAQLIFVFLVETG FCHLVG
10541	24442	A	10623	67	430	LARRTWKNOHSSTHGCDFFFFFFFF LKKGVFFFPPEGHGHRRFFFINIKFLN YKRRFFCLFEDVLMISVGPPLAFFFFF WRGGFSYLLRCV/LTFLALGAPLFAPM FFLFLFGEL
10542	24443	A	10624	3	207	PGGQLGSECSGVRMEDVL\TLKSLIIG ESGVGKSSLLRFTHTDFDELAATIDP SSVNPNARNAATP
10543	24444	A	10626	151	380	KMLFGQVQWLTPITIPALWEAEAGGSLE\ LRSSRPALKRSETSSPSPSLPCQKKKKK KFPFRAGGQMLEVPFPGRVGAG
10544	24445	A	10627	210	3	NFCQVKGFQKQSSQIKGFGKNKKKGG SFFFFFFETESHVS\RLCSGTIIIVHC SLDFPGSSDPPTSA
10545	24446	A	10628	237	2	LCFLSGASCSPYIDVYEVNGVNPTFII LTNKTNTFGPLFLIIFFGETESLSIA\ RLDCSGAISTHCKCLPGSRHSP
10546	24447	A	10629	1	352	RGPLSIQDYISKALFFLLFGFLLLLLF FEVRSCSLTQAGVQWCNHSISSLQSPT PG\RSPSPDPASAS
10547	24448	A	10630	48	200	AIKPKNLFFFSETKSSSVTQAGVQWRDL SSPQPPPP\SSDSPAPAN
10548	24449	A	10631	209	376	SFLWKFCCLKGVPGCVRCQSA\LLWGASR LGYLGVRDPLYEAVCPFSDLKLCAGRTT
10549	24450	A	10632	141	1	AGFFFFFFLFFLETESRFVA\RL\QCSG AITAHCNLCWGSSNYHAS
10550	24451	A	10633	18	522	PLYSLTRHTPREA/KDNLKSTQLLSVI DAISEGPIEGPVDGLKSVLLNSTPVLDT EGNINISGVTVVFRAGEQEQTPEGFES SGSETVLGTEVKYDTPITRTITSANIDR LRFTFGVQALVETTSKGRNPFSEVRLLV QIQRNGGWTEKDITIKGKTSQYLASV V
10551	24452	A	10634	127	2	NLSPLFFFFETGSRSVTQAGVQWSDLGS LQTPPP\GSRHSPTK
10552	24453	A	10635	336	452	RIFFFLFETEALSVAPAVAQWFDLGS LQ SPPP\GSSESPA
10553	24454	A	10636	259	3	GTRIFFFPNSSPLSFPPVQKKSVSPFFF SF/LFFFFETESRSVT\RLCSGAISPH CKLHLPGRHSLASATRNVLRLPWRHA SCA
10554	24455	A	10637	96	413	GDNTSQHSAILINYFIFFFTFLEFF/ETG SHSVAQAVRLEYSSVITAHCNFRLRGSS NPPKKKKKGGAVLKDPPWGGQSLPGLATY YFFPYRGANKNLLGDFWEGPLFV
10555	24456	A	10638	180	473	CYMGRKAWLVLSNLLTLKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKK/EMPVKQKNRGRALYKK KKGRRPFFLFWPFFFFFLGGGKKHPGG FRRKKFFFGGKKKK
10556	24457	A	10639	312	480	ETVDSTSGEDDVNIAEMATKDS E D Y I N L V\GKAVAEFERTDSNFE\RGKMMSKSI
10557	24458	A	10640	2	516	MKPLENLSQTASLARGATLLRPVLRRLC GLPGLQRPAEAEMPLRARS DGAGPLYSHH LPTSPLQKALLAAGSAAMALYNPYRH/E ERPRISTSTLDLGKLSLPEGSLGREYL RFLDVNRVSPDTRAPTRFVDDEELAYVI QRYREVHMLHTLLGMPNTILGEIVVKW FEAVQ
10558	24459	A	10641	56	455	PLCSYIQFIYHSHKFNNSQISLVHTIPLS KLFQYFSQLYSIYSYLQHF I H L L S I F I TVFCIVFYWVFWHLISVPMYICVCLCTN VCVCV/CCLW
10559	24460	A	10642	272	33	GRWFLFLGPAKYFLTGGRFPSDFFGPLK INPPFFFFFDDTESHSVAQAGVHWHNL GYLQ/SPPPG\SSDSPAPAEFHHTV
10560	24461	A	10643	285	1	MGNFLKRFKNEKKFFFPILRAHPFNFF PGKSPFKTPRRALPLGVPPKHPFFFFF FSETESRSVARLECSGMISAHCNL\NLH LPGSGYSPAL
10561	24462	A	10644	100	466	FLLKFRLEVPSSRVRCQSA\LLGPTSQL GYSGVRDTLEEAVCPFSDLKLCARRTNT LFKTVRQGHLSLQRFLLPFVQLCPVPRG GVYGRQASLSCSGVHPVRASPPCLCPK VPPPS
10562	24463	A	10645	260	460	LKPHAERETIDKGRLPYYSFFFFETESC FVAQAGVQWHDYSLPPPP\PGSEGSRA
10563	24464	A	10646	360	504	QIGHICAYVEKTELRLIFFFLFFFRQS CSVT\RLCSGTILAHCNLC
10564	24465	A	10647	241	45	WEVEVPRVAPCHILKRDYFIIILFLFLF FEMESYSFT\ELECSSAISTHCNLCPPG SRDSPGIPPH
10565	24466	A	10648	76	462	FLWEYQEKAHILWSLFSKLILSRSRFTV KEKVRQKPGILFIYLFIFEMESCSVAQA GVQWRDLGSLSPQKKKDS/DQSKAITFV EGINSKRGGWTGPHF/HCSLKMIFLI
10566	24467	A	10649	3	359	QTQREPTMELTPADKTNVKAAWGKVGAH AGEYGAEALERMFLSPFTTKTYFPHPDL SHGSAQVKGHGKKVADSLTNAEAHEDYM LNALTALNDLHAHKLWVDQVNFKL\LSH CLLVTTA
10567	24468	A	10650	266	3	TPEKKKKIGGLGAPFGYPKKIWPNNFF FFKKT K F F F F Q R V G W A P P K S F F F F F F EVESCSVAQAGVQWRDLDSLQSPPP\GS RGSP
10568	24469	A	10651	278	461	KKIICGFFFD TGSCFVAQAGQQWRDLRS LQSPPPG\SSDSLTSASRVVGMSRHMRA VF
10569	24470	A	10652	161	456	VFFFFGENIAFVENKTLSYHFMFTRMT AAKMMENYKGCWGWETIGSFMPCWLESK RVQSLW\KVWQFFKWLNVKLLYGLAIPL TGICPKLKKYVQGY
10570	24471	A	10653	91	486	PCFNHGH T T W Y M Y F F S L S L I L F F V F S L K PVILAYKTFSPFITIRVLLQRRHRQKFV LDGFNGVDQNNILGSI CVSLIKIFFLTE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SCFVAEAGMQWCNIGSLQAPRP\GSCHS PGISPPVLG
10571	24472	A	10654	267	470	NLHMRCEKEQNFNKLSFKDLFGLGWLWF FIFCFWRRILTLSPRLEC/RG/MIFAH NLCPLPGSGHSPASA
10572	24473	A	10655	775	1401	TFPSQIRYGLRKRPNSLTLSPRLECSGA ISAHMQRPPPGFTPFSCSLSPSSWHYRR PPRPAICVCVCVCVCVCLVETGFHRVN QDGLDLLTS/S/IPPASA/FPKCWDYRR E
10573	24474	A	10656	287	454	LPLIYFLYFYETECHPLAQAGVQWRDLS SLQSPPP\GSNDSSASASPTVPTSAM
10574	24475	A	10657	212	64	LFLSKFYFFEMESCSVAQALQWCDLGS VQPLP\PGSEDSPPASAWGYLD
10575	24476	A	10658	368	473	GFIDHTRRRPECP/LTDEWIKKMWHIH TTEYYSA
10576	24477	A	10659	358	1	ILAVFCFCGSAPGFEGGKLTFFFNNGRE TFLALVKTPPPGKARGPVFISKNKKIPE FKQPPNPNSFFFFFTESHTIARAG VQWHNLCSLQSPPPG\SSDSPGRWSLQR TEIAPL
10577	24478	A	10660	2	235	KRDLIRHYPKEDIYMANXYLK\CSLT MHTETLIRTTMRYHLILIKVTIFKKT DNMTAVGVHICNPNTLTGHRGIA
10578	24479	A	10661	9	538	CVTVRIPSRPTRPLSSDRSNPGRFLSTS NSSLY/EKDKRNKAYFTK/RPSPVNDII ST
10579	24480	A	10662	374	38	SPLWKLHLRGAPGCIRCQSA\LLGGVSQ LGYSQVDRPLEEAVCPFSDLKPRAGRTT TLFKAQRGRSLQKFLPFVQLCPAAR GGVYRGRQASLSCSGLHPVRASRPLCSR R
10580	24481	A	10663	268	47	ALIPLSSLTISAFHLLLETVSTSSPKM ECSGAITSHCSFNLDPSSPSPTSASR/V IGTIGARHQQLMFIYFC
10581	24482	A	10664	64	451	FSSERKSHMSLTNLQKLEMIRLSEGLS KAKVGQKLVRHLQTVSQVDAKEKLLKL IKSATPVNIGMIKQHNLIADIEKFGMIW TDCQTSRHTVLCQRLIQSK/ALTFLNSM KAERGKEAADEKLEVRRG
10582	24483	A	10665	355	474	ILFYFIFFTESCSVAQAGVQWRDLGSL QAPPPG\SRDSP
10583	24484	A	10666	317	481	GHTCPWQTFFFFLFRDRVLLHHPGWSAV TQSWLTAALT\FGPKRSSCLNLLNDWD
10584	24485	A	10667	57	329	VKNTQWKGDSL FNKRV\FKNWASTYRRI KLD/LTSYAKINSKWIKDLNVRLEIVKV LQVEYPSFKILNGSVLDFVFFYSYGIFA LHLMGEHP
10585	24486	A	10668	86	468	ENYKIPLMGGKNFLFPISIPPYFFFFSR LGLTLPLRLKCSGDHCSLQPRPPGLKRS SCL\GFPKCWDYRNEP/CVPR
10586	24487	A	10669	254	25	GSHICKVPAIYSNTCTSSHEGDGGVVG GCSSGSTTHSPVADSFVVVETVSL/S VTQAGVRWCDLSSLOPPPPGI
10587	24488	A	10670	206	3	YGRPRKLCNIGLKSGLDPTHWGQHRVI SFFFIMETDSRSVAQAGVQWHNLSLHP PPPG\SSDSPAS
10588	24489	A	10671	20	355	GFTSQSELLYSIDPITRPTDQVTIGISA

1194



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10607	24508	A	10691	240	406	DGIRRLSFFFFFFFETKFGFVA\RLGR GTIWNVNHLHLPGRDSEASASQVAGIT
10608	24509	A	10692	343	3	QVPLNLSLHLKLGMLFPGCINGSLSQFL QFFAQISPYQTGFPSFYKTSIYHNSLHQ YSLSLPYFIFLFFFSFFFFLQKSHSVS \RLECSGMVSAHCNLRLLTATSTTQVQVILV
10609	24510	A	10693	196	3	YDAGHTKKTLHFPTVYPFVLFVCWWECKM VQPRWKIVRR/FLKKLNTKLPYDPAIPF LSVHQKELRT
10610	24511	A	10694	245	391	KTDYQPGAVAHFGRPRREDHPRLGVDK PDQLEKPVSTKNTKLW/SWWL
10611	24512	A	10695	252	389	KTGGKVLFFFETESRVAQVGVQWRAL RSLQPP\QPGTSDCPASAS
10612	24513	A	10696	385	1	PPNKAAMTSSKDNKNLHWGKDTLLNKWC WESWIVTCTITMKLDSHSPYTKINPKWI KD/LKTIKILGENIKKTVDIGLHK\NM SKTSKAMTKILDLIKLSFCPAKEIISR VNRKSTEWKVFASYLN
10613	24514	A	10697	296	430	KHIQARRGGS/CGN/RQHSRPRRADHL RSGVREQPEQPEKPHL
10614	24515	A	10698	280	468	DYLC/SLSIYLSIYLSIYLSIIHQFIY HLFYIYHLSNLSSISIFFTKWLS
10615	24516	A	10699	15	393	RSVGVLGPVRCQA\LGSDSLG\SGG SGVRDPLEEAVCRFPYLQCTGRITLAF KAVRQGHLSLQRLLSF\VLCPAPIGG AYRGRQASWSCGGLHPVRA/SMLCLCPK EAWAMAGAPPPASLPPLS
10616	24517	A	10700	176	1	DWTNFTTFLYNFKPSSIMPYLSHLFKT LR/MWPGAVAHARNPSTLGGRGGWIMRS GDE
10617	24518	A	10701	494	80	FNKKDIHSDTPSEGHQLQRPNVETLKKM GRNQCKGENPKNQNASSPKDHNSSTPR EQNWMKNESDELIEVGFRRWVITNSSEL YKG\DVLTQCKEAKNLENRLGKVLTRIT SLEKNHGGLMEVKINIAQLCEASAGWR
10618	24519	A	10702	264	410	KKGPLFTPPGGGGG/PQKPPGPLNPGG QRDSSFFPPPGGGNTGETPPGG
10619	24520	A	10703	125	3	NRGNKGQV/QWLMPVIPALWEAEAGRSP EIRSRDQPRQHGETL
10620	24521	A	10704	184	2	RLRVLAPCRHLPRAPRTWPKRPFFFSFF LFFPQTQSHSVA\RLECSGAISAHSNLC FPPTRP
10621	24522	A	10705	187	406	LFLWKFCRLRGVPGHVRCQSAL/LGGASQ LGSSGVRDPLEEAVCLFSDLQLRAGRTT TLFKAVRQGHRLRLQRIIL
10622	24523	A	10706	82	410	ILRGKFGKHYFNRIWREALRQSLSLFN FIIFSNFLASLHKPEMETELKGSFIELR KALFQLNARDASLLSTVSDSDFSCRKFS R/CSKCGQ
10623	24524	A	10707	390	2	SKDCRTAKIAACSFLWKLRSRGAPARCK PELSCMRCLSA\LLGGVSQSGGTGIRDP LEEAVFPLAELERCVGRSAALFRASRQE HLSLLKMHPQLPLPSGALSQADGSFIYK PLTGASAFLEMPQERR
10624	24525	A	10708	229	392	YSWWRQMHSVAHAGVQWCD/LVSLQPQP PG\SSDPPASASLAARTTGAGHNLQIF
10625	24526	A	10709	193	2	RYLCYQDQHVILLILLLLLLFLRWSLTLSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLECSGTIMAHCSLDS\SSNPPTISASQA AGTTGACYH
10626	24527	A	10710	180	11	LLFFFETRS/HVSQTVVQCGMISGHCNL RLSGSSDPPLASRVAGTTGKHQNIWLS R
10627	24528	A	10711	234	408	MKLIMLKVILFPQIHLQIQPNFYQNIFF FETELCSVAQSGVQWHNLSLQHPPP\G SSD
10628	24529	A	10712	312	470	TGPHCVT\RLECSGAI TAHCSLDFAGLS TSPTSVSQVSGTTGTWMKLETIILS
10629	24530	A	10713	64	392	PKMVIRISSETSLYASLPLQMKGQRQK/ CEPQPKKKKKKKKKKKKKKKKKKKAR G
10630	24531	A	10714	169	427	NNQKTNNKMVGVSFYLSIIILNVNELNA PIQRHRVAEWIKKEKKKK/DPGICGLQ QTLFFYEDP/HDPLRLKIGGW/RKYYP S RGTQIK
10631	24532	A	10715	176	410	ARSSWGLHTAVPVAFSLRFLLEIFLDR DTRCSPPAAFFFETGSCCVA\RLEGRGA ITAQCSLNLGSSNPPTSASRVA
10632	24533	A	10716	234	389	NSGNMDRYKDVQNTIIONPICWPGTVAHA CNPSTLGGRGQIL/RQGEFETSLA
10633	24534	A	10717	190	2	GPFPHPGGFLRGFFVPNTIPPTFFFF FFLRRSLSVAQAGVQWCDLSSLQPLPPG P\SNSPCQ
10634	24535	A	10718	201	1	WPLFLPKMFFFFFKRFPHMGPSPVWGAQA KKKKIFFFLTGSHSVT\RIECSGTISAH CSLNLPGPSH
10635	24536	A	10719	195	419	EYHTSLVTCGNPCVYRSNNKLNQTSRRK VITKIRABELNEIETEK/LQSGETKIWF FEKINKTGLELLGSSDPPVW
10636	24537	A	10720	218	407	GKKNLAFKKKKRKEKKRKSQSNMNS AKIEARTNIKLVVKGHWKNCIIDA\LQ KAFGDNA
10637	24538	A	10721	231	409	GTQLHLGGFFFFSEKELSFCFWF/MFALF EMEACSVT\RMECSGTVAHCNLRPLPGT SNSSA
10638	24539	A	10722	40	401	PLCPSESSGNTLMASSDPSTPAVPPNT THPPLCLSKSHLPLRPKQGLPSGNLLQL PLTLIPLLGAPVACWQLPQQCTLTSTFF FETKSHPVAQAGVQWCCGLSLQPLSPG\ SRDSPDSAC
10639	24540	A	10723	210	14	HVMGLLLLFLNKLTVNNFGWLAGFWCLG FFWFFSFFETRSGSVT\RLECSGMISAH YKLCIPGSSH
10640	24541	A	10724	347	462	TFFFFFFETKSRCDIQAGVQWCDLCSLP PSS\PDSSDCP
10641	24542	A	10725	169	386	DKKQAKTIKWGKNSFSNKWCWNNCIATG KRMKLDP\YLTPYKK/INSKWIKDLSI
10642	24543	A	10726	257	54	PLFFFFKRQGLTSLPRLECNGTVAHYN LKLGSRLDPTSASP\SAGITGISNPAR LFTYLNPTHLQT
10643	24544	A	10727	2	401	NNYDRAETQIYQYMCLNPTFYCLQETHL TCNDIYRLKVKGRREIMQIENKRVGVAI LVSDKTDKPTTVKKKLHYIIKGSIQPE DLIILCTYSPNIRASRFIKRIPDLRKEI A/HTVKVGDFSISLNLRSRQNT
10644	24545	A	10728	154	1	PMCSLLGLSKGGIIFFFFEAEFCSSVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AGVQWRDLGSLQPPPPG\SSDS
10645	24546	A	10729	34	151	PRPPVPSLLDRGRLOLWRQRLRHRAHS NGFIGGKQKIMKLLKNYVRPVG/VAVA IMFDPDPYPRSWIEDDFNYGGSVASAT VHIRMGSLVENNKS
10646	24547	A	10730	2	408	VFLLTVRTLICRSVGVWWRSTPDLVCLG ISSGGCRTANIGLYQMLLPDHSSGSFCL RGVPGHVRCQSA/LLGGPSQLGYSRVRD PLEEAVCPFSDQLHAGRTTTLFKAVRQ VHLTLQRFLRFVWLCPAPRG/GVYR
10647	24548	A	10731	274	89	ENIPVFNPPVCSPLLPQPE/CEYPKL CKLCLKLHKHRVYF\FLFFFFETEPHSV ARLECSG
10648	24549	A	10732	251	1	TFQMMQKCFSHRKIFHNLLDKASYKIVY KEDPFPSSLSSSVSLKNNFFLETESC SVTQAGVLWCHLSSLQPPPPG\SRDSP
10649	24550	A	10733	375	1	APFPPLWVRGSPFSPVFPHPKLPPL AEILGFFKERKWSIRKPCLFKVKKLVS VWPGLELQIFKFIGEFPFSPSLVGRKP NFFLGPVFFFFFEKESRSA\RMECKGT ISAHCNLHLPGP
10650	24551	A	10734	82	398	SFLWKLRLRGVPVSHVRCQSA/LLGGASQ LGYLGVRDPLEEAVCPFSDQLPAGRTT TLFKAVRQGHNLQRFLLPFVQLCPASR GGVYRGRQASLSCGGLHPVRAS
10651	24552	A	10735	2	341	TFCATSWLESGVEDGPRSRISYRISTFF FFFKGAPEPKEVRGRPKPLAPTSPLGA HGTTLGSGWTPSIGGWQPPPPPRENPK GEHPPAPVAGDTFQ\PKKPPPIKVFFP K
10652	24553	A	10736	171	1	RVFYLLAFALFVDTGSPFVSQAGVQWCD HSSIQSQTSG\SNDDPASAYRVAGTTGV
10653	24554	A	10737	190	1	EKHTTVRKIPKMEEMADSGSNMLRIIIF LFLFFETKSCSVT\RLN/CSISAHCN LHLPGSSNS
10654	24555	A	10738	252	413	GLLGLQNFYSYKVLTKAHLKKCSWLDV AHAYNPITLGGRGW/IQEFQTSNTV
10655	24556	A	10739	101	249	AGSTSRCI/QELSDLLEHLEQENCLNPG GRGCSEPOSCHCTPAWVTETQKK
10656	24557	A	10740	185	403	LGLPVHTMKSNYHYHLCHHHHHLQH HHHCHCHYHS/HHHNSQHPPPPPPPP HHHHHHHHHLP
10657	24558	A	10741	119	425	IKFHLHSMERTHLFLWNCWAHKQRNCFK ADFVITDDIKQLCPPQSWWTRAGKLPLG AGRGGSHMLSHFWRPRHADILYLGVL DQPGQGETPSL/LKNTKSSW
10658	24559	A	10742	112	2	GETFFFETGSSSVA\RLCSGAISAHCN LHLPGSSKSP
10659	24560	A	10743	188	3	PPPLFFFFFFFFFKTGSGSAT\RECTA HCNCLPGSSHPTSAVQVARTTDCNH AWLIFV
10660	24561	A	10744	176	3	SLYSKNKNPSHLLFLPIPIKFFFFFFET EFRSVAQAGVQWHDLSLQPPPPG\SSD SP
10661	24562	A	10745	250	1	GPRIFFLKEFYPRFVGKNPAPGGFFS GGKKPGFPFNPRIKFFFFFFETFRS VAQAGVQWHDLSLQPPPPG\SSDSP
10662	24563	A	10746	155	3	PPHPFPNPLPIKFFFFFFETFRSVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AGVQWHDLSLQQPPPPG\SSDSP
10663	24564	A	10747	157	1	TPRPFPFNPPPLKFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10664	24565	A	10748	157	1	TPRPFPFNPHPIKFFFFFFETEFRSVAQ AGAQWHDLSLQQPPPPG\SSDSP
10665	24566	A	10749	153	2	PPPLSVVTPAPLRFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10666	24567	A	10750	157	1	PPPPFLFFPRPLKFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10667	24568	A	10751	155	3	NTFPFFFTPLTPKFFFFFFETEFRSVAQ AGVQWHDLSLQQPPPPG\SSDSP
10668	24569	A	10752	86	406	SFLWKLHLRAPGCMRCRLA\LLGGVSQ LDYSGVRDPLEEAVCPFGPKLHAGRTT TLFKAVRQGHLSLQKFLFPVQLCPAPS TGVQEGRQASLSFGGLHPVQSSR
10669	24570	A	10753	364	469	GQFLHSLD/SHWKKSEDFCLWFPHSEN VSAIHQDH
10670	24571	A	10754	250	61	GEKKKKKPRVFFFFFFETEPGSVT\RL ECSGVLSAHCNLRLLPNPNDSPASASRVA ASAKLG
10671	24572	A	10755	66	446	SFLWKFCCLKGVP GCVCRCQA\LLGGASQ LGYSGVRYPLEETVCPFSDLKLRAGRTT TLFKAVRRGHLSLQRLLPVSVCLCPAPR GEAYRGRQASLSGGLHPVRASRPLCLP TQALAMVGAPPPGSL
10672	24573	A	10756	252	482	RLPRQPVRKWWAGVRGCCVWGVVSKSLQ RSTTLDWQGPQRGGPILFFFFFFETLCH /TRLEGNGEISAHCDLCLPGSN
10673	24574	A	10757	205	488	PLESLRSPGLPLSWRTASSVSPVICIYY IYIYIYIYTHY/HIHTHTHTHTHT QYIFVCVFLKDRVLLCHPRQSAGARSW PTRTSASQRQEM
10674	24575	A	10758	272	471	YSYVLFFIFLGIESCSV/AFSAGVQWIN HSSLQLQTPGLKQSSHLSLP/ASASPVA GTTGMRYHARLIF
10675	24576	A	10759	17	342	GTLSSGAQVLIGRIESTVVGLKPWALG GCPSPRAVHWLLASSDWRPSLQDGAEGW KKGEANGNHR/GIAVISDQIDFKTKTI KGD\KKSHYVMKGPQQBAITINI
10676	24577	A	10760	42	498	EFRRGREKEREKERKTEERMEDRERKA EREREKERQEGRRERERERERERERKR ERERKRERE/RHEPGSL
10677	24578	A	10761	1	305	ASWDDPAHNNFNHIPPVVAAHFFFCRL DCPPWAPRPPAPR/VLL/TPAAAAAAA AASRPEKKRAENVGATPPRKRPPRWEE RRGPRKGSAPPGRGAGRAR
10678	24579	A	10762	364	2	FPQKQNGQYLPLFPKPTGLCGKGKTRLG FFLNIFYGKKKKKRGRELGFPPFCQIWGT SIYRGSMDYFFFFFFWRQVSLALLPML C\RMIRVHCSLDLVGPSNPSTASQIA RTTGTCTMCHH
10679	24580	A	10763	152	484	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10680	24581	A	10764	208	420	SFLWRFPLRGVPGHVRCQA\LLGGASQ LGYSGVDRDPLEDAVCLLSDKLKAGRTT ALFKAVRQGHLSLQR
10681	24582	A	10765	319	85	GKLLNNNRFCGSKFQGMFFFGETESPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITQSGVRWHDGSLQPP\PPGSRDSPASAS\RGITGARKHTQPIFLLVSNS
10682	24583	A	10766	122	3	KFFFFFFETEFRSVAQAGVQWHDLSLQPPPG\SSDSPSL
10683	24584	A	10767	240	86	RAPPPFFEMESCSIAQAGVQWLSLGLLQAPPP\GSCHSPASASCELMFSKI
10684	24585	A	10768	244	85	RAPPPFFEMESCSIAQAGVQWLSLGLLQAPPP\GSCHSPASASCELMFPKI
10685	24586	A	10769	35	296	EVKSPSARQPPRLGSEHLRPAAPSGREVGQPPPGQPPCPGGEG/PPPPGSPDW EVRSPSARQPPRLGGEPPSSRLRTGHDDD GGFV
10686	24587	A	10770	260	484	MDEELLLMNEQRTWFLVESSPGEDAVS I IQLATRDLEYDLNLVEKGAAG/LERKH YSFERSSTVDKILSHNTACY
10687	24588	A	10771	248	393	TQEGKKLINWPGTVAHACNPSTLGARGG RTTRGQLETK\LANKIKPCL
10688	24589	A	10772	239	2	SFLWKFCRLRGVPGVRVRCQSA\LLGGASQ LG\SQSGSVRDPLEEA VCPSSDLQLRAG RTSALFKAVRQGHLSLQRLLSF
10689	24590	A	10773	158	455	LFFTLCPSLLQHIAMVLELGLKGPKSTIQ PIFWVFLQTEP/HFLVTPVR/CCLPLL KLFCLLVFCMESPSVPHAGECSGVISAH CNLCLLGSTDSSASPSRV
10690	24591	A	10774	166	403	KKTFLGEPLFWGGAKKKKPGKKNPGFFP RG/IKPRVFFSRFFFFFFGPPPKGFPQKS FFLKSLPGFFLFGGCPPPFFFFFFFEM ESCSNTRLECSGVILAHCNLCPLGSSDS P
10691	24592	A	10775	208	1	RLCFFYFRKALLGKAQIKNIAFFPRKGS FFFFSETESRSVAQAGL/LDCSGAISAH CKLRFPGRSQSPAS
10692	24593	A	10776	192	29	IFRKEFPCLNFFLLFFETESRSLAQAGV QWRDLGSLKAPPPG\SRSPASRDTGV
10693	24594	A	10777	275	490	KPGFFLLQMAKVYMIFFFFEMEFC\VA QAGVQWHDLGSMQHRPPG\SGDSPSCLP SI/AGIPG
10694	24595	A	10778	340	3	LKVPVGKPRSTLLGVKKVPFFGNKRKKF LALFFFP PPPGEGFSTAFLAQKPTPRV VPALGF PKNQSPSPFFFFFFETKSCSV TQAGVQWGLRSPQMPPPG\SSDSPASCL
10695	24596	A	10779	313	1	ANPFGGPGGDPFSSRVFPFGPKNETP FFKNKTATKKTGNKGWAPSPHRGGPK KGPALWDKKGKNLWPPFFETESHVST\ RLQCSNTILAHCNQCLPGS
10696	24597	A	10780	116	422	ILEDNTNIQTETLLAIREVQIQTTLRNH FTLTGMAL I /RKTDNNKCWRECKIETL ICCWRECKMLCNEVGTALEIVWQFLQSL NIELSYDLAMPGFIIFPRE
10697	24598	A	10781	120	418	TQTTGAPQLHLASRWLSRSGGLTSSPQE IPKLFWSIESPLGSSKHLSQLVFVCLFV CSFVFEMESCSVARLECSIVISAH\CTL HLWGSSHFHASASVA
10698	24599	A	10782	134	1	SSFFFLCQTESCFGVQWHDLSLQPPSTS RAQA\LSLPSSWDHRR
10699	24600	A	10783	2	435	CSHRGDSYSSQLSGIRAGDLGGGGKDI FRLPPTTLNIFAGKESYDVVCV THERMC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LC/SCLFIYMCLCMCVHV/HYTHEACVF MCLCL
10700	24601	A	10784	432	161	FSRAGFH/RVSQDGFDDLPS\CLPPLGL PKCWDYKREPPRPAPKLMCRQVHRKCTW LFIQIGSTLFKTNGLSAVAHAYNPNTW GGRGERIA
10701	24602	A	10785	270	442	NVRLRLGLALSPTLECRGTIMAHCRDLF PGLMQSSHLSHRVAGTTG/TCHHAWLIF KFL
10702	24603	A	10786	12	424	LIQLPRLECSGALICARNFTY/SLGSGD PPTSASQ/VLKTTGVCHHAQL
10703	24604	A	10787	350	3	DSSSVQTNKGIPGQVLSLSCAVKASV LVI I PLHNALSSWLVPALFLWKSQVQVK SQQAHSVSGLC/MHYRSHTHAHTSPH RHRHTYTYARAHTHHTQML SAYLPSKQ PSGSL
10704	24605	A	10788	155	3	HAFFALCIRNRLECNVILAHCNLC/RL LGSSDSPVSASQVNGIAGACHHAQL
10705	24606	A	10789	188	2	RRDLSSLQPPRGGQ/MRGCIYTHHTHT HTHTHTVHWGWGKRHHVPKGMKSANG ESGRAK
10706	24607	A	10790	19	405	IRPTISRVERGINSLVASEGQRLPWDGI ACSQGLVVQQTWGPGLGFPSSLGMPHR PTFRDLNSEPAPGVANVSGTLSTPLPGA SHGLLVFFFETESHFVAQAGVSWGDLRS LPPPPPG\SSNSPVSAS
10707	24608	A	10791	157	1	KPGPPFPYGPGLKIFFFFEFETFRSVA\ RLECSGTISAHCNLHLPGSSDSP
10708	24609	A	10792	157	1	QPRPPFPNRPKFFFFFEFETFRSVAQ AGVQWHDLSLQPPPG\SSDSP
10709	24610	A	10793	83	387	SFLWLKHPGGAPACMRCLA\LLGGVSQ LGYTGFRLDLEEAFCPSLKHAGRTT AVFSAVRQGLSLQKFLLPFVQLCPAPR GGVRG/RQALLSCHRLHPV
10710	24611	A	10794	204	419	KGVYGHSGSFSPAPLACFRDKTLFPVS LWKEFVHSPWCKCTLPPQPLWKTWVRYLK NFKME\IPYVPEIPLG
10711	24612	A	10795	207	2	RRGFTMLVGQNSLDPSTSRSAHLSLPKC WDYRCKP/PAPS/LREGFSYLLHSLHP TPAPGSHHLWAALIC
10712	24613	A	10796	2	237	FFFLRERILLALSPRLCSDANMSHCSL NLPG/FSQSFCLSHP\SRWDHRHMPYP VKFFGI FVGDRVLALFPKLISYII
10713	24614	A	10797	342	40	DRVFFCSPRLECSGAT IARCS/LRTPGL KQSSHLSPKCNHRCPPRPARCSLNE SHSAKKWPGQSTDSSACEVQPTSPFPT VPYPTLLSPSAGHGRGR
10714	24615	A	10798	209	2	CSVLAVILNPECIYVVPWLELLAHDPIP RLVCPSKFFFEKFCPSVAQAGVQWHDLG SLQPPPPG\SSNSP
10715	24616	A	10799	142	2	IFFFFEMESRSVARPGVQWSDLGSLPP PPP\GSSDSPASATPSPMQS
10716	24617	A	10800	276	2	ILPIIIRNTCCCFLLKESRSCSVTQARV QWHII/GSLQPTPG\SSNPPASAFQVA TGAHHHTSLIRNTLIIINWEKNTKLSG CTSMHFRFL
10717	24618	A	10801	12	364	LHHYKTVSGIYKCLCVLNGPPTFFPDF LPPLGLPYSLRHNNIEISPINNPIASK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YSRERMSCISLTNLQTLVMIKLNEESLL KANS DHKLCCLLR/SVYQVVNAYEKFL
10718	24619	A	10802	235	3	HRPSEDLDFFPHWAVMRAPQYPSWDTRE GGPRSFLFLFLFFEMESYSVAQL/EGTI SAHCNLCPLSSSDSPTSRLCSL
10719	24620	A	10803	349	1	NQTPFFFFFPGGTETTSTLCS\YGLLI LLKYPEVA/ESASQRDPWEAAVWRWLE GPGSAQPPSAPAKGQELDPVVGQRPVPS PDDHVQWPYTNVAVLLETQRFISVVKRTL TLDTLTY
10720	24621	A	10804	365	3	IDVCNVCVRKQYRGFCQKYRAWISPVY PHKCGWHRVYNTPTPHCETEWLWVILHA QEH/TFSLTGRHTHTHTHTHTHTSKL APPASRALFGVAHVEAQKALASPSSGRY LAITMFVQPCI
10721	24622	A	10805	406	96	CPPEFSEESPRLLKFRVGGYLTPOVSKC GLGVVRIKFVFFWSPPKVQTSLFFFSKT GSHSVT\RECGDTILAHCDLCAPGSGD PPASATRVTVVGLPPCPAR
10722	24623	A	10806	58	369	FFFFKGDRAQNN/SGERCLLNKGWYDI WISTCKMKSTPYLTLHTKISSKGLKDL IRAKRIHLKKYIGINLHDLGLK\DFL NMTPKTLATKEKIDTLDPIKIK
10723	24624	A	10807	126	1	KEPFFFFFFFETESCSVAQAGVQRCLSS LQHQP TG\SSDFP
10724	24625	A	10808	204	415	HLGFDLSLTICISLSDGLKYKATVFLVFF FERESNC\AVWAECONGPISVNCNLRPLG SGSSPASPSRGVEIT
10725	24626	A	10809	168	2	KISKRPFFFFFFFETGSHYVA\KLECSGV ITAHCSLDLPGSSNPPTSASWVAGTTGT
10726	24627	A	10810	97	389	LAVSPSLSLSLSLSLSLSYLGLPYSLRR SNIEITPINTPAEGSVCSSEKGHMSLS FNEKIEVITLSAQDMSNTKIG/RKLDLL CH/TSQVVNAEEKFLK
10727	24628	A	10811	24	416	LEYIARRYLGVVWLFFFFLNRQGEKSR GPFKFFPRGFFSTRNGAPGGPWGFLP WGGGPPVGFQKQGGGAP\PPKNRFPK GGPLTQPNLEKTPINPKGPPTRGFFPS GPPPKKGAGPPPIFRVGEF
10728	24629	A	10812	60	435	KKRKNFPQKKISPYFYPLKWFKTPPLWV KNQTPPV/CCFFEAPFSLKKPPRGLKKG /WGKNFPPPLVPQKKKKKDTAGVAILVS DKKDFNPTKIKKDKGHYIMVKGSMQQBG LGCPDAWVPS
10729	24630	A	10813	618	1519	FWFGVNCKSVCPFLPVLFCFVVCWCER GVLSQRSMGQAQSKPTSLGTMKHFKKG FKGDYSVTMTPGKLRTLCEIDWPALEV WVSEGSMDRSLVSKVWHKVTCKPGCPDQ FPYIDTWLQLV/YRPPPY
10730	24631	A	10814	179	15	KVKRLKTPFFFFFFFETRTCSVAQARVQW HNHSSLQPQPPGPKRS\PTSVSREAGT
10731	24632	A	10815	61	422	NCFFLKGPDLFFFFFFFLLQIVFI YKFFAFLQMEFRSLPRLDKCNCAISAH CNLSLPSSWDYRNLPRLANFFLFLVET RQPASA/FLTCWDYR
10732	24633	A	10816	170	440	RQGLSLLPRLECSSMTTAHCDLKLSSS NPPISAPHIALG/LTGLCHHTQL
10733	24634	A	10817	322	443	FIFIFYFFETRSHAVAQAGVQWRDLALL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPPPP\GSSDSPA
10734	24635	A	10818	134	3	KKAHLPFFFFLEGTESHVA\RLECSGT ISAHCNLCLEPGSSVSV
10735	24636	A	10819	76	245	FLLRKGTRQGGPLSS/LLFNIVRDVLAR AIRL\EKKIKDIQIGKEAELSLFADMI IF
10736	24637	A	10820	233	440	FFFGALKKWKSMTHKKVERGKRTTLNG GGIKAATASLKKHLQGWGKVMLMANKL LRGERAW/FPPIRG
10737	24638	A	10821	293	402	RNPFFFLTEPHSVAQGEVQWCNLSLQ PPP\PGS
10738	24639	A	10822	168	1	PLRGLSDSSLGIMKRMATDLSSLQPLPP G\SSDSPASASRVAGITDSHHHAWVIF
10739	24640	A	10823	97	405	LCVNICFNFPWLGVEWLNHIIGVGLTFF FEMESCVARLECSGAISAHCNLL/LPP SFGSSDSPASVT
10740	24641	A	10824	186	2	EPGTISLVALKLQKWPRR/SDHLRLAVR DQPGQHDETPSLLKNTKISWAQWQAPVI PALEPV
10741	24642	A	10825	199	1	KKTQIGGAPGGALFFFFFFETGFPFVA\ RLQCSGTNQACSLNLLSSSNPSFPALQ VTGTPSACP
10742	24643	A	10826	252	381	GQQEFFFFPCSVPOAGGQWCNLSLQAPP PG\SHSPASASRVAG
10743	24644	A	10827	77	427	IPQVHCPMSPPVPMACIPRVSSFTSWVF HNLLPPSECPLGPLVPASSHPRPCVCCR PCTSW\CPLWPRPPCSNSPV/TCVPCL PCLCISEIPSCVPWP/WTYSSLCPMSHV PDSPCPLP
10744	24645	A	10829	20	518	SFAFSLLOHLTETSFAINSCSEATLLFL SVFL/RAQTLTAPCQTRGPRRGKDRGSG SSSPSGPKATKESSVERRKSFDSWGHFR AA\QRLMDNQAERESEAGVGLQRDEDDA PLCEDVELQDGDLSPEEKIFLREFPRLK EDLKGNIKLRALADDIDKTHKKFTKAV
10745	24646	A	10830	351	3	LHFSFPLQHRQNIKVWLMRASMQRHSRT HGAFPLHQDEIQTRPRLRSAASSGPSLL SDHILSTLPAFTCANLSSRFCS SSPCSC SCLRA/CCTCHFDLSTLIHAHTRTHHT HTHTMY
10746	24647	A	10831	8	376	GMLPAHLADVLRHNSVGRPKHMRVMAGA LEGDLFIGPKAE\EHRG
10747	24648	A	10832	336	38	GVATEGVGEAAQGGEPRQPEQ/PPPQPY PPPPQQQHEEEMAEARQA/AGAPMDDG FLSLDSPSYVLYSDRAEWADIDLVLQNV GNPNVVQIYSDKYTLWK
10748	24649	A	10833	206	1	TYFFPPPPGLFFIAGIFFFFFFLETGSH/ SSLRLECSGIITASCSLNLDPNDPPAS ASQVAETTCATMY
10749	24650	A	10834	226	376	RISQAIISFYFYFLFETESRSVAQAGAQ WSDLSSLQPPSPGV\SDSPALPS
10750	24651	A	10835	213	1	DRVLLLSPLRGCSGMITAHCNLHLPWFK RFSCLCPPE/SSWDYRCPLP/PPRLTSV FLVETGFHHVGQAGLR
10751	24652	A	10836	351	447	RENLWLTVPVLPALREAKAGI\LEPRSSR PAWAT
10752	24653	A	10837	71	472	SASTAPMAPVKKLVVKGK/K/KKKQVLK FTLDCIHPIEDGIMDAA/NSTNYEQFLQ



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						ERIKVNRKAVNLGGVVTIERSKSKLTVT PEVPFSRRYLKYLTKKYLKNNNLCDWLC IVANSKESYELRYFQITQDKEEEK
10753	24654	A	10838	37	382	SRCIMAFYLYGIRSFPELWKSPLYLGVGP GHSYVSLFVAGRCGVRNQRLCSVKTMS PONTKATNVIKARYLRKDEGSNKQVYS VPHFLIAGACKERSQMNSQSEDHK/LA/ PVRNAV
10754	24655	A	10839	313	617	AFFLIVFQYVARERERSRS/VNCGLYQ HCYFRTL
10755	24656	A	10840	309	511	WEQGSWEHVLQAPCSLIAPRITHAYTHT HTHTRHYTHLYPH/APTSIL
10756	24657	A	10841	269	450	TPWPLKKEFFFLKWSLALVAQAGVQWR DLGSSDSP\LQPSRFKQFSCISLPSSW DYR/PC
10757	24658	A	10842	420	1	LERGNGTRDRRKGLSHCHQPMDSVLP PLCHPPPLVLTMEEEITMLFIDIGSSMY KAGFAG/DDASRAMFPSIVRCPWHHGVM VGMSQKDSYVGDEAQTKHSILTLKYP IKHDIIITNE\WDMMEKIWHHTFYNKLHVAP CI
10758	24659	A	10843	431	1	GEHSWASDLAEDVTKVTRGPLGLFWGL CSGNLSFSGCVPGLPAGAVPPWVPVFPQ GGA/SWVWKGPSPTLHLLLRTWGLAGG VGGRSLGRWRAWPGNPGSQGQGAAPAHQ ATGTPRSRTGSTGGIETVTILEGSHVSG MGIR
10759	24660	A	10844	55	297	QRWPGTLLGVQPG/APPDSTSASGSGGA RGGPVPTLEGNTGSRKWDPCWGSQNS PSSDGSKPPPGPLTSKVCDSDRLSE
10760	24661	A	10845	109	427	QTGPSAAGLLEFARGPLQTLFAWVPAAV AAEQQIFVNRECCCLIVLEFCLRGVPC CVRCQSA\LLGGASQLG\SRGSGVRDPL EGGSCPFSDLQLHAARTTALFTA
10761	24662	A	10846	17	416	SFLWKFCLEVPGRARCLSA\LLGGASQ LGYSQVDRDPLEEAVCPFSDLQLRAGR TTLEFKAVRQGHLSLQRIILPFVWQCP APIGGVYRDRQASLSCSGLHPIRA/SRA AVPTQASAMAGAPPPDSLPPCSLSSN
10762	24663	A	10847	265	429	LSGASCCFLSLPIVLFALLLSVLSFSF CAWCVPWSLSPTLFLTFVLHFL*RFIS CF*VNSNPKNLTFMVNPGGKMGKIGLAL ERICICGCSLVFPEAILETSCQNLFC TYACAGVLSSVYDYLALLAVSFLFL* FFSLFFFFLYLFLFALGASLPGLYLL LYFLLLCCISYSLF
10763	24664	A	10848	12	462	QTLGTRKMEGLFATFIAPTILGLPDALL IILFPPLLIPTS*YLINNRLIITQH*LV KLTSKQMITIHNTKGR*SLILISLII IIVTTNLLGLLPYSFTPTTQLSINL AMAIPL*AGAEVIGFRSKIKNALAH FLPQGTPTPLIPILVII
10764	24665	A	10849	2	462	TTLHAFGTMKREAFITLLCLFTSANSRG VYARDAHKSEAAHRIKDIAEKDFLALVL IAYAQYLQCCPFEDHVKL*NEVTEFAKT CVADESAETCDKSLHTLFGDSLCTVATL RETYGEMVDCCAKHEPVRYECFLQHWDD CPNLP*VVRPEVD

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10765	24666	A	10850	164	1	RGFQVRGE*NSGRETER*RERE*KLARE RAIGQEREREKSREAGRERERKKE
10766	24667	A	10851	417	100	MMLVVGNLETRLWSQAQTIPCTKQRSSL FFPVLNAAIFRSKSKVLNCLYFLGNTL FSWDLIPEILFPLSHYHHYHHHHNHQY *KS*QWSASNTRFQGILDKNSY
10767	24668	A	10852	339	3	ETTHSEARRGRSAAASCRGSALRRGRFP ESRRGREAAPVCPRHVL*GAQSKQAAV AGKRSGRTHASRWPKSLFPPRRRISLK RALHFWQQSADPSPSVSRIPPHGVGSS
10768	24669	A	10853	1	373	LQQKGMKRKAGQSEMAPAGVSLRATILC LLAWAGLAARDRMYLHPHFLVIHNEST* EQLTKANAGKPKDPTFIPAPIQAMTSPV DEEALQDQLVLVAAKLDTVDKLMAAMVT MLAIFLGFRIYG
10769	24670	A	10854	1	423	VSCSFLKLTMKHGLLLLCGFLLSQSG VNYTEEGFFRARGHRPLDKKREEAPSLR PAPPPITGGGYRARPAAATQKKVER* APDAGGCLHADPDLWV*SPTGCQLQAL LQLERPITNTVDELNNNVEADSQTSSSF L
10770	24671	A	10855	343	3	RGCEAHPLPRSEGPAGSALAQPVMYCTI FAGTLITAISSH*FFT*VGLEINMLAFI PVLTKKINPRSTEAAIKYFLTQATASII LVIAILFNNILSGQ*TLTNTTNQ*SSSI I
10771	24672	A	10856	147	1	TRTPTGQCVPKSMFLGAVAHSCNPITL GG*GRRIT*GPEFDPPLANMV
10772	24673	A	10859	189	422	NHTMDDFERRELIRHKREEMRLEAERI AYQRNDDDEEEAAR*RRRRARQERLRQK QEEESLGQVTDQVEVNAHNSVP
10773	24674	A	10860	90	273	SHQEIEQNSAMAPRKRGGRGISFMFYCL RNNDQRYMT*RL*SGIGWMLSSGRMGY ALPG
10774	24675	A	10861	25	411	APCAKPCGDWRSRGLVWAMSGCNARKG DCCSRRCGSHL*N*IPTDWPLN*FPLTS AKVKECFPKESIYSQTVY*SPG*KM*T *DKEHPRYLIP*LCIQFYHLCWVTGTGG GIILKHGDEIYIAPSGV
10775	24676	A	10862	33	302	SRRATLIYVDMENGEPGTRVVAKDGLKL SGSPSMLALNGRSQVSAPRFRGRTFNAPP SLPIATIRALGTVNRATEKFVKTNGPLR Q*QPRS
10776	24677	A	10863	1075	1521	YCHTGKGEQLGERFCEGVSRRGPAERGS DSQTPWPWPLCAAAGTSAGTSHSGSSSG AFSSWPCWTAAEPAARKRGRPAGSWSSP ATGAPGRCRHRILSRGAGGSAGFVCSGL AESGL*ESSSPGRSQG*PQGQRHPQPNG LPAPPSTSV
10777	24678	A	10864	245	418	TSKLAFPI SIPVIYANKVCP*FSKKKKK KKKKKKKKKKKKKKKKKKKKKKKKVVF FFEGPGFFF
10778	24679	A	10865	132	398	LNMGKGDPPKPRGKMASYAFFVQT*REE HKKKHPDASVNFSEFSKKCS*RWKTMSA KEKGKFEDMAKADKARYEREMKTYIPPK GETF
10779	24680	A	10866	115	455	LLTRNMDRLILLAGMPGLGQGPPTDAP AVDTAEHVYISYLALLKMLKHGRAGVPM

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						EVMGLMLGEFDDDDYTVRVIDVIAMPQS* TGVSAEAVDPVVIQAKMSDMLKQTKPEMD
10780	24681	A	10867	64	483	QGERPAAAMKI*SLTLLSFLLLAAHVLL VEGKKKVKKGLYIKVDSE*KDTLGNTHI KQKSRPGNKGKVFVTKDHTNCTWAVEQE EGISLKVECTQLDHEFSWAYAGNPTLCL KLTDEIVYWKPVARNLRLQNDIMIYSPQ
10781	24682	A	10869	229	1	DTTILKLGRLLIILQWLLSEGKSHMSFTL NQK*EIIKLSKECMSKAELSQKLGCFQ VGSQVMHAKEMLLKEIKSAT
10782	24683	A	10870	934	515	KKVLLCLPGLGCGGVILAHGSLALPGSS SLHLSLQSSWGLTGM*VDARLIFVYFPR EMGSCHICQAGLNSYNSSIPPTLVSQNV GTTGVSHRAQLAPVFCFCFVTLVDVKAL HFGKQENRIFFFFIIFPGSRDEDRVA
10783	24684	A	10871	373	424	EFKTNLANMG*CLKSQHLGRPRCANHMR LGVQNQLGQHGEIPFLK
10784	24685	A	10872	1	469	RSRSGDSLPAACDRPSGASALATCETIFS AISCFWDLPAAPSLRLTPSCQPTMSSQIR QNYSTDTEAAVNSLDNWYLQASYTYLCL GFYFDRDDVALEGVSQFFRELAEENREG YDRFLKMQRGRGRALFQDIMPAAEDD* GKTHNMTAAMGLET
10785	24686	A	10873	244	2	NIYSCKETFSVPLLAIHVHFLVGRGGS QGTEMLWHRVDLRYREQAGHSGSHL*SQ HFGSPRQVDQLRYGVSDQRGQHGE
10786	24687	A	10874	83	427	ISLNMIRIAALNASSTIDDDHE*SFTRH NTQTKEAQEAKAFALYH*ALDLQKHDI EESAKAYHELLEASLLREAVSSGDENEG LKHPGLILKYSTYKNLAQLASQREDLET AME
10787	24688	A	10875	94	1	KSQKACNPSTLGG*GGWIT*AQEFTTSL ANT
10788	24689	A	10876	2	413	GVTRGFNMRIEKCYFCSGPIYPGHGMMF VRNDCKVFRFCKSKCHKNFMMKRNPCVK RWTKAFRKAAGKELTVDNSFEFEKRRNE PIKYQLELWNKTIDAMNRVEEIKQKRQA KFIMNRL*KT*ELPKVQDIQEVQLN
10789	24690	A	10877	65	417	RFAGAGATPEARAWPTDVHAAEEEEKEMD LPDLASRVFCGRILSMVNTDDVNAIILV QKNMLDRFEKTLEMLLNFNNLASARLEQ MSERLLRHRTL*DMKPDLSGLFRPIRT LEWKL
10790	24691	A	10878	4	442	APTPDAMGHFTEEDKVTITGLWGKVNVE NAGRETLGRLLVDYPWTHRRFDSFGNLT SGSVIMGNPKVKAHGKNVLTSLGDAIKH LDDLKGTFA*LTELHCDKLDVDPENFKL LGNELETDMAIHFGQDFTPEVYAYLQNM VTVVAN
10791	24692	A	10880	1	419	GKHIRQYHEEKETGQRINIEHYLGNML AKNLLFEKEREAEKEKSYEIPTKNIQG QMTPIYPVGMGNGTPCS*KQNRPRSSTV MYICHPEKHEILSVAEVTTCYEAVIL TPLLCSPKYRFRASAVNDIFCQSLPG
10792	24693	A	10881	54	335	REIFTMSGALDVLQMNEDVLKNLAVIT HLCCTKTDSPEQIIYGS*TEYIYSIKL NRT*QNLMLAVP*NYDI*NHDEVMTVF

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						NNTLQMFEF
10793	24694	A	10882	216	3	MSIKSMSICCLRKKKGKHFQIRGK*NSG RETERERERERKRERERARGQERERQKT SEGGREERERERKKE
10794	24695	A	10883	3	390	GELKCSKEKCQSMSAKSRTIWIIGAPFL KGQPRGGVEEGPTVLKAGLLEKLEKEHE CDVNDYGDLPFADIPNDSAFRIVKNPRS VGKASEQLAGKVAEVKRS*ISLVLCVN LGGGLECLCGHAKVYSR
10795	24696	A	10884	3	375	STMRAWIFFLLCRAGRALAVPQQESLPD ETEVEETVAEVTDVSVGANPVQGEVGE FDDGA*ETE*DVVAENPCQNHCKHGKV CELDENNTLMVCQDPTSCPALIGEVEK VCSYDTLTFYSS
10796	24697	A	10885	95	2	KCTQGPSAVAHACNPNTGRGRGWIT*G QEF
10797	24698	A	10886	1	114	MGFHHVSQDGLDLVTL*GACFSLPKCWD YRREPTLHAH
10798	24699	A	10887	1	368	EPTMELTTAEKTNGKAAWRKVGAGAGEY GAEALERMFLEFPTT*TYFPHFDLSHGS AHVKGHCCKVADALTNVAHVDDMPNAL SALNYLHAHKLRDPVNFKLSSH*LLWT LSAHLHVEFT
10799	24700	A	10888	336	9	FRGQVIPALFFPFQTTLSYFQTGPQN* TPFFQKILKLTRGGGKLLDFQTPGRLRQ KREDPLFPGV*NCN*P*SHPWWGTKQNP VSKKKKKLKTSSIFVHRVSMSP
10800	24701	A	10889	3	362	GFLAPLEMQELGTPMNRILQLTAEQE TFLTPALLLPIPHQTYSTASAVPLAKPD T*PKDVGILALQVHFPAQYEDQTDLENY NNVKALKYTEDLGQTLMGFCSVQEDINS LCLTVEQP
10801	24702	A	10890	66	333	TLPGNIGISFVERVMEVLRPQLIRIDGR NYRKNPVQEQTQHEED*DFYQGSMEC ADEPCDAY*VEHTPQGFRTTLRAPS*LY TPIVG
10802	24703	A	10891	405	49	IPWMGTERTRASAQRDVAGPARNPACPL PEQCFPGPAEWGTPLTPPGSC*LRPGER ERHGPWCWGPRLSSGQTHPPSPQGC NTCPCHKHQELLAGGVAVFYKLFYRYG NSPKWDL
10803	24704	A	10892	2	197	PQPLRVLWTAHLAAMAPSSRTSLLLAF LICLPWLQKAGAVQTVPLCTLFVHAMLQ THRAHQVIDTYQELEETIIPKDHKYSF LHDSQTCL*FSDSIPTPSNMEETQQT SNL*LPDIPAPGFCPDLPALASKGWCRPNR SAMHAFLPRYAPNASRPTGH
10804	24705	A	10893	3	334	DQLPEPLKVLWTAHLAAMAPGSRTSLP PYALL*LPWLQEAQAVQTLFVSRLFDHA MLQAHRAHQLAIDTYHEFDETYIP*DHK *SFLHDSQTSFCLPDSIPTPSNMEET
10805	24706	A	10894	3	341	LLTPGVSDAICYILDSGYIIMSDTFTAY VIG*RFEVNG*HATVRFAAVVPVALPW LGV*WDNPERGTYDGTHEWTVYFKCRHS TGGFFIRSNNKVNLTDFVTADKNLYVLD Y
10806	24707	A	10895	25	351	AMIQTRDLQGGRAFGLLKAQQD*RLDEI CTQLLDDLKYSNDEDLPSRLEGFKKYM

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						EFDLIGNGHIDIMYLKMLYLKLAVPQTD LQLPRSTIGEVYSGSGETISYPDFLM
10807	24708	A	10896	364	38	FSQFKIAQFLKKIPFPGFSPFFQNGGNF LKFSKFFPNKRGFPPHFF*KRGPFFCP KWGPQGHIGAHGPPAPQGGKIPFPQVPK KMGIKGPTPPPGFFFFFFFFFFFSW
10808	24709	A	10897	136	3	STLKHR*RPGMVAHACNPSTLGRSGRI T*GQQFKTSLTNMVKP
10809	24710	A	10898	193	269	GNKYCLTILLLLLLLSFKRQSLTLLPTL ECSG*TRTPGPKGSSLLNPS*VAGHGGV CL*SQLRRLRWEDHLSPGV*GHSDPRL HHCTLTWATE*DSVS*KTTTTTTTK
10810	24711	A	10899	316	374	CCCCCCCC*CCCCCCCCCYKETNFE QQ
10811	24712	A	10900	38	206	VYCVLVFTICTLLCNTSLGLFHPEFFFF ETESCCVAQAGLQWHHC*SLRLLPHRII
10812	24713	A	10901	364	2	DYQHISPEKHCRPEGSGMVYLMCRKKK RKKKNLSTKILNPQPSFIL*KPRNSARK S*QKEITKIGADSLIENRKRKIEKIYIN ETMSWFIEILNKIDQPLARLTMIERKDS TKFRNERG
10813	24714	A	10902	132	3	ATSSPWGYSAVRVAILLFLYFSNKLAF VLYGFV*NYFLQEI
10814	24715	A	10903	234	352	NFCFFETGSCSVT*AGVIMAHCSLDLPG SSNSLTSVSEE
10815	24716	A	10904	250	356	TMEMMLDKKQI*AIFLF*FKTGDKAET TLNINNAL
10816	24717	A	10905	280	322	QT*SLILVSLIICIATTNLLGLLPYSFT PTTQLSINLAMAIP*L*AGAVVIGFRSKI KNALVLCSTPLPTSTMLPVHMDTSSD IHPKI*SIR*QTCIQHRLLLWLKC
10817	24718	A	10906	271	365	KWRPGVVAHTYNPSILGSRGGWIT*GQE FKT
10818	24719	A	10907	135	358	LRYKLTNPKLTLTCLGLIFLKGNIVNIG QCNGVHM*YQHFGRPQDCLSPGIQQQH GQHKESLSL*KSLKISWS
10819	24720	A	10908	107	212	IKNEGMGQVRWLMVPVLPALWEA*VGCTP EVSHSWL
10820	24721	A	10909	165	383	PKNRPFIPLKRSSISNPGDFQKSLRPG LTPMGPHFKRGNYSYDENLENLCPVGGNK GPGSH*GLLTCETCRGF
10821	24722	A	10910	119	291	GGYRFYVKDTF*K*GFWPLTLFIILKPL AGHGGACLSWRMLRLK*EDHLSLGGRG CSELWLCTLA*ATE*DPVS*KVRLALN FVYNTKTFPSRAWWCMPVVLATHEAEVGG SLESGRSRLQ
10822	24723	A	10911	283	2	SDNTTDTFLPFYKYIFPITWEQGETWK KNPRNSRLKKTLRSETIAQIPLKCNLWP GMVAHACNPYTLGD*GGWVT*GQEFETS LANMARPSC
10823	24724	A	10912	1	360	PHAFGTMKWVTFMSLLFFLSWANSRGGF RQNAKPKSEVAHRLKDWGKKNFKAWG*MA LAQNLKQGPFFENHGKLGKEVPEFAKPGV ADDAEAENGDKWLNLTLLGNYPVAAVRE TYGERAEC
10824	24725	A	10913	270	361	SKTWPGTVAQTCNPRTLGSQGGWIT*GQ EF
10825	24726	A	10914	157	1	VFFQLSRLAWKGFSRFFVFETESHVA

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						*AAVQWRDLGSLQAPPPGFTPFSS
10826	24727	A	10915	1	357	LEEWGPEREFAEEKEKNTKKKKIKNS TPPKKPARKGEEKPGPFKRAITTFVAR IPLFCLKGFLWPSC*IIGRSSPTPGSKG HTGAPNCPPCPLAAFPKDVFNPNKPMVE AVKNPIL
10827	24728	A	10916	102	471	PSTPIILTSSYPHYVKSSVTSTFIISLF PTTIFMCLYQEFIIISN*HLPTTQTTHLS LSFKLDYFLIIFILLTFLVTWSIIEFSL *YINSNPNINQFFKYLLIFLITILILLT ANNLFQLFIG
10828	24729	A	10917	2	138	REPTMVLSPADKTNVKAUVGKVGAGAG* YGAVVLFWTWLTNLNVIDS
10829	24730	A	10918	178	393	LVLCTVLLMWRFFHFDLSILKAQDVTE NLSNPTVLRGETGPSAVAHTSNPSTLGG *GKWITQGGQEFETSLA
10830	24731	A	10919	278	124	TAWADWGSNETPFLKLKPKKLT*GGGVC LEFQVLGRVRPKNPNFLNQGFN*PKFR PWTSTWGAQN*FV*KKKKKNKNKKP*NS RHTPPP
10831	24732	A	10920	221	243	IIIGSPLIDIKISKCFKLIVAFGQAQWP VIPALWEAEAGRSPEVGSPPA*PGSLK VHVDNNWESIN
10832	24733	A	10921	33	292	GTMWLEIRHAVEVQCVLVSELVIPTSGD KPBQC*DHYLIT*YLILGKWI**ISGA LEKKKKKKKKKKKKKKKKKKKKIKITGG FI
10833	24734	A	10922	108	3	KLAVYGSVCL*SQLLGLRL*EDHLNLGH GGCSEP
10834	24735	A	10923	106	2	KLAVYGSVCL*SQLLGLRL*EDHLNLGH GGCSEP
10835	24736	A	10924	195	2	ASLFKSQNLNRAFIYLFYVFIFETGSL* PMLVCSGVITAHCNLHVLGSGDPPTSAS QVAETMVL
10836	24737	A	10925	127	2	YVCILKNLKGKPGMVAYACNPSTLGGQG GWIT*GQEFKTSL
10837	24738	A	10926	639	282	FFLSIRGWVQQFMPIIPTPWGLKQEDHL RPGLRDQPVQNSKTPSLKI*KLARRGG ACL*SQLFRKPR*ENCLSTGELKPKGGI FIRLVQNKIPTTRGEKQKQSHTGSYQCP KIKKKG
10838	24739	A	10927	1	363	ALLTQALTCRQAGAEAPHAGATPSLMPP SLPQGFDRDCSPSDAAYTMENTIDKKQNG VILFKFKMGHKAQTRNINNAFGPEI ANKGTVQWRFKNFCKRDESREDDE*YAQ PSKVATDQL
10839	24740	A	10928	53	379	TEAELLTLYLLPNALLNHFTSPPLMFAD RRLFCTNHIDIGTLYLLFGA*AVVLGTA LSLLIRAELCQPGNLLCNDHIYNVIVTA HAFVIIFFIGLPIIIGFGN*LFPL
10840	24741	A	10929	180	350	EPMAKGKTESPGPKRCGP*I*WVISQRG TLRFRGAGLEFFMGEFLRLGENLLEIPRG A
10841	24742	A	10930	361	379	RRYWWLG*VQWLMPVIPALWEAKAGRSP KARNL
10842	24743	A	10931	121	543	HRNTGSTHASAHAYHIVHTNP*PLTGAL SALLMTSSLAMGIHFHSITLLILGLLTN TLTIYH*WRDVTRESTYQGHHTPPVQKG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LQYGIILYIT**VFFFFAGFF*AFYHSIL SPTPQLGGHWSPTGITPINPLKDPLLNT S
10843	24744	A	10932	227	339	VGGVKSQVQLLLNCHFSSR*MKKKKKKKKK KKKKKKKKKKKK
10844	24745	A	10933	64	409	DQRNKS AHLRAHLK KKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKRGEL*KKIN WAFFLPLLKRKFVGENFLKKNFFWGGNI GGQISSKKYRGGGK
10845	24746	A	10934	2	362	NKLSGPYPPEKVGVTLPVLMNPLAQLVIY STIFAGTLITALSSH*FFT*VGLEIDML AFIPVLTKKINPRSTEA AIKYFLTQATA SIILLIAILFNNILSGQ*TITSTTSQYS SLIILRAM
10846	24747	A	10935	154	3	GCPLSPLEFNIVVKVLVRAVMQEKEIKS IQIGLEVK*SLTDNMILYLGN
10847	24748	A	10936	250	363	TAWPGYLYSFSFLY*ETTKIWLGA VAHA CDPSTLGGGR
10848	24749	A	10937	199	339	NVLGILLVFRIIVEIYKCGRLWLGTVAH TCNPSTLGCQRGQTT*GRE
10849	24750	A	10938	130	240	KNEQDPRDL*DNDKWPNIHIGVPPEEDK DNGTERVFD
10850	24751	A	10939	35	235	FILVENTKKMCICPLLNMIIYAILYLFVP SVFL*EENKQ*GITEKKKKKKKKKKKKK KKKKKKKKIKPGGL
10851	24752	A	10940	179	12	DQPGQHNTLSLQENKNKSSWVQCCV*P QLLGLRLWEDCLSPGGRSC EPCSHSG
10852	24753	A	10941	297	278	INQDNELT LINQSSKQIKHKINQTLRT KMNENLFA*IIAATILGLSATVQIILFP PILIPSTSKYLINNRLITTQ*L IKLTSK QMITIHNTKGRT*SLGGD
10853	24754	A	10942	3	318	FGGGRGVNRYPDAFVLSVLLPSRLLFPH LFPHLFPLPPFLGLAPYCFRTL*YF*K* *LYYSQSIIFFFYREMNKLLVFWAINL FFLYYYNYMEMWT LICYWK
10854	24755	A	10943	190	3	KLSHKQSVYFKTPFI*KNHVLFK*KNLW VYPNDKFFFFFFESLALSRLQCNGTIL AHCNLR
10855	24756	A	10944	281	1	KKWLFSSSYSSLYGNGLFLIPPFLRVSGF GKGFWKKFFFLRARGALFWGSP LKGFPL GFFWVFFFF*DGVSLLLPRLECNGIISA HCNLRFP GS
10856	24757	A	10945	169	319	NGVEDAFKNMVLGWAQWVTSVIPALWEV KVGGSPEVRSFRPTRPI*KYGFRLGTVG YICNPSTLGGQGRIT*GQEFQTNPANM VKPC
10857	24758	A	10946	312	1	FARPGLLKS WDFQP*PLDPVWGGFFKRF PENWLEFEIFPFLII MAKRKLSKSLFP FPFLG*FKD*GQKTPFFFTVSLLLPK LECNGAISAHCNLC L PGSSD
10858	24759	A	10947	208	329	IFTGDRSRNNRTG*ARWLTPVIPSLWEA EAGGSLEPKSLR
10859	24760	A	10948	116	374	FYFGYLLFFFCFFEMAPCSRG*SWSARG QSFCNLI FPGSSDLYVSAFRVARITGAR DHACIIIVFVDGGCVDTTITSGLAGWL RG
10860	24761	A	10949	264	434	QLAFCTDTLTSVREQCEQL*KCVKARKR IELCDEQ*SCRSHTD*CTDELDFDLHA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10861	24762	A	10950	226	429	T NFGFRLDKTVFFSKIRINAWAQWFMPVM PELWEAKAGGIT*AQELETSLSNIVRPW LYKKFKN*VWWC
10862	24763	A	10951	188	433	YSAEWKIDLGIEVFWVGKMTYKQ*FFWF VFKFLFF*RQGRTLSSKLEWMSVITGHC NLDLLGSRETFASAFQVTWTIGSCHS
10863	24764	A	10952	298	445	LFSKCSSKSIKEEGPGVVAHACKPGTLG GRGGWIT*GSEFESSLANMVK
10864	24765	A	10953	244	1	KTPQGLVVFCLFKKSPKLGKGVSMGVL ICFFLKSRINLNFNPRGLGQRKNFFFF ETDSYSVAQTGVQ*HNLGSLQPPSC
10865	24766	A	10954	199	3	QETKKEQNKENKQIK*STRKKHRQGTN KTKERGERQTPPVGNRQPTPLGIHARPR RRATTSPRA
10866	24767	A	10955	157	3	YSYTFSTFIITTSILIIQTLSGHGGACI* SQLLGRRLRQDNHLNLEHGGCTRA
10867	24768	A	10956	263	357	GLSLKVLQTQWLGAHAHACNPSTLGGRGG *IT
10868	24769	A	10957	333	2	KWKADMLIPLVIKSFFLGIFFKMFTNSK RYIFLLQLLAQHSSFFSFIRCMEL*WPY PIPLCYGQSNQPSV*LAYCRDLFNELIF FFFFETEFHSCCPGGISAYCNLCLSC
10869	24770	A	10958	130	228	GSSFLGGSPPSVAQAGVHLPDHGSLO*DK SPSVQKMSKWIGCSGACI*SQLLRRLRC QGRISP*GQACSEP*SGRCTPAWATEGD PPKLLPYTTDS
10870	24771	A	10959	250	3	VQACISITGALYQRRNAEDPQTARPISG FTTSIAMRLMLLTCSGHIWVPVADLAFSG IMP*GLFFPSRQNLALSPRLECSARA
10871	24772	A	10960	199	326	VLGRMWSNQKNYTLARM*KIK**NNTR CWGGCGATRRIHC*QECRI*KCQPQSL WRTV*QFLNTLNIR
10872	24773	A	10961	323	3	LLFFHLPDNWQH*YVFCHYNLSFLQFYI N*IIQLVVFVWLLSMSIILKSHPCFHS K*LSTVTFFFRQSRVSRLWSGAISAH CNLCLPDSSDSCASAS*VAGSC
10873	24774	A	10963	120	3	PPFFFFFF*EMRSCFVAQARVQ*CDQSSL *PSTPGLKQSSC
10874	24775	A	10964	168	441	LTPVIPALWEAEAGRSPEVRSSR*SPP
10875	24776	A	10965	19	207	APLKLNVAMELSLGQWDVSRSNLWEIPL KKGDTGRVQWLTPVIPALWEAEVDRTPE VTSVTRC*PLKLNVAMELSLGQWDVSR NLWEIPLKKGDTGRVQWLTPVIPALWEA EVDRTPEVTSVTRC
10876	24777	A	10966	209	1	TKSALSNMVVTTHIGLCKNFCIVL*DRV SVTQIGVQWHDLSLQSLSPRLKDPPTS ASRVAGITGMHLV
10877	24778	A	10967	109	1	DYLRSGV*DQPQGHGKTSSLLKIQKLAR LVGPIISC
10878	24779	A	10968	141	2	GLAMLPRLENIIFRPGTVAHACNPNTLG GRGGQIT*GQEFKTSLSLSC
10879	24780	A	10969	175	348	LVYECKHLLCVFNTSLFFPH*TCYK*RG VLWLGEVAHACSPGTLGGRGGWIMASGD RD
10880	24781	A	10970	108	2	KTKKLHMRSGVVAHTCNPSTLGG*GGWI T*GQDSC
10881	24782	A	10971	184	2	SFLWKHLRGVPGRVRCQSAPTRGASQL



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GYLGVRDPLEEAV*LFSDLKLCAGKTTT LFLV
10882	24783	A	10972	245	339	SQISGPGTVAHACNPSTILGGRGEWIT*G QEF
10883	24784	A	10973	295	340	KRVFF*ARKKNPFLSPLWGLTLENPLGF RLFNLNPFGLKISQFFFPRI*PLAFFF WGTLPRLNLKFGPFFFFFFFFFFFF*DG VSFCCPGWSQARRYIEINISLSTCPRA
10884	24785	A	10974	186	340	RPYLTIIRFKGHPPNEPIQ*SFFVLFICYC FDTESRSVTRLECSGSNSAHCNL
10885	24786	A	10975	253	491	FLECTSLKKRQRVHPGQHSKAPPTKELQ TTGRGGALLQSHLLRRLRQEHCLGPGVG SYSEP*LHCTPAWVIEGDSSKK
10886	24787	A	10976	141	1	SFSFFKFSPPTGDMIGFF*HFFFFLRRSH SVAQAGVQWCHLSSLKPRA
10887	24788	A	10977	3	138	HEETGFHLVSQDGLNLLTS*STHLGLPE CWDYRREPPPGREGDF
10888	24789	A	10978	186	323	YESRSATQAGVQWCELGSL*PSTSRFQ* FFCNLNSTWDYSGLAPS
10889	24790	A	10979	183	3	IKILFPFFFLRLSLALLRLECSGTFS AHCNLCLLGSSDSAS*VAGITGTTTSPM QLV
10890	24791	A	10980	309	55	KNFGPNWVKFLGGKGGEMAFLGKFFFPF FFFFEKESWVFQ*MQWGDFRSLQGP PGVTQISRLGKIGGPLFKKKKKRERGN M
10891	24792	A	10981	637	838	SQHLGRPMRVDQLRPGV*DQPGQH GEMP SLLRIQR*AGHGGTHL*SQVLRVRQDN CLNSGGGGCSE
10892	24793	A	10982	275	2	RNRTLKMEFLSWFWGFWNWLLNMIRPKN VKDSTSKSMENDTSPWHELFKELGKINA FDTPDLSLVRGKFSDSIHNTFDHM*RTK EYNEARA
10893	24794	A	10983	98	346	GHGHATLRGLCVLTFSEHITALSVSGTN DAEDCCLCETQKPCGYIERNLLYLLIK DVCRVPAVV*VVERVYSLISRYSLWRD
10894	24795	A	10984	30	410	LPEFTGRPKRTRTRGFSTNHTDIGTLYL LFGA*AGVVGTAVALLIRAEALGQPNLL GNDHMYNAIVTAHAFELIFFIVLPIIG GFGN*LVPLIIGAPDMAFPRINNICE*L LPPSLLLLLASAIAE
10895	24796	A	10985	141	360	QTLRTKMENLNFASFIAPTILGLPAAVL IILFPPLIPTSKYLINNRLITTQQ*LI KLTSKQMITIHNTKGRT
10896	24797	A	10986	3	347	HELRTKVNHELIASFMGPTSLGLPAALL IIL*PPLIPTSKYLISNRLITTQQ*LI KLTSNQMITIHNTKGRT*SLILESII I IATTNLLGLLPYSFTPTTQLSINLAMAI PL
10897	24798	A	10987	46	317	KSMTPIRKINPLIKLINHSLIDLPTPSN ISA**NFGSLLGACLILQITTGLFLAMH YSPDA*TAFSSIAHITRDVNYG*IIRYL HANGAS
10898	24799	A	10988	245	1	VSCLEGLKLTNRKDIHTKNPSVHHHHQR PKVDKTKMGKKQNRKTGNSKKQTASPP PKK*SSSPATEQSWMENDFDELREE
10899	24800	A	10989	255	1	SCLPWANWISVQNHKKTFLVIRTFPI GSFHVT*LLGPPLILISPPRIFFFFETG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SFTVARAGVHSGAISARCNLRLGSSNSA
10900	24801	A	10990	166	307	GEKPGWGLIWGGLVGRSSWASCQVLELL*EMVFRHVAQAGLKLLSSSNPPASASQSAGITGVSH
10901	24802	A	10991	109	330	TNQFKTKKEREAGKKKVKELERERERGRK KRKEQRKNEKERR*P*NMD*RRIRERNH SFDVYEFLICGLLNLLHV
10902	24803	A	10992	244	326	GRYLKGWLDGPA*AVVLGTALSLLIRPE LGHPAILLGDIDLISSVIVTAHAWSIILV RVIPIIIIAGFGN*LVPLIIGAPDMAFPR INSISF*LLPPSLLLLLPPPI*QMRAGV GEREVVR
10903	24804	A	10993	101	2	KTFWARFVGTCL*SQLRRPRQEDHLRL GGRGC
10904	24805	A	10994	177	1	TPSLLFFVNIICFCLNPGGGCYSEQKLC LCTPAWVTE*NSISRPSQNNRQSRQVN HLF
10905	24806	A	10995	214	326	KEERKNPRAIRVV*PWGFFFPFLKEISL FLFVFRFWHGYPFGAFFSTQKWLVF*T MVLFFFFFF*VSLLPRLECSGVISAHCN TFLPGSSDC
10906	24807	A	10996	184	379	LCCMVYHFPSSILLLYL*CKLFFSPKLEF SSCCPLECNGTVLAHRSRLPASGDSPT SASRVAGHGGTCL
10907	24808	A	10997	136	3	GRVDGQHIMTHQSHAYHIVKPS*PLTG ALSALLMTSGLAM*FH
10908	24809	A	10998	274	363	PWAYAEPLTLHDATYST*SLIRASFTL FIA*TTLRLLP*SFTPTQLCMNLAMA IPL*AVAPDIGYSSMITNALSHLLPQCT PTPLISILGIETVSLLIQIPITLGVRR TANIT*CHLLMHLIGSATLSISTI
10909	24810	A	10999	305	1	NLHTTPSQIPLT*PLPNINIHNLHLLTTT Q*IKYLILIPSNLPHNKNLKTAYSVPP SPNLHLPSSSNPASASQVAGNAGARHY AWLIFVFLVETGYSLV
10910	24811	A	11000	154	2	IVVGILQSRRCGR*SQHFGRPRQADC FTPGVPDQYFTLLPEVVFFLV
10911	24812	A	11001	142	367	GVCLYQRISYIKKTKKLSQGLFYFLLL LLLF*EGGSHSVTKLECSGGVSAHCNLC LLASSHPPTSSSQVAGTTG
10912	24813	A	11002	60	385	GNTLLSHTLRAHLIENLHAEFIDRTILG LPAA*LIILFPLLIPTF*YLINIRLMA NRH*LIKLTSEMITIRNSIGRT*SIIL VSLIITATANLLGLLPYSITRTT
10913	24814	A	11003	214	83	SKKSASPLTFNIVFQVLNDSVREERTRY TEMEKEEIKLS*FVD
10914	24815	A	11004	241	368	SYLL*PSP*PLTGALSALLMTSGLPMRF HFHSITLLILGLLTNTLTIIYQ*WRDVTR ESTYQGHHTPPVQKGLRYGIILFITLEV FFARFF*AFYHYSLAPTQL*GHWPLT GINPLNA
10915	24816	A	11005	3	396	HEPHALGMPLTADLPSMASCSTSLLLL LHLHLPLWI*EARAYQAACSKLFDHAM LQAHRAHQLTIDTYQEVEETYIPEDHKY SFLHDFQTSFCFSDSIPTPSNTEETYQK SNLELLRISLLLIESWLEP
10916	24817	A	11006	156	335	FGCCCCFLFF*LVYCCYVMMLYIYVLI

1213

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10933	24834	A	11023	180	353	IFCFCIFSRDGVSVCPGWSQSPELMIH *NTKIS*AWQRPVKIPATQEAEGESLE PG
10934	24835	A	11024	155	1	PQARRGGTCLQS*LLRRLRLRQEDRLSP GV*GYSEL*SCPCTPAWETERLV
10935	24836	A	11025	22	325	KLILLYDPQLTFIFLNTRAVVAHCAFCC WPIHFVFGNYGFVFSCLFTFIFVYSGKA DLFFKPKKKKKKKKKKKKK*KKGG RGLKNSWGGPIFWGFPK
10936	24837	A	11027	127	259	GQVQWLTPIPTLWEAMVGGSTKLRSR PFFSTP*PCIVMILYG
10937	24838	A	11028	37	408	IASGALFFFKAAGKRDFKTEGAYQRO RTIFKNKKRARREKTGRNLRGNYKNMG RGLKTPRGALGGPYLDKKGPLRGKGPFO GGTLLGGGPKIKIQGTL*IRRNYWPYIR RYNRFKKRQKNM
10938	24839	A	11029	146	3	LLVLKDLPRIMVRSAPTYIYIYTYLYIY IYIYTHTHTHFIT*VLFC
10939	24840	A	11030	268	435	LMCLRNETHN*F*KVE*WLGAGAHTCNPK TLGG*GGRIA*GQEFETRLRNIVRP
10940	24841	A	11031	322	2	KLPHLQQQCVKVCYKPFLLKNGKIGHGG VCL*SQPLRRLRQENHSNPGQCTSAWVT QRDSVSKNKKKKRMEKYFSSVRQNKPVK HTKRMSPTKADTKSTHCGGGRV
10941	24842	A	11032	251	380	HKRLHTIYFVPLKKMGPGLVGHTYNP STLGGQGGQIT*GRE
10942	24843	A	11033	64	324	FWFFFFFFFFFLNPPGGGKKKKKPPPL GKKKKRKGKGGKKFFSPPPRGGGGPKK ISLKRVLKFF*NPPGGTKKGGGPFLLPP GSP
10943	24844	A	11034	420	534	CPGVVAHAYNPSTLGS*GRQITIDREIE TILANMAKPH
10944	24845	A	11035	196	1	KNGHSLPPGPQKGTTPFKKKKTPKINLS ELGKSKAYSWPGTVVHACNPSTLGG*GG WIN*GQEFE
10945	24846	A	11036	10	248	PSDR*LFSTNHKDIGTLYLLFGA*AGVL GTALSLIRAE LGQPGNLLGN DHIYNVI VTAHAFVIF
10946	24847	A	11037	32	405	DYVSKRKEKREKRNIVLETSSISHLVE WMLCSRYHPLIKKRSSVRILIALCPQK VRDMS*GIGSKKQWDSWLSIWIKMESD PFLIPYPKINA*RLKDL CERINLKIIK REYLHDYRVKKV
10947	24848	A	11038	337	448	KNPRGFFGKNPFFWGGPFGGPPPKKMG FGEKKKF*FKRSKKKKKKKKKKKKKK KKKTG
10948	24849	A	11039	307	415	RFVCSTIKVLRDLSSDRSNPGRVLSTSN SSLK*KKK
10949	24850	A	11040	213	403	VHRGIKYFLNKLDPDFPQTFKK*G*RL GAVAHACDPSTLGG*GGWITLQGTFETS LTRMGKS
10950	24851	A	11041	104	2	SAFFF*ETESCSVAQAGVQWCDLSSLQL PPPGFK
10951	24852	A	11042	177	3	AYTAYICVCIHIYLYK*MYICINHVCK ITYLYIYKYLKYNALYLHIGFFSFLHTI S
10952	24853	A	11043	314	395	TVYILNLSINSVQSVLLSVFHLRLHQPR GRVQWLTPIPALWEAQAGGSP*VRISQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IKTPA
10953	24854	A	11044	310	403	RGKGGKKPRNPGGGKS*ALTKKKKKKKKKKKKKKKKPGGALKKKPRGGQKKTGGGKKKFLPKRGAKKKPPGDFGKKNQIGGGEKRGKTPPKKKKKP*GKKKNLKGKGGKKTpkSGGGKKFPFPRVV*KKKLPPGG
10954	24855	A	11046	181	3	EGPLSLSLLEFFFF*RQISLLLRLLKYSGTIIAHCSFKFPSSRNPPTSASQAASTTG VHH
10955	24856	A	11047	392	41	KESRSLSQGGREKGPFFKFLAPPAPKFKRIFRPHPLKKGPKGPPSPS*ILSLKKKGGPPILARWFNNSCPQGFPPPGPPKRLGFKGGPPPPPLF*KKKPPFLGGENQVKNF FFFF
10956	24857	A	11048	147	307	TVIFVFLLRKGLTLLPRLESGMTMAHLKS*PPGLKQSSCHSLSSWDYRRRRRG
10957	24858	A	11049	118	1	HGKIPSPLO*HK*TAGYGSACLQSQLLRLRWESRSISI
10958	24859	A	11050	54	284	RKIRRGGLHLWSNLLGRRLRWEDLLGRRLWEDRLSPRRGGCSEPLCHCPPAWATE*DPVSKKKKSLFVEKPGGG
10959	24860	A	11051	130	340	HNMHFAAHGSRINFDFFFFFFFFPERGFPFCPPVGRAGTHFGLLEPFPSRV*KQYYWLGTVAHVCNPSTLGGHVGES*GQEFKISLANIVK
10960	24861	A	11052	140	337	NIIMFFFFFFETVSFLLGLLEGKGTIWN*NLCLPG*GDSPLGCS
10961	24862	A	11053	197	428	IRSINNPTVASQYSSEWKSHIPLILNQNLDMIKFSEEGMLKAKIGLLRQTGVQVVNAKEKFLKKNQSATPLSI*IRK
10962	24863	A	11055	180	1	ATIALYSRLGDYARRFHLRRKKEQWQGMVTHVYNPSTLGGQGGRTA*TQEFKSSLG NIA
10963	24864	A	11056	158	426	FFPLPLPLPTVSLFPRSPSDAEPKLDCTAAISAHCNLP*FSCLSLPSACNCRRAPPRLTASASRGAGIADGVSTQCSMVPRLECSGV
10964	24865	A	11057	220	421	YALHLNMKNNSYF*MRKKKKKKKKKKKKKKKKKKKKQNKKDPGGA VYKKIP
10965	24866	A	11058	162	464	SCSVGLKLFMSKTSLSLSYYCLLLLLTLHYYYYYYYYY*SLVFM
10966	24867	A	11059	1	134	APENRVDPRVRKTLVPLILPITITLANPCKKD*YPYVKISIAIC
10967	24868	A	11060	382	273	SSCL*PQLRLRLRQEDYLS*GA*GCNEL**CHCSPA WTEQDPVSKNIHTYIHSQSINYGSMIGYIHEQKGIADHKPIIAEPE DSTYPRDHT
10968	24869	A	11061	298	378	SCSASPCSSRHGWSFCG*QTCLLLAIALRCLPWLREAGALHTGPGCRLFDHAMLQAHKAHQLVIDTYQEIGENYIPDQKNSFLLESHTSFCSDSITTPSNMEETQQKSNLKLRLISLLLIETWLEPVRFLTRIVANN
10969	24870	A	11062	39	486	RPTRPDAYHIVKPS*PLTGALSALLMTSGLGMRFFHFSITLLILGLLTLNLTIIYQ*WRDVTRESTYQGHHTPPGQGLQYRIMLFITSEVFFFAGFF*AFYHSSLAPTQQLGGHWPTGITPLNPLEVPLNLTFGILAI GGSIT*AAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10970	24871	A	11063	269	429	ATWQKLP LQIQKNYPGLGLVAHACNPST LGGQGGRI T*GQEF LNQPANMVNTH
10971	24872	A	11064	248	65	IIEGQAQWLMVPV I PALWKA EAGGSPEVG SSKPA*PCDEPASASQ SAGITGVSHRTQ LILNS
10972	24873	A	11065	176	1	LFPPPKKVPPWGNTQFKSICLYTTNFFF FETESRSVARLECRGTISPHCKF*LPGS RE
10973	24874	A	11066	2	397	MVLWTAHLRAMAPGSRTWGLLT FALLCL PWLQEAGAVQTVPI SRLCDHAMLQAHRA HQLAIDTYQEFKETYIPKDHKYSLLNDS QTSFCDSDSIPTPYNMEETQOKTNLEVL RMSLLEIDS*LRPAQSNKR
10974	24875	A	11067	172	399	QILYL*KYAYTVTMQHL SHPIL*KKKKK KKKKKKKKKKKKKKKKKKKKKTGG
10975	24876	A	11068	192	3	PKLTPMLKLIVPHI ILLPLT*LSKKHII *INTTTHSIIISIIPLLEFFNQITSNLFS CSPTFC
10976	24877	A	11069	204	345	DKSGEHSKTSSIQKNLRLGAVTHTCNPR TLGGQGRWTT*SQEFQTSF
10977	24878	A	11070	3	416	HELPQPLRVLWTAHLGATAAGSRTSLLL DFALLCLPWVQEDGAGQTVP*SRLFDA MLQAHRSRLGIDTYQEVVETIYPEDRK LSFPDDCHTYFCF*HSIPTPSHLGETLL TSNLELLRLICLVLIDSWLEPARILTS
10978	24879	A	11071	108	2	PSPFFFETESCSVT*AGVLWRDLCSLQA PLPGSSC
10979	24880	A	11072	400	278	KVK*LRQENQWNSRGRDCSEPRSRHGTL PWTTEQDSIPKNKTKPKYKIS
10980	24881	A	11073	139	3	KLACCGRAHLSFQLLRRLRREDHLSFGG *GYSEPWSRYCTPASRA
10981	24882	A	11074	17	421	DHVGQPRWLMVPVILALWEAEPGGLLEP KVQDQPGQNCKSLSLLTIKKKRRENFPG RGGTQLCSQLRRLRVGCCIDPKLHNCL PAWMTERDPTFKRE*KNNDVLEAKNFFT ILTFMNTTKEKMVAQRIGSLFHG
10982	24883	A	11075	412	1	QFFFLGVCCPTQIFGVGKKGEKKKKRG FPPRVFFFNPQIFSPFFFGPFFFLGK FPPFFGERFLFFSKSKFFPGVFKRGFP FPPKNFFFF*RIF*KWFSPPKPFFFFF FFF*DRASLCHPGWSTVAQS*LTSC
10983	24884	A	11076	279	410	VFCCVAGRDGAPGVKAHFFAAQKPWDGG FPGP*SAGVGPPPIPR
10984	24885	A	11077	12	386	IAHLLLSFYHKDTGTLYLLFGAGAGVL STALSLLIRAE LGQPGILVGNNDHIY NVI VTAHAFGIIFIIPIIIGCYGN*LATL IIGAPDMAFPRINNISFGLLPTSLLLLL AYAIVDAGARTGW
10985	24886	A	11078	412	3	LATLSLSLSLGFPPYSLRYKNIKIRPINN PTMASKCSSKRKTRTSFTLNQNL EMLKL IEKSTAKAKRLKVRPLVPVSQVVNAEEK FLKEIKSAIPLNIQ MIR*QTS LIADMEK VSVL*IKDPTSYNIPLSQS*IHSK
10986	24887	A	11079	78	443	RHRLPSDTCLTAAPV*PCKGSKKKKKKK KKKKKKKKKKKKKKKKKKKKGGGFKKNS GGGQNFAGGKKIFFFFGGGVFKNPLWIF WKKTFWGGKISGQLSQKLSLWGEKKI FWGCGGETSF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10987	24888	A	11080	395	2	KRVPKKKPKKNSPPGGRKGGSP*SPPF GGPDQPIF*VGGFDPPWLTPEPFFFKK KNN*PGKGMPLILKSLGCGWKKKIFTP GGGLPKN*KETPPPPPGGKKKIPFPKKK KKKKKRAAADLELVPTRP
10988	24889	A	11081	24	182	TVSTTKCFSLIPYYGRKDM*KI*IIQ KKKKKKKKKKKKKKKKKKKKKKRGG PP
10989	24890	A	11082	173	3	NNVICYILYIPSVPKYKTTLNMRGSAFF FFFFFI*DGVSILCHLGSAAVARSWLTA
10990	24891	A	11083	284	391	SVAHACNPGLGG*GEQITRGWETFSL TNMEKARL
10991	24892	A	11084	257	3	TKKLREVNMLGWLYYMREEARPVDYVHW RGPEYSSLTKTIRNVIVKGHQHY*KASA GRGGSRL*SQHFGRRPRADYKSGVDRDQ
10992	24893	A	11085	42	171	ARRMRAGIHRVSQEGDLLTS*SAHLGL PKCWEDRRREPLRLA
10993	24894	A	11086	176	325	FKRSKKKKKKKKKKKKKKKKRGGAL LKKF*FKRSKKKKKKKKKKKKKKKKK RGGALLKKFLGGPQISGGGKRFFFFFF
10994	24895	A	11087	67	379	KKKKKKKKPKTKKRTGPVRQNVWRGSL SEGRAPAEGPQGGSTESPLLVGRCIL GLREPGVPPAAYGRFLRDYMNISIQKLE KQRQP*GLPSLTGAELIKH
10995	24896	A	11088	128	326	KKKSGGGVFFFTIGGGGHFFGGGRFFFF FFLGGFFFLKFFFF*EKFFFLGGNLVKH SSKKSSWVGW
10996	24897	A	11089	109	2	KTHSRPGTVAHTCNLSTLGGQGEWIT*G QEFETSL
10997	24898	A	11090	52	347	DHSLLELQMKLYASAQAATTKCHRMGGL NNTFLFLFLSLFFFFLKQSLALPRLK GRGPILVN*KLPLRGKRDSPPSPQCVG ITGLAHPRLILFF
10998	24899	A	11091	386	48	IHLQPPLQICTLKFFTNKNPHLFTGCP KYALIFLCFALVKTFGHHVQAGLQIV PLCPDRLGLPKCSD*RREPPHPAKKQFF IDRVMLCYPGWCPALGINPSSPVGLPKR
10999	24900	A	11092	164	3	VYSLLLRCPPS*ALTAKFINRCTYIHVC MYMCEPYAYTCLYTSTHIVCMYIY
11000	24901	A	11093	148	325	CLKLQPFGLGVVAHACNPSTYFISYQ*L SPVIPALWEAKTGGSPVSRSPARP
11001	24902	A	11094	162	3	LLGLKRP*IFFFWGGKFFFFFFFEIES PSVAQAGVQW*CNLGSQPASGRV
11002	24903	A	11095	259	358	LRPGTVADTCN*GQARWLIPVIPALWEA KAGGSLEVGSRLAWP
11003	24904	A	11096	254	2	SWGFIPEERERENRYWDRQQGHAI VSN IVINAFLYRYTEREKPGVSLSPRVECSG MIVAHCNLSLVGSSHSAAAS*VAGTTG
11004	24905	A	11097	132	3	KKKKRQPRVVAHACNPSTLGGCGGWIT* GQKFRTSLVMVKP
11005	24906	A	11098	2	455	LNLEQLIEPLEVLWTAHLEALDPSSRTF VLLAFALL*LPWLQEAGAVQTVPLSRFL DHAMLAHRAHQLAIDTYQEFETYIP* DQKYSFLHDSQTYFCFSDSITTPYSMBE TOOKSNLELLRIYLLLESWLEPVQFLM SMFGNNLEYDT
11006	24907	A	11099	2	375	QLPEPLMDLWTGDLVAMAPGSRSTSLLA FVLLWLP*LQEAGAGQTVPVSRFLDHAM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LQAHHRAHHLAIDTYQEFETYIPKDQKY SLLHDSQTSF*FSDYIPTFCSMEETQQK SNVELLRICLLV
11007	24908	A	11100	1	359	LQLPKPLTLVLTGTAHLPMCLAYATALIL GCALLCLA*VE*ARAAQTVPSNF*DHA MLQAHHRAHQLAIDTYHEFEETYIPQDQK YSFLHDYQTSFCLSYSIATPSNMEETQQ KSNLELL
11008	24909	A	11101	1	370	LPEPLTDLWTAHLVPMAPGSRSTSLLLAF ALLCLPWLQQAGADQTV*SWLFDRAHL QAHHRAHQLAIRTYQEFETYIPKDQKDS FLHDSQTSFCF*DSIATPSNMGETPQKS NLELLPISLLL
11009	24910	A	11102	2	361	AHLLAMAPGYRTYLLLAFAILLCLPWLQE AGAVQTV*SRFLDHAMLQAHHRAHQLAI DITYQEFETYIPKDQKYSFLHDSQTSFC FSDSITTPCNMEETQQKSNL*LIRICLL LNEWMEP
11010	24911	A	11103	8	366	PLRALWTAHLAARAPGSRSTSLLLAIAL CLPWLQEAGA*QTVPISRLLDHAMLQA RAHQLPIDTYHEFEKTYIPKDKHHSFLH DSQTSFCF*DSIATPSNMDETQQKSNLE LLRIFLL
11011	24912	A	11104	3	341	EPLRDLRTAHLVAMAPGSRTYMLLAFAL LCLPWL*EAGAAQTAPLFRFLDHAMLQA HRAHQLYIDTYQEFETYIPQDQKYSFL HDSQTSFCFSDSISTPCNMEETHQRSNL E
11012	24913	A	11105	240	329	RNWPGAEAHYYPSTLGGGRGRQIT*GRG FE
11013	24914	A	11106	2	316	HEERERERERERESAIVRQIHTQGEGLT ELVFPYRRPAPSGLKFTFVYVQEHILGV GGNGLSPLQIGVILRDGRGLAHIRCGTR NKILRILKSQGRAPDLS*DLV
11014	24915	A	11107	169	1	EDGHHSGHLHKKQKQPAWPSMVHTCNP NTLGGRGWIT*GQEFETSLTMEKPCCL
11015	24916	A	11108	192	355	GMSLTGHSNYIILNLFNLPWCVAHTCN PMTLGGQGRFT*GQEFENNLAYRGK
11016	24917	A	11109	145	383	EVNKDKGKYHVSQGIQSFYSYVAYVYFRK LIYTMMTIVNSALLYTELVICQGRRLV FDFGF*FWFFETESCSVIQAGEQ*CDLG
11017	24918	A	11110	199	400	TRAGFFPPFKKFLKGPGPAPPFNLNLF GGRGGGFF*IPKKKIYPLLLPFLKVQKT PSKPPFFFFFLRQVLLCCPGWSAMAR SRLTRA
11018	24919	A	11111	373	177	QFETSLGTMSGPSFYLN*KSARCCHTC MRFQLLQQRSDHLSSGVHRCNSP*LH RCTTTWVTK
11019	24920	A	11112	204	399	NHFWDVVYHFSPPFFFFFEKNLCSVPR AEDQGMNLS*LNPLPPGLKQFFA*PSQE AGIIGPGHH
11020	24921	A	11113	192	16	KKTENNR*RGYGETETPAHCGRACKLG *PLWKPV*QFLKKLKMCLPYDPTIPLPA IFS
11021	24922	A	11114	113	369	AGGQGPNFLQKPGPPGLKGPPIPLPG GGNYGGGPPSRGIF*FFEKKGFGVVKV GPNLRG*RDLPAPPSKGAHPLNGGFFSR N



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11022	24923	A	11115	250	387	ILCDVEHSLWPGVEVHAYNPSTLGGQDGR IA*AQEFETSLNNIARL
11023	24924	A	11116	192	1	VCDLFWKPSPHALTRRRTSVFHLKR*FS WLGAVAHTCNPSTLGG*GFWRIT*AQEF ETSLGNMV
11024	24925	A	11117	289	202	VFYCQ*KFIRKKKKKKKKKKKKKKKKKK KKLSKKIKKMDQQKLRSPTIK
11025	24926	A	11118	412	421	RA*PTEQVTLGITEQSYSRGHINNRVHD LDVGS*HPDCAAAIKGSFVQRLKGY
11026	24927	A	11119	16	472	DLRKPSATHAFADAYHTGKANP*PLTGA LLTLLMTSGLTM*VHLHSITLLILGLLT NTLTIIYQWRREVTRESTYQGGHTPPVQK GLRYGIILFITSEALFFAGFF*AFYHSS LAPTPQLGGHWPPTGITPLNPLEDPLLN TSVLLASRVSIT
11027	24928	A	11120	304	346	GLWHATGITP*PLTGSF*LLLMTSSLAM *FHYHSITLLILSLLSSTLTIIYH*WREW TRESTYQGHHTPPVQKGLRYGIILFIT EAVFLARFC*AFYHSSLAPTPQL*GLWH ATGITPLNPL
11028	24929	A	11121	174	420	FISALLKSAIQRNAMFSTYYALTCTVG TAVSWSSVS*PQRNMMS*VHAPAMAGR LVCHYIRVYRRFEHVCKRAVHGQYP
11029	24930	A	11122	299	466	IFILHEICTTFFFEETRHFCH*AEVHWCS LGLLKPPPPGLRCDPSTSPSRVAGTRPS
11030	24931	A	11123	138	1	NPFNEKNPPPKGPGPKNAFFFFFEMES CSVAQARVQ*HDLGSLQP
11031	24932	A	11124	241	499	NQRERS*HLYLLYNTVCLTHGLPIIIY SAYQLAIYDLLLRDALARLQADLADRR RGLQPKKRFAFKTRRKDAASSTKVDAAP GI
11032	24933	A	11125	252	391	PLSLDLQSNASLSHFTSPPLMFADR*LF STNHKNI*TLYLLFGAWA
11033	24934	A	11126	45	459	AFLKNHPLET*SNHSFDLPTLSNISA* GNFG*LLGACILIQITTLGLFLAMHYS PDASTAFSSIAHITRDVNYG*IIRYLHANG ASIFFICFLHSGRGLSYGAFLYSQT*N IGIILLATIATAFIGVLP*GQISF
11034	24935	A	11127	109	301	QDSLMRKKSKNRSPSHER*RSKCLERKR SGDKKKKKGGPPKKKIGGFPFGQMELK PFSILGGF
11035	24936	A	11128	322	2	SCHHVSSLGDRARPCLOKEKKKKERKKVG DFNTPLSMDGYQHWYQARKIIIMDGT TK*KITRK*KIRNQ*DLTDVYRTLHPRVK YTFLSLAYGTFSRTHIRGQAI
11036	24937	A	11129	182	2	FLPRGFQPPPVVVPGLGFLFPSPSRD PGFSPMPFFFFFFFETESCSVS*AGEQW RNLG
11037	24938	A	11130	138	1	GWVFFLVVFSFSLFFFLR*GLSLSP TLECSGAITAHCSLKLPLGLS
11038	24939	A	11131	304	83	WKKTDFPRKGRNSASRLPSDSNCNSSL SLLQGLSLLYRFWTYHVTGKGSQSRPQEQ VLGYHARKNSR*VHRVK
11039	24940	A	11132	247	225	KNFWGGPPLRGCKKNFFFFFGGYKK*L LLCLVNMYI*CV*YI*HKRIISDPKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK K
11040	24941	A	11133	242	3	KKKKIFFPPRYFWAPPYFFFLGPPPPFF

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						FFFFFFFFFFFFFFFFFVF*TFHLS PRLECSGTSAHYNLHLPSPDC
11041	24942	A	11134	361	2	ASQSAGITGVSHRTRPETHGFKDT*RKPA EEFVTHI*ITLMSCNIESPEKVCADL IRGAKEKNLKVCRPAGTPIKASRITTRK TPCEGSNTRDRFQMRIHKWLTDLHSPFD GRVGGRV
11042	24943	A	11135	1	370	IRQTFQKREIVGIILCYWNVGYSQLH *SSRMLWIFHFYRVYISVKVILVILVPH EKKKKKKKKKKKKKKKKKK
11043	24944	A	11136	273	2	GGRAGQQILFCRGITWLGPPRSCQCTFRS PPGLAL*PWECSLPPALKIRFSPFLPF FFEMEFSLSPRLECNVTVAHCNLRPLP GSSNFP
11044	24945	A	11137	130	354	GQLNKLSPYPENVGTYLVLINPLAQP VIYSTIFAGTLITALSSH*FFT*VGLFI NMLAFIPVLTKKKKKKGGPL
11045	24946	A	11138	366	2	LVEMGFLVRQNGLYLLTS*SARLGLSK CWDYRREPPCPASDWVILTSPLIHALD GKEHTHTHTHTHTHTGLGICQSSLGKQS GGWGWLSANRGQFSPFAVCLVVSFLPEV PVVTSALFT
11046	24947	A	11139	228	1	CRAGRGLPAAVLIILFPPLLIPTSKYLI NNRLITTTQ*LIKLTSQMIAIPNTKGR T*SLILVSLIIFKATTNLLG
11047	24948	A	11140	157	337	HIPTPPHTTCPERPSIRHNSIYYLKRYC LLRIILSLPLQTS*PLTGALSLLMT SGLSM*SHLHSITLLALRLTYTLTIYQ *WRDVSRHSTYQRHHTPPVQKGLRYGII VETTSKDIVESGLF*AFYHSRLAPTQL *CHWPPSGITPLN
11048	24949	A	11141	188	3	IPTPGGPPPLPPQKVLFPKNPRAPPGV FFFFFFETDSRSVVRLECSGVI*AH*NLH FRGSR
11049	24950	A	11142	224	3	SVSSPCISNTHKVDVRSSALLQESTSSR EVMTCGHFYLIYET*LRSLAQSAALAC SGTISAHCNLRPLPGSSN
11050	24951	A	11143	262	371	SYCGPGVVAHAYNPSTLGGRGRIT*GQ EFETSLTN
11051	24952	A	11144	244	379	TIGKQRCHAGIEEVSQAPWLKPVIP AL*EAEAGGSLEPRSLR
11052	24953	A	11145	1397	1565	DRLESLEMHIPGVYPNQWNTNFYLFYI FEAESHVAQTGLQ*RHLGSLQLPPQV
11053	24954	A	11146	284	1	GRGRQGGSSGKGEGRAMDITGGVLGK GQGAGEAFVEVWEKELRGFKVEGEDMD KERVVD*GL*GGRERERERERERERE RERERERESLV
11054	24955	A	11147	64	286	THALAWTRNQIRSGHGAMCLYSHLLRK LRQNDHLTPGV*KCLEL*LHH*TPWT KPTAKAIFNLKKKDSWD
11055	24956	A	11148	230	358	VSVSLIIFIATTNLLGLLPYSFTPTTQL SINLSMAIPL*AGAV
11056	24957	A	11149	81	367	QTLRTKMKNVVASLIDPTILGLPAAEL IILFPPLIPSCKDVINRLMTTQ*LI ELTWEQMITIHNTKGR*CLILECLIMV IATTKLLGLLP
11057	24958	A	11150	257	2	SVCAVITKYLRLLGCFADAADTQRPLPPA TVKLTMFNIAHGEPLGCI*LFVDKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PKTAENFHALSTGEK*FSYKGS CFHRI LP
11058	24959	A	11151	257	1	WRCGEKETLIRCWWECKLVQSLGRVTWR FVRELKLELFPNPAIPLLG IHPKEKK*L DPCTCMFIVALVTIAKMWNQPKCPSMDL V
11059	24960	A	11152	17	367	NHKDGKKTEEEKQSTSPQKDCSSSPAM EQSWTENDEDELREEGFRRSNYELQEEI QTKGKEVKNFEN*DECITRITNTENCL KELMELKAKARELCEECSRLSSRCQLE ERVSA
11060	24961	A	11153	213	2	TFCHFFFFFFETESGSAVQPGVRWCDLGS LQAPLPGFPTPSWRQRLQ*AEIVPLHSR LKLHFKKKAGVFSC
11061	24962	A	11154	1	347	GTSNHFPFLYTYQVHNSTDYPRNRCCLN PSLRPHTSSKPLPARPHIMTHQSHAYHI VKPSP*PLTGALLALMTSGLAM*FHFH SITLLILCLLTNTLSIQ*WRDVTREST YQG
11062	24963	A	11155	223	3	YSTNLKILRNHFILFF*DRVLLCLPGWS AVASSRLTANSASCLSLPSSWDYRRAPP HPANFCTDRFHHVQVG
11063	24964	A	11156	143	1	RGFLNQCPSONFPFFETESCSVTQAG MKWYDLS*MQPPPPPRFKLV
11064	24965	A	11157	149	355	LQPLPPGFKRFSCRLRLTSWDYRKDVDS ALLSNYVT*KYISKTLCRHQSP EIVREF LTAMKSHKLT KVG
11065	24966	A	11158	156	370	RSDGCQKIPRNM LGGWSVLHHTVDEQ*G PNRYIKKCSASLIIREMHIINTVRRCLT PATMATVRRKTTSVG
11066	24967	A	11159	298	4	HFOVVIMWRQLVKGR LQAQKNAAFTDSH THLCYLKCVYFCVCVCMCICVFVCV*SR AL**SLYLF LCIKAVKAGHSVSGLESQH YGR LRQADHLRSGV
11067	24968	A	11160	364	285	NSWGKIKILKGK*PPPKKIFFPKYPQS FFLSPP*KKKTNFPHPRKYLSPGIFLK APPPLIFFFFFFFFFFFFFFFFFFFWG
11068	24969	A	11161	198	406	KSVYMTLKKKRGSFHERGDVPAICNFFF *IHIYMCVYIHC VYIYIYTHIYIYTH QIYIYIYIYIYIY
11069	24970	A	11162	95	376	KIITKHNIARTNPTFCIMN*LEITLQG EPKLRPPKPDKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKGGGGGFKKKPGGGP KIRGGEKIFFFFLGGD
11070	24971	A	11163	343	391	WR*LSSTNNDILTLYLLFRARAGVLR AVSLLILAEQGP GNLLGDDHIYSAIDP AHAFAMFFIVIPMIIGGFDN*LLAVRN GAPEMAIPHINNISC*RLPPSLLLLLAS AIVEAGAGTG* TAYPPL E
11071	24972	A	11164	1	158	QPMTPNRGPLSP*PLTGALSALLKTSGL AM*FHFHSITLLILGLLTNTLT IQ*WR DVTRES
11072	24973	A	11165	265	466	KLLTSLSPFNLLRETNQVGLLELSQAKY KKT PRLGTVAHV CNPSTLGGQG WIT*A QEFETSLANMA
11073	24974	A	11166	204	458	KRCLLPFPDSNTQSSQCRREQIGRAIR KILTFETQNIKRLKTEKQLLKLE*SGK ITAHCNLDLP GSSSPPTSASQSAGITAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11074	24975	A	11167	256	3	S KILFFKPGVLSPPWGGVNFQLMFPQGG PPKKKRGPPLSPPKKGPFFFFFF*ESR SLLPRLECSGAISTHCNLCRLGSSRTRG
11075	24976	A	11168	1	457	HRTPSVRTPNCRGDPVRVRSSTNHKDIGTL YLLFGA*AGVLSTALTLLIRAELEGQPGN LLGNDHIYNVIGTAHAFVITFFIVIPIT IGGFGN*LVPLIIGAPDMAFPRINNISC *LLPSSLLLRASAIIVEAGAGTG*TVYP PLAGNYSHPGAS
11076	24977	A	11169	343	428	GR*LFSTNHKDIGLLYLLFGA*AGGLST ALSLLIRAELEGQPGNLLGNDHIYNVIGT GHAFVITFFIEIPITIGGFGN*LVPLI GAPDMAFPRINNISF*LLPTSLLLLLAS GIGEAGAGTG*TVYPPLAGNYSHPGAYV DLT
11077	24978	A	11170	91	2	PRQDPSFFFFFF*TESGSVAQAGVQWCD L
11078	24979	A	11171	219	1	IFKSKILCLPPPEPNFFFFFFF FFMRHGGACCSPSYLG*GERMT*ASRV AGTTGVCHYAWLIFVFL
11079	24980	A	11172	292	365	RI*SLGQAQWLTPVIPITLWEAKVG
11080	24981	A	11173	251	1	ICDLQILTHGITTCVKMGLTTLFVSGIT FLIHSLAIKFGV*KNPS*LGTVVHTCN LSS*GGRGRIA*AREFETCLGNIVRP
11081	24982	A	11174	200	407	KIFETDVYVKCSNLCWASISFSNYFG GPFYLN*FLSYFSFLETESHIVAPLE CSGMILAHCNLCL
11082	24983	A	11175	11	155	STNFFLFSETGSGSVLQAGVQWPGDLL ASSHSPASAS*VSGTTVDAA
11083	24984	A	11176	140	1	PSTFPDVVAMRRVSCSKGDKGQV*WLT PVIPAIWEAKAGGSPESI
11084	24985	A	11177	210	1	TDEELLMDQQRK*FIEMESTPDEDAVN IVEMPMKDLEYVINVD*VVAGLKRTRDC SFERSSTVGKMLSN
11085	24986	A	11178	133	148	STSTR*LFSTRKDIGALHLLFGA*AGV LGTAVSLLIRAWLAQLGSNKEA
11086	24987	A	11179	236	1	KFWKKDPLTKGGCPLKKGGGGIFSKKK KNVFFPKKKFKGGKKKNNFFPKKKKKK KKKKKNKE*LFISFAHIAVHL
11087	24988	A	11180	210	1	QSLGQENLQVFFPLFGP*PNYLDKGEKW IRVGKIWGHLLLLFFETESRSVAQSPRL CSGAIAHCNLCPL
11088	24989	A	11181	292	348	KKGALFFSPGG*KKNFPPGGKKKGPLFS KKKNPP*KKPGEKEKTRFPFLGGLGG GFPLAPGGKPPRNRVLAPPNPNGGKKK KTPFSQKKKKKKK
11089	24990	A	11182	168	3	KPEASMLRMDFFFF*EAGSHSVAHAGVQ WYCSSLQPTPELSDPLAPSSKVGGIT
11090	24991	A	11183	87	351	KGIKWSLNIQRGVQPHLSYNYSFSSFF S*DWVLLRLECSGTTTAHRSNLPGSSD PPTSASQAAGTTGMHCHTRLIF*ETGFH HAVQ
11091	24992	A	11184	55	344	TSLNLCFFFFFFWGEKSPFLPPGGDEGPL FGQLDTRPWGIEKIFFAPPP*KGKRGVP PGGEFKNPPAPKGEPPLS*KK*NQPGQ GAPPCYPFLGGGAKKIFSIQGRVSN* PKRGPSSPPGGKKGDFSPQKKKKQRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EV*PNSPSGAP
11092	24993	A	11185	344	190	LVETRFHRVSDGLNHLTL*STRGLGP KCWDYRCEPPRPANTANSLNPFPM
11093	24994	A	11186	135	3	IFPKVFGGPPFFFFF*ETESRSVAQVG VQWCNLSLQAPPPGFT
11094	24995	A	11187	305	14	IMLITSIRRSRLSSTAEGILSRLRICG RVAKYLINNRLITTRE*LIKLTSKQMIT ILNTKGR*SLILVSLSVVGYHFL*G* FD*SLLLY
11095	24996	A	11188	198	1	LEQTFNMFPNPKSIISTPSFGFLFKIS FPFLFFFF*DEVFLLLSRLCNGTILAH CNLCPLGSSD
11096	24997	A	11189	352	3	QLCNTPLPKTNHAMLTSNANTLIYRRS AIAAASSPPIFPASKILLNSRLITPHQ *LIKLAQKQMIAPNTKGR*SLILVSL IICFEVSLISHCWVISRLLMRYLEVGI NRGG
11097	24998	A	11190	270	137	CIINRLYVCVYIYIYIYI*IFYMYV YNILCILGHRRESGVI
11098	24999	A	11191	18	342	ACRKRKMSSKFALRATGNCYYSCTFCSI SFPHPK*MPCYQKKKKKKKKKKKKKK KITV*K*SKTKNIKGLGAR*ELSLA*L LGEPPIFAKGHPLMLKNVEICKRP
11099	25000	A	11192	169	3	ERSGIIRVYQD*NQCLAWSLA*KIHPW LAAVAHTCNPSPSGGRHWIT*GQEFK
11100	25001	A	11193	407	1	KRACFRWLTLISTLWEAKQENCLNAGV HDQPGQHGETPSPQKIKSAWHGGPRL* EVRWED*LSQGG*GYSEPCSHHCTPAWA TERDPV*KQKRSIPWKELASERKDSGR RWLVREMPSCQASVIQVRRISF
11101	25002	A	11194	110	412	VCGFRLHSPAILMPLMPSYFRHSNT EIKPISNPTVASKRASEKSCSLTLNQ KLEMIKLSEAT*KAEVGQKLGLLHQKV SQVNAKEEFLKEIESA
11102	25003	A	11195	34	155	AWHEGMHHSVDGLNLLTL*DACLGLPK SWDYRRKPPCPA
11103	25004	A	11196	289	453	NQPGKSFMSSTFHFMMFTLVHAGV*W LDLGLLQPPPRFKGFSLHLPWGDR
11104	25005	A	11197	177	432	KWEKQAQTLGGGNFPKGKTRVGKNFEK LKGNNPFLCL*KRGRKGTGPWKKPAPS GERGIPGKKGKTGPPGFGPMEKIKRG K
11105	25006	A	11198	139	3	AMVLSLSPRLECSSMIMAHCSLGLSGSSD PPTSAP*VARITGMHHP
11106	25007	A	11199	150	492	GDPLPGHHPV*EVRRPFARQLPRLRSEE PLRPVATPSGK*GASLSGSHPIQEGGGG GQPLPGHLPHPGWRSGVKPPPGQSARPG GEGHLLPATPTGK*GGPQSGQPHLSGGR RE
11107	25008	A	11200	239	64	YQKYYYYYFF*ETESRSVARVKSSGLIS AHCNLHLPGSRLQLCLFPTS AVFGQESH IT
11108	25009	A	11201	31	396	ILTMREIVHIQAGQCGNQIGAKFWEVIT DEHGMDPTGYHGDSLDQLDRISVYNE ATGGKYVPRAILVDL*PGTMDSVRSRPF GQIFRPDNFVFGQSGAGNNWAKCHYTKG AELGDSVLDV
11109	25010	A	11202	85	407	VLLPHSEALEGADTMPHSYPALSAEQKK

<b>SEQ ID NO: of nucleotide sequence</b>	<b>SEQ ID NO: of peptide sequence</b>	<b>Meth od</b>	<b>SEQ ID NO: in USSN 09/515,1 26</b>	<b>Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence</b>	<b>Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence</b>	<b>Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)</b>
						ELSDIALQIVSPGKGILAADECVGSMAR RLNQIGVENTQENRRLYRQVLFNADDRA KKRIIGGVIFFHETL*KQDDDGVT
11110	25011	A	11203	302	115	THLDHVAIYLSTLYLSIYHLSIYHL SIYLCRF*LID*DRVSLYFSGWLQMPGL KPSSCF
11111	25012	A	11204	130	348	GNAYGGPCSVLVQRT**IPALTFPSTCL DSKFQRDLVTLRDFSNFTSNTVAEIQA LTSQGSEGLDGA LGWGQ
11112	25013	A	11205	232	62	ISARNEGFNTLN*RITFFFFSSHCLSR LECGGMILAHCNLQLPGESLEPGRQSLO
11113	25014	A	11206	161	2	KKRGFLPLIEPFCTQEIQLR LGAVAHT YNPSTLGGRGGWIT*GQEFKTS LAN
11114	25015	A	11207	251	3	PNHLPKAPSPNTLRIRFQHLNFRGAQQ TFGLQHKLTSKQMITIHNTKGR T*SLIL VSLII FIATTNLLGLLPHSFTPTQL
11115	25016	A	11208	145	287	GFRLLK*INQKYSFLKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKK
11116	25017	A	11209	436	110	ISGRGEQKFKFYSPAPFFRGINPPPLGG E*NQNLIKPP*KKI FLGSPKV PKKKGGPQ KILKKGPGGGP PLFPPLGGQG GGFPE SQGFKTTPGKKKKPPPKKKKKKKK
11117	25018	A	11210	217	2	DKWSVLHINYNILSSSLVHVLFKYLEN* K*KKNLWPGMVAHACNTNTLGGQGGRIV *AQEFETSMGNTVKC
11118	25019	A	11211	146	3	QKVSHAQYRCLSWG YFFFIFLET RSRS IAQAGVQWRDLGSL*PPPA
11119	25020	A	11212	187	384	GLICFYLT CFYFI FYFILFYFSLLCYVM LCYVLCYVMLCYVMVCYVMLCYVI*DRV SFCHPDWSAA
11120	25021	A	11213	373	482	MIKLRHRLGTVAHTCN PSTLGGRGQWIA *GQ EYKTS
11121	25022	A	11214	64	362	ITGVSHFTOPLPFIGGLALSPKLECRGM IIAYCNFELPGSGDSCHLSLPSSWNRY MPCMPS*LKKNF**RQGLTVLSRLEKDY LL*D FSALRSFPWGR
11122	25023	A	11215	181	368	CDSA VPLLDIYPTEFKADLK KIRIPMFI IALFAVAKR*KQPTYPSIDKWIKKLWAG CGGSRL
11123	25024	A	11216	268	369	TTRPDMVVHTYNSSTS GGQGGTIT*AQQ FKTSLT
11124	25025	A	11217	90	3	IGQAQ*LTPIIPALWEPKSGGSPEVRSL
11125	25026	A	11219	277	272	SLTAPGL*SQLRRLRWEDHLSLGQSSF SEP*SCP TPAWVTQ*DSVSKKEKKKE KKRKEKEKVNP QPKATESPGQALIGSHS LQVQKRVYAHPIL
11126	25027	A	11220	19	343	LELEV EPEDVSELLQSLDKNYLSCFLKR FLENKYTPGEDVVNTIKMTTEDLKYNTD LVDKAAAGLERINFNFEGSSSVGKM LSN SIAWYSEIFYEROSQFMWQT*LLA
11127	25028	A	11221	266	356	FFEMESH TVA*AGVQWC DLGLLQSLPPG FK
11128	25029	A	11222	105	2	RFVCSTIKVLRDLSSARS NPGRFI*TSN SRPRKS
11129	25030	A	11223	145	350	RKGRQLLD*DLGWV*WLTPIIPILWEAE LGGSLEARSSRP AW
11130	25031	A	11225	155	348	PLFFFCFHRTF Y*KSVCRFPKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKKKKKKMEGGGGGANTKFLY GENRKPPPLFFFF
11131	25032	A	11226	271	3	NFLSVFNFTTRICLGMCFLSIFLLIFGGS LKYQLFLAQGFFFFFLHYFFTSSIHSSLL Y*MLDFLDLFFLYLFCNFNFVSFLFCI LSKFF
11132	25033	A	11227	3	413	SPAEPHRSYTMWNVKVGVNGFGRIERLV TRAAFNSGKVDIVAINDFIDLNYMVYM FOYDSTHGKFGHTVKAENAKLVINGNPI TIFHERDSCIKRGDAGAAYVV*STGVF TTMDNAGAHLHG*ATRGIIISAPSAD
11133	25034	A	11228	48	413	VFVLVSCGFFFFFWEKKICFFWPGGKK RGKIGGTGTFGPKGKGNFRGPPPKNKEK GGPPPPNNFGLKKKKFYQGGQGG*KT RNFGKPPAPNPPKGGDLGGGPPTQGQNG FLKKKKKQKK
11134	25035	A	11229	172	404	EFENS CSPGWQRRGVMIPGVTVEDMNQQ EIRALVALLLKKSRLKVPPEWDTTKLA KRKELTL*DEKWFTY*AASTT
11135	25036	A	11230	247	2	QPKKKS VSKKKKKELPCDPAIPLPGIYP KEKKSVYKKNLHLRVYCRAVFTIAKIW NQPKC*SGDK*IKKI*YIYTVDLRR
11136	25037	A	11231	1	372	TETTVEVAWCELQDRKLTKSERQRFKEE AEMLKGLQHPNIVRFYDSWESTVKGKKK IVLVTELMTSGTLKT*VHQYYS*PRSM REFDFLNRSTSTFLVVPKKGTVLPTV TVLAYFLAHKVL
11137	25038	A	11232	311	464	KKATPRNLCKWPGTVAHACNPSTLEGRD GWIT*GQEFETSLTNMVP
11138	25039	A	11233	64	418	VPVASRRRRRCGRVGGGKAMADLDKLN DSIIQRLLEA*GAKPGKKVQLHENEITG LCLEPREIFLRQPILL*LVAPLKICGDI HGPYYDLRLFEYRGLPPKSNYLFLEDY VDRRQH
11139	25040	A	11234	233	421	PTTSNMRSLRLRGASS*KKTAGPQQRNL EPALPRRWGGRSADNPPSGSLRKS GKNM QKTPGTA
11140	25041	A	11235	343	1	NNTHGLSHSSVGRNPGAVGSGSCMSGIK LSEGLRSLLEAVCISRAAVIKCHSWVAS NNRHFFSPSSGG*KSEAKVWAGPCSL*R RVPSLPLPASGGSRLHLCVCGCVTPPSAF TW
11141	25042	A	11236	122	419	RTPRGPKPNPGLQRKTFLLIGGRIKTYL GIFGKDLYFWGGKNWDTLPKI*RSREN KNF*REKWNLPYPGCLKNGARQQHFA HLILRLDTKTYMLAF
11142	25043	A	11237	1	379	AFNHLHAGHGLSGAAMKSLVLLCLAQ WGCHSSPHGPWLIYRQPNCDP*TEEAS LEAIDYINQNLPGYKHTLNHIDEVKVW PQ*PSGELFDIEIDTLETTCHVLDPTPV A*CNVRQLNEHAVQ
11143	25044	A	11238	1	397	QTMTNRRGPLCPSKDLRSSHVISLPLHS ATHTRPTNQHTNHI PMARRSTRKHIRR APHTTCPKRPSIRDNP IYYLRNFFLRRI FLSLLPLQSPYPPIRRALAPNRHHPAK SPRRPTP*PLTGALSALLKTSGLAM*FH FHSIALILGLLTNTLTIIYQ*WRDVALE STYEGHHTPPVQGLRYGIILFITSEIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFAGFF*AFYHSSLAPTPQLGGHWPPTG ITPLNPLEDELLNTSVLLASGVST
11144	25045	A	11239	267	3	FVSVRITPIYASATWLSYVWVWASSPN VCPGDRVALSPRVECSGTISAVRNLR PGSSDYPASA*PADGWAPPQYRCPPRL ANF
11145	25046	A	11240	391	31	VFFFFFFFFFFFFFFFFFFFFFFFFPPPF LKNPFEPNPPNFFFCPKF*ILFLN*I*F *IKF*I*KIPGFLLNPPFFPPFFFPF GALFFFFFF*EGVLPSPGWSAMSHLLS EKRKLTPRMSYN
11146	25047	A	11241	371	491	KIFLCWARHDAHACNPISIFRGQGGHIT* GQEFKTSANMV
11147	25048	A	11242	1	221	HRIDPLCRNSARAFFLSTGCHRVSQDG LDLLTS*SAHLGLPKCWDYRCKPPRAL NCFRTISQLLNLCIKD
11148	25049	A	11243	382	333	TYKIKDFKTF*RWFHPNISRVEAEKFL SRGQRGDFLARPSSESPGGFTLSVR
11149	25050	A	11244	169	477	TQKDEKESTTTTKNAENSKGQSAYSSPS DCNTSLARAQN*EEAEMDELTEVGFRRR VIMNFVKLKGHILTQCREAENHDKTLQK LLTSITSLAWNINDLMELK
11150	25051	A	11245	200	462	SLIYNELCTIHILYQYVA*QRS*CFQQ LMSFY*RTLKNLKESELCKVALLYPSFLK WKRGLWLTGVTADT*KPSTLGGQGGRIA*A QEF
11151	25052	A	11246	484	301	IFCEKKGL*FQLRRVRWEGPFNPGNQG CS*LLSSPCPPGWITE*DPVSQKKKERK RNQVMELVSAQENKKNKPRSVGLQACARS MLAFSTTPR
11152	25053	A	11247	226	458	NTVAVDWGPRCFFSLLLSHAENCDMWFT KIELFIFTNHLLLKQDLEMLW*GQAHAC NPSTLGGRGGWIT*GQEFETS
11153	25054	A	11248	304	436	SPSRCRK*KIG*AQWLTVPVISTLWEAKV GRSLDPRNSRSATWY
11154	25055	A	11249	216	451	THKYLFFYLGYNPMLYIERETGSCSIA* AGVQWYSHGLLHP*PSGLKRSSQVAGVI CLANFFFFFFLKKWSLVVLPRLG
11155	25056	A	11250	260	474	DKYFLLYPLKALNVVLGAHINI*KVSKI MC*K*DKNMYNFFFSF*DGVSLLLPRL CNGTILAHCNLCCLPC
11156	25057	A	11252	193	496	MTSCYSFYL*IKDASMVKKKKKKKKKK KKKKKKKKKKKKKKKKKASSSQAQDYS KADYK
11157	25058	A	11253	348	478	DLGWLKLGTVAHYTNSSSTSGQGRRIT* GQKFKTSANVVKPC
11158	25059	A	11254	174	475	MHHWVLIQDIDDNT*NCNLHFLCSQL KSIQKFKKKKKKKKKKKKKKKKKKST
11159	25060	A	11255	292	48	LPLTCHRPVAVSHTHLAFSNPTAGTIF* TRSSWNAGTFIIFKIVTFLLFFF*ER VSLKLTRLERSGAI PAHCNHLPEF
11160	25061	A	11256	347	16	TQSADWCITYNPPARHKSSPSPHPTQ*PS WLHLVDPAWVWELPTSPAPSACTPQP LGSRWDPQPSQKQCPSGRLGPQSPPO VGLGKAGWRSQALPVGLTRSIESHWW
11161	25062	A	11257	238	590	APGAYIFPQQHNPTDSQVIFSLTASHLL ICSPLCISVLHFNMGNIIDENRNAHVHA RACAHATHHTHTHTHTLYLMNYRETL



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MLLKTRGRATGSHARCIFS*SLQACP
11162	25063	A	11258	310	461	LSFGDVLQLESDRPGAVARTCGPSTLGG*GGWIT*GREFETSLANMLKPR
11163	25064	A	11259	461	174	MGEHRVSQDGLDLLT*SSAHLGLPKCWDY*CEPLRLAPVGKLFKCVGYKLVLCCHGSYMSMVIKIRMPGLIWSLEGGSAAVVHRYSIWEISFGC
11164	25065	A	11260	343	472	LLRRLRQKDCLSGGGQCSEPRLDYCTPAWVTK*DPVSHKQE
11165	25066	A	11261	229	3	VKMKLQ*VPVKVKI*KYTPLLGIYKELKAGFGRNTCTLMFIAALFTIANRWMQPRLP*IGECVNNM*YIHTMES
11166	25067	A	11263	163	399	KLLPGTRNLHAMEHPIFGWLRNPHATAQG*HPLSQSSSLALHGRADHICYPELCTSSSCIAGYPN*EGMFASQHRVH
11167	25068	A	11264	316	427	TNKKHII*IINTTTHSLIISIIPLLFFNQINNLFSCS
11168	25069	A	11265	184	418	KTPPGFFFEKNPFFWGGKKGPPPPKPNLPLGGKKKFLRGKGGKTFFFFF*KIGSSSSEPPPPGGEQAPPPPKSPRR
11169	25070	A	11266	219	13	KFFFSLEHQNFQGGGVPLFPPPKGEGFLPKPKQGFTITPLKQKIKPPPPGGYSGPPRVL*KGPPHIFYK
11170	25071	A	11267	3	173	SHHARPETGFHRVSQDGLDLLTS*SACGLPKCWDYRREPPRQARKLYCLGMRTNE
11171	25072	A	11268	157	2	PVDITHVKTTVGLGMVAHACNPSTLGGRGGRIT*ARGSRFLPPHWTSELR
11172	25073	A	11269	291	468	ISEGKRSLFVILHFIFFETGSCSVAQAGVQWCDLDSL*PHIPGPK*SSHLGLHTGACH
11173	25074	A	11270	29	478	GWNPNQQDIGTLYL*SGARAGVLGTALCLLIRAEELGQPDLLGNHINYVIVTAHAFAIIFFFIVTPIIIGGSGN*LVPLIIGAPDMAVPRINNISF*LLPTSLLLLLASAI AEAGA*TG*TVYPPLAGNYSHPGACVDLTIFSLHLAGV
11174	25075	A	11271	61	474	PYNQGGNDAAHAWPHLTKWRSQGTTEICREPEGAWQRPSQPRHLKGRSPGQLRALSQNLPSYSGGSHLLSAYVVPDTISKHFINTIGWLGTVAHACNPSTL*GEDRWIY*AQEFKTSANVL
11175	25076	A	11272	277	478	KIYQPVKIHGPRPGAVAHTCNPSTLGDRDGWIT*GQEFETSLANMNSPSL
11176	25077	A	11273	350	11	KEKTAGQARWLTPVTPALWEAEAGASPEVRSSRPA*PPP
11177	25078	A	11274	138	3	NYINLYAWLGAHACNPSTLGGRGCGWIA*AQEFKTSLGNAKP
11178	25079	A	11275	359	219	FVIKMGFPQVGRDGFNPLAS*SAPLGLPKWWDYRH*PPRLALFFFF
11179	25080	A	11276	262	3	FCMSLVHLFSSHSDNYFTSFSL*IFNIPSGPFLFAFQDTLQ*P*DFIYFYFETESP SVTRLECSGAISAHCNRLRLVSSNSPASAS
11180	25081	A	11277	285	1	VKKGDSVSKIFRKKKKRKDKIRLHFMITTVNNLGLIEGNLNLMIKEYKNPTANIILNGERLKAFSL*SGTRMSFLTPTTF*ILVDTQQVYIFMSH
11181	25082	A	11278	160	3	TDKEVPLINAQRKWFLEMESIPGEDAMN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IV*MTTKELQYYINLVEKVLARPE
11182	25083	A	11279	334	488	PLNTCGY*NLN*NFQPGSVAPACNPST LGGQDRWIT*GQEFETSLANMVK
11183	25084	A	11280	527	356	FFVFLVETAFHHVAQDSLDTLTS*SSRL NLPKCWDYRHEPQRQAKNVGEFSETRSI Q
11184	25085	A	11281	486	248	VRQLFSLLLPRLECNVISAHCNLRPLPG SCDSSASAS*VARITGASGSQAVVLQVQ CLQPVPQPGELLRVDLFQLVVLQR
11185	25086	A	11282	38	157	STGLHHVSQDGVDTLTS*STLPKCWDYR HDLRPPASQRL
11186	25087	A	11283	474	339	FVFLVQMGFHHVGOAGLELLTS*SACL LPGKWD*RHEPTDPAK
11187	25088	A	11284	2	462	LETTRTARWNSVIALRHHNSCPYKMANL IDKVCSDYSKDWPFPIFLPLLRPPYCL RHHNMETRSINPPWPSPKCSSEKTNEEG MLKVEIG*KLCLLCQTFSKDMNAEKKFL KEIKSATPMNTSMIRKQNLIDHMEKVL VIRIEYQASHNIL
11188	25089	A	11285	65	280	SRAVEFNLLTT*SACGLPGKWDYRCEP PHPASP*FSKLLSSNLKTYLSSL*DSHS GFYSFVCSGLIILI
11189	25090	A	11286	244	488	MRLGRVPSVLFYVVRMQREGIILEAENK PSPDIESVGALILDFTASRTIRNKILF IIFPG*GILDSPNVP
11190	25091	A	11287	345	445	KRPGTVAHACNPHTLGG*GRWIT*GQEF WTILA
11191	25092	A	11288	223	500	SPGTRPKVLECCSTLGRQATLLLGEGWL WGQSHRLGVQSQCCLCVLWDLTCSLSCS FQIIKLR*RPGVMVHTCNPSTLGGCGGR IAQGQEFK
11192	25093	A	11289	157	22	LSCQEVKGEIGEAETCWAQWLPPITPAL WGAKEG*SPEVRSSKPA
11193	25094	A	11290	305	497	KLVNCIYFKGVSMVRELYCNKIV*WLG TVAHIYNPSALGGACGWIT*GQEFETSL TNMAKPRL
11194	25095	A	11291	478	1145	QHVQACPERPQMMGTLERSRAVASKIGH SYSLDSQPARAVGKPPWQQACTRVTELT EATGKLIRTSKIGKHPQSFQPAATQK LRPASQQGVQMKTOGGASNPALQIGSHV MCKSSQFKSDQSNPSTVKHSQPKPFHSV PSQPKSSQTKSCQSQPSQTKPSPCKSTQ PKPSQPWPPQSKPSQPRPPQPKSSSTNP SQAKAHHSKAGQKRGK*HANSRDL
11195	25096	A	11292	352	468	TFFPGQHGKIPSLKIQKLAGHGDACL*S RLSPR
11196	25097	A	11293	295	24	ENIQGSKKNERQHMHNGVGTWNSNPGFV STWVYRNCLACLDISFSFIKWKSHKDT SMGMFTAALFTIAKT*NQSTCPSMVDWN STTRTS
11197	25098	A	11294	274	429	ECEPVQTLWKIRKFLKLIKIELPSDPAI PLKGINLKEVKSVP*SDTYTPMCI
11198	25099	A	11295	168	469	PSLGNKSETPSPKKKNLFLGFFPYFREK LVGILLKTVLQKGAGGVFFGPKNPPEKN PDEPLDSPKTFRRLGAFVKTFPKGLKA AVVFPALV*PQGMGG
11199	25100	A	11296	37	348	IKIFNKTLKYFKKKKTIKKKKKGGGGL KRPRGGPRIYPDGARKNLPHIGTAKKH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGYWEKNPHGGGGNTGPTPPQKTRPLGG KNNLKRVRQGEKPRPRLGGGKTRSQLFSC HA*P*VQGEKPRPRLGGGK
11200	25101	A	11297	93	388	DEYASDNCCYFPGSSHDSQVKQIGSQFT TQIQAHNLAKPRRAL*NHS*PMEMRSK CLLLAYKKKKKKKKKKKKKKKKKKKK PKYLSSRGKDH
11201	25102	A	11298	61	243	YYIHRTTVFMCMN*GLKDNVDK*TIDL LCKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKPQGGGA
11202	25103	A	11299	250	341	IYMSLTGLQNL*EIHLLTHKDSHLQVK GWKNIFHANVNQKQTGVALLISDNIDIK ATTVKKKKKKRENPTILNIYVPNTGAPKF MKHLLNLKNERDGTTVLG
11203	25104	A	11300	3	285	DAWERKKRSQMNQKTTNKVAGVSPYLSI MAWNVNELNFLIKRHRVA*CIKKTSMI CYLQETNFIKDTLRLKIRGWKKIHFHNR N*KLAVVY
11204	25105	A	11301	175	407	AENNPDLVLQKA*TSRGTFMP*ILLRVK RGSNSRNNRCWQGWGRTGMLLHC*QECK LVQPLWKTVWRILPDLESEIL
11205	25106	A	11302	75	280	YHLNLVLYPHPPKNRVC*KKKKKKKKKK KKKKKKKKKKKKKKKKRGGLKKNLLGGP FFPGGKKKNFF
11206	25107	A	11303	299	3	IHASFLFRGCITLAFTVRCSHRSITSSE TSDLTHYYYYYYYYF*LASQSVALAGVQ WDQLGSNHPPTSAS*VAETAGASHHARL IFNFFVEMEVSLYC
11207	25108	A	11304	137	323	FFTNGRHRKEKKSNKDQLNLGLHDFLD NPLLLF*KYLGREKKKKKKKKKKKKKK KQKKKK
11208	25109	A	11305	64	481	RPTRPHVYHIVKPI*PLTGALSALMT CGLSM*FHFHSITLLILGLLTNTLT *WRDETRESTYQGHHTPPVQKGLRYGII LFITSEDFFAGFF*AFYHSSLTPTPQL GCHWPPTGITPLNPLEVPLNLSVLLA
11209	25110	A	11306	142	330	FFTNGRHRKEKKSNKDQLNLGLHDFLD NPLLLF*KYLGREKKKKKKKKKKKKKK KKKKKK
11210	25111	A	11307	259	440	RPWIRDNPIYYLKSCFLRTIFLSLLPLQ PRPYPPTRRALSPPNRHHPAKSPRSP*PL TGALSALLMTSDLTMLGHFYITLLILG LLTNTLTITIQ*WRDATRESTYQGHHTPP VHKGLGYGIIILFITSKVVFARFF*AFY HSSLDPTPQLGGHWPPTGITPLNPLEVP LLNTVRL
11211	25112	A	11308	433	3	FPPPDIRHSRSLGFPPSFGAGFLNFAF SKGQEPALPGGFYYPSPKKNLAFCSPP LFYWGKFGSKFSLGVGLFFP**SPKSF CQFLENKGFFPEKSFFKFFPPAGGCVFF FSEGGFPFCLFLFFFDRLVWCHPGWISV ARS
11212	25113	A	11309	2	423	GRVGDR*LFYTNHMDIGTLYLLFGA*SG VLGTALSLLIRAEQGQPCNLGNDHIYN GIVTDHAFDIIFFIAPIIIGGFGN*LV PLIIGAPDMAVARINNISV*LLPSSL LLAYAIVEAGAGTG*TVYPALAGNYSH
11213	25114	A	11310	234	1	TFFGKFPFCLKFKPAQRGGENTPGPFPF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LVFFFFEMESRSVAQTGVQWRDLLGSSN SETAS*VAGTTGACHHARLIF
11214	25115	A	11311	406	211	LSLFLHSLISTHGARPDPVGLVPTQDG LDLLTS*SAHIGLPKCWDYRRAPPCPAC GFDLHLPND
11215	25116	A	11312	379	398	KT*NFTVRGSIPLLNIPMASMTFSKKK KKKKKKKRGGLKKNPGCAKFNNGGRKRK IFSLKGGEKKNPGGILEKKPFFGGGKKK ENPPKKNKGLREKKKF*RGKGGKKPQKG GKKMGSSSAKTPTWG
11216	25117	A	11313	390	489	RYRLGVVAHACNPSTLGRGRWII*GQE FETSV
11217	25118	A	11314	286	434	ILWYMNYSIKLLKIIYKLGAVAHTCN PSTLGGRGGWIP*GWEFETSL
11218	25119	A	11315	322	3	FTFYGCRQFQVF*IVTKNDRIIFSSYTK NLLKIYLGly*FYVPLLRKSLKKTGS FESNLSFK*VFLWSGTVAHTCNPSTLGG RRGWIA*GQELETSLTNMERPR
11219	25120	A	11316	251	389	TFFFFEREHFVPQVGQGGSLGSLQAP PPGSHSLA*ASPRCWDGG
11220	25121	A	11317	313	80	EYICPRCLSPGFRD*PGQHGETPSLQKL QKSAGCGGAHLRSQLLRLGDRVRHCLK KRIYLSLFSNLVLSNNRFQII
11221	25122	A	11318	145	410	APKTLKVALTSAAAARESTICQLGVDEL VIFLELNRSTDQRPGAVAHTCNPRTLGG HGGWIT*AQEFKTNLANMVKTC
11222	25123	A	11319	393	3	NFFKIIFTLSPPLPLIFTPPFFFFFKKI PPKPLFFGVFHSQTCPIISFFKNFYPL FWFSNPFFLLFSPSRKGPFPFSRFFFK VGNPLFFLFFFFFFFFFG*EGVSLLLPR LECNGTISAHYYLRPRV
11223	25124	A	11320	135	1	HRDVKLEYAIRKMEVRPGVAHACNPST LGRGGWIT*GQEFETS
11224	25125	A	11321	282	2	NSESVLIKEKGDREKVLFSLLFSKRKV LBSKTFPTLHSGCKKRSYFLKITSSFL *PRVECSGVIIDHCKLKLGGSDPPTSA FPVARTTGM
11225	25126	A	11322	149	30	WGGGQVRWLTPIIPALWKAEGGSPEV RSS*PVWPCLY
11226	25127	A	11323	316	399	STLGGRGAQIT*GREFETSLANMPNPIS
11227	25128	A	11324	223	397	IIKAYQ*DVNREQIKTIIYFQNKLKCI KKMIWPGAVVHVYNPSTLGG*GGWIT*G QE
11228	25129	A	11325	3	396	NYSTAALFLRGIHWGRWGTLYYGSSPI YCRGLNSTLGLYPLNASSNPHPRKLCKP KIYTHIAKCPIGHKIIYPYANTPIH*HH THTHTHHTL*DSLLWPGVVAHTCNHNT LGSWGRQIT*VQEFKTSIA
11229	25130	A	11326	113	442	KRYIQIRAHSEVLCGHELWGTLHNPVQT IQTWEPFPYLPPLCSRVTSGKSHRFVPL LFHL*NRNNSHHHHHHHHHHHRNPC* ECCRAHSDSYAVWSDKVSQEPVAAAM
11230	25131	A	11327	145	3	ELDIKPPNPFCHTGVQ*CDLGSPQLLP PGFK*FCLSPSSWDYRCA
11231	25132	A	11328	189	1	KTNLLLTHSKRLRLHLQSSVFQC*SKSEK SNVCT*CAFSCLPKLFWLGKVAHACNPS TLGGRGG
11232	25133	A	11329	193	405	ID*QTLTKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AYTSKKKT
11233	25134	A	11330	209	11	GKRGTPPTINNIFNFF*EKGSCCSS RAC*CNGEI*AHCPRLRLPGSSNSPAAAS RVQETATTPS
11234	25135	A	11331	38	390	VDQSTVCKMGQSAGCGWGS DKG I KAGCL K*QRQKKKKKKKKKKKKKKKKKKKKGGG LKKKLFLGPGGEKFFFFFWGPPFFFGGR FLKRGGGKKPGYKKNKISGHPFPFLGGG KKKKR
11235	25136	A	11332	38	326	VDQSTVCKMGQSAGCGWGS DKG I KAGCL K*QRPKKKKKKKKKKKKKKKKKKKNRGGG FIKKIFFGPGGEKIFFFWGGFFFGGG FKKRGGEEKNLF
11236	25137	A	11333	1	234	RTRGKNWMAFIKEGWVPTGRMGGSFIKH SFLESKNTWLGKKKKKKKKKKKKKKKKKK PHDKIKDLDFDPV*NKKQNI SIP
11237	25138	A	11334	244	398	INHLYSNKNDLIFLLVFLYLF*RRPG EPPLIKGWLPLYLGGVNLNRKDPL
11238	25139	A	11335	174	1	HQVYPYVKQEHYKQDSCQYIKYMNWVP DAVAHGCNPGTLGAQGGWII*GQKFERT RG
11239	25140	A	11336	148	411	LEFFPHCYLLNAPSILYLNPKVYVNLH LCVSAVCLLPVHSPHRTCLY*KKKKKK KKKKKKKKKKKKKKKKKKKKGGAPFK KLLF
11240	25141	A	11337	237	453	GQRPLLSFREKGSFFFLLETEFCFAPQA EGQGHNLG*LQLPLWG*SNLSVSSSQEV GITGAGHHPRLFFVF
11241	25142	A	11338	65	347	VCRVDDFVPEARTRFFKSI*EAWNKNKI KPLLSTFSQVPGSENEKCTLDQAFIGI LEEEIINHSSCENVLAISLAIGGVTEG KYGSVLFCLK
11242	25143	A	11339	158	393	VPCTHSEGIRKGRKCLPKTRENAREERD KKIPPGLC*AGKLFPPQESSTWPGKVH AWNPSTLEGRGGWIT*GLEFKTT
11243	25144	A	11340	117	3	GIRPGAVAHVCNPSPLGG*GRWISRDWE L*TS LANIR
11244	25145	A	11341	292	60	SGQGLRLRGAFRGKVQAKBWMPIPKLGC LVKDMKIKSLEEIYFFSPPIK*FEIIDF FLGASFKDEVFFLFVCLFVCF
11245	25146	A	11342	149	30	TQIFPPPPPPGKKKKFFPKKKKKKKKK ERKKDRKNKQK*KGPGVGVSPLPFPPLG QGQGGFPQGLGFKTPLAPKGKPPFP*KT QKFPRRGGPPKIPFLGGGEEKPFSPG GQGSNPKPFPPPPPRGKKKNFFSPKKK KKKKRKKERKTEKTNKK
11246	25147	A	11343	120	504	GVHDCRLWDDMTRRPPAAAATACPAGRP PPRREEHSQLLLISFQGFWD*QQDVN TPNLDHLAREGVKAKYLMPPLVMTSPS HFTAITGKRHSAHFTRCPSNPQRPSFPV IRSKSSVSSREVEVA
11247	25148	A	11344	213	399	ALVIHCLTTTIQVSGLSGSKYLMRQGMV AHGCHPNTLGGRGGWIT*SQESETSLAN TVKPCL
11248	25149	A	11345	308	3	NPTPRSGDLWVEEGSPGAGNWGCLSEQT LRAIIKATTSYSFYCYFFETGSHSVAWA RVQWYNPGCSICGSSHLPTSAS*GAGTI GMHHHAWLIFLFFVENE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11249	25150	A	11346	189	433	GHCRAGTSLTLTHLGGSAMLELIHGLCLGRMKFIHTTCIILFLFLSATQAGGQGGDLS*LQPPPLGFKQFSCFSLPRSWD
11250	25151	A	11347	257	3	KWGELCFLTIKEERMGFPLAKKRKIKGVF*FGLFFFFFETESHVPAQAHCNLSLSDSYSPASAS*VAGITGACHHNQLIFIFYE
11251	25152	A	11348	159	434	LSPSCRDVGTYSAHAHPHTHTRVRAHTHACTHVRATHTHHTAHGSHLTKEQPGLCTLPGSSW*PGLGGRAIATAQAWVHCAGIITAAHPP
11252	25153	A	11349	240	406	AFKKLAKNNSMGVNRSLSRPGVVAHAWN PSTLGGRGRQIT*GQEFETSLANMVKP
11253	25154	A	11350	163	360	PQLQLMKFLQN*LLERLRPQNGNLNLEG LACSESRSPCAPVWRTERDSVSSPQPRPGAGGRPSFF
11254	25155	A	11351	145	406	PLNSGAKPTLPPWSPRRPELNAPPPPPG EKEFFFFLGRGFLFAPQBEAGGENIV*G KPPPPG*REFFAPPPGDDGNKGAPPPPLFL
11255	25156	A	11352	122	337	ILWVLLLVRESLKFFFFLLLLFFLFFETDVA*AAVQ*SDHSSRQ*PPGLRGSYTS AFRIAGAIGICHHL
11256	25157	A	11353	325	416	KCVYIMGWA*WLTPVIPALWEAGAGRSLEEV
11257	25158	A	11354	260	415	LEELQNTACQKLEPFLSRTETKQGCLLS PRLFNIVLEVL*AVRQKEIKGI
11258	25159	A	11355	160	2	ISEISTKRNNYFLKNWLGVAHACNPST*RG*GGQTTRGQDFQTSANMVKP
11259	25160	A	11356	160	3	ENLKLYNGSPFLKI IWLGMVHTCNPST LGQGGRIP*AQEFKTS LGNVRRP
11260	25161	A	11357	235	408	GQPLPAALFFYQWHLHFKELLAHPWCKT VWRFL*PLKKEGPHDPAIPLLDIYPKNK KW
11261	25162	A	11358	11	393	QTERTPTPKPHLYVSFPNSQDPQLQGG KLITNRKNTHTKTPSVCHHHQRPKVDKTT KIGKKQSRKTGNSKNQASPPPKECSSS PATEQSWTENDFDELREEGFR*SNYTL KEEVRTHGKEVKNL
11262	25163	A	11359	283	475	FMVSVSIKVYFFIFIFLFFEMESC SVTQ AGVQWHDCLSLFC*VLASSPGNSSPVR
11263	25164	A	11360	266	407	LEIHHSKTL*FWLGIVARACNPSTLGG* GRWIT*GQEAIIILANIVK
11264	25165	A	11361	93	1	DVLSILLPRLECNGAISAH*NFRIPGSS NSS
11265	25166	A	11362	131	377	MEEMIKGRGLSKPPALSSYLTLKSS*LK RVRARRRRLFKSRFSLDLQVAGFFVCLF VFWDVSLCHPGWSVVQSRSLTAALT
11266	25167	A	11363	212	392	QAEECAPLFIGVKEPPKNLTHWLGTVAH TSNPSTLGG*GGQITWGQEFETSLANMA KPCV
11267	25168	A	11364	141	3	NELWLNHQNVLWLGTVAYTCNPSTVGR WIT*V*EFETSLGNMVK
11268	25169	A	11365	215	384	ANFNIRPEISLASKCPSEKRSRTLLPLN QKLEMI*LSEEAATSKARTG*KLGLLHQI
11269	25170	A	11366	48	373	EPWTRKEVLKISSSLKIHCVLSILCLIL MPTLECTAAIMAYSNLPLPGTSCPTCA S*VAGTTGACHRAPTVLKIFLRDRIFFF FFTNVTPWCHTPADPAIFKANAR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11270	25171	A	11367	310	2	GLICLNRENAYFFVIRQISMSCLEKEKP ARYSSPYAKSVTRGEKRRQRFLLSRAPP IPFLFFI*IV*AESRSVAQAGGQWLHFS SLQTPP*RRSDSPASAS
11271	25172	A	11368	303	50	MFALTNRGVQGSPIVFLGVFLISKMGFT CFKGFSRKFVLVFFLGVFPSSFFFLRAR VLLCCPGWSPITLGIK*SSCLGLPQCIVLT
11272	25173	A	11369	109	419	QSNASLSHFTSPPLSVADR*LFSTDHGD IGALYLLFGA*AAVLCTAISLFILDWLG QPCNLLRNDHIYVIVTAHAFARIFFIG IPIIIGGFGN*LVPLIIGA
11273	25174	A	11370	112	258	GGRFKGSNFTSAGMQRNIFFMGPPK*NS RAGV*QRGEGKNPGVTKLNRL
11274	25175	A	11371	823	1078	SQHFGMPRWADHLRSGVDQPGQHGETL SLTKIQKLGRGGRCL*SOLLRLRQEN CLSLGGRGCSEPRSHHCTPAWATQ*DSV S
11275	25176	A	11372	184	420	IKQOKNFLALVKELVQLLWKTVMQFLK KLNIELLCDPAILLGLIYPRELKMYVHT KTCT*MFIVELFIKSKK*KQPTC
11276	25177	A	11373	234	44	LATITDRLLALSDSAIPLGIYAKEKKS VYQKDNCTYIFVAALFTVAQI*NQPKCP STRTRGS
11277	25178	A	11374	73	456	PPIGSPLVPYIPSPALSSPAQPRMGSH CLIPSASCHPPLETDFLSLLPHTFCLAV FTKERFSPPPSPYPRF*KFLRS*KFSF FLPPFLFFGGTVLLCLSGWSAVAQSWLT AASLGLSSDPPTSTS
11278	25179	A	11375	43	456	EFFHHVGQDGLDLTST*SAHLGLLKCDW YRREPPRPASDGHY*TDATGSLPSSGTT *IRTKPSQAPASWGLWNLAHHPRSHPS CPMANLICSTLSSFDGSGPGTGPGGWCP LGLSGSPARAVFKDSSCSLHPLATGI
11279	25180	A	11376	288	484	EWVLSAVGGSQYGVCLPFLHCFIFETE SRSVAQDGVQ*CDLGSGLSLPPG
11280	25181	A	11377	129	1	NFNALNLRAGAVAHAYNPShLGGEDGR IA*GQEFETSLSNTA
11281	25182	A	11378	307	1	DSEIPLGLAKFWNHRREPPCLALFTL NQKLEMIKLSEEGISKAKTR*KAGFLCQ RVSQDVNAKEKFLKEIKRATLVKTQMMR HQNSFIADAQKVVMAWMK
11282	25183	A	11379	200	397	CISLFSHYKDLPETGSGFIKKRGLIGSH WLGAVAHACNP SILGGQRRIT*GQEFE TSLASMKPC
11283	25184	A	11380	167	1	SNGLYSREARMVQHTHTRPGVVAHTCNP STLGGHGRIT*AQELKTSLGNIVRPC
11284	25185	A	11382	12	395	AHSSFLSLDLVVFATCPHRAETQTGHR FSTLLPLSALYPK*DYFKKKKKKKKKK KKKKKKKKKKKSGGGA
11285	25186	A	11383	160	2	TMEMMLDIK*I*EIFLFEFKMGLKAAET TQNINNTFGPGTANEQTAQRWFNK
11286	25187	A	11384	274	389	GQAQWLTPVIPALWETKAGGSLE*GQAQ WLTPVIPALWETKAGGSLELKNSRPSLG NMVKPP
11287	25188	A	11385	389	37	WSYESSWSFIFKSFLFSFMISAYDM*YA SQILFTPKLYRTHPYFLVLFLILSILV ILETGSRFVSRLECGGISAYGSK*LG SGNPPAAASLSSRIPIVHQCSDLA FN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PEFEM
11288	25189	A	11386	214	374	KGGRFRKGSKFTSPGGGEKNFFIGAPK*NSRAGV*KRREGKNPGVTQLKKGVG
11289	25190	A	11387	142	410	RFVCSTIKVLRDLSSDRSNPGRFLSTSN*KKKIKKKKRGAPFKKKNFYRGGGKYFFFGAPKINFLGRVFQPGGENPGRSPFKGAWG
11290	25191	A	11388	144	1	CLSNEDSIKTPKGLGTVARTCNPSTWGGRNGWIT*GQEFKTSANTVK
11291	25192	A	11389	167	2	RNISSHLNMAITKQTNNNNCW*GYREIITHIHC*WEFKMMQLLQKLVPOKVKHT
11292	25193	A	11390	2	412	SDQVQDAGRLISSEASLLGLPTATFLLC LPTGFALCTRVPGVFLLRSTVILREGLPTLVTSFYLNYYLLKDLVSIQSHWGLQLPMNFGETQFSL*QKLV*KEKESMPGMVAHACNPRNLGGQGLIT*GQEFKTILA
11293	25194	A	11391	1	206	TGRLAGHRVSSLPIRGGRAEAPLTSRTGRLNQDGLNLLTS*SARLGLPKCWEYRRQPLRLAVISGFLT
11294	25195	A	11392	262	388	VSK*KKKKKKKKKKKKKKKKKQ
11295	25196	A	11393	78	414	ICFFLRAPPFFFFFFF*TKIFFFPALNSMANFFFWTPPFLGGIFLPPFFLEGGGPGLASPPGGAFF
11296	25197	A	11394	238	11	IKWETAGRSSACL*S*LFERLRRENPLNPGVHG*DEI**HHCTPAWVTVRPLSKYINKNKK*ARLAARCGSRL
11297	25198	A	11395	340	1	KHILVPPFINVSEIQRYSLV*HLLFVGV*NLFFFLFLSFKKPVLCM*IICHEIISP SKPKCKASHLSFV*KKNSNLWLGAHAACNPGTLGARGGRIT*GWEIETSLTNMEK
11298	25199	A	11396	363	245	QMDLNRHLSKDDK*MANQCMNRCLTSLAIRQMQUIKTIMI
11299	25200	A	11397	292	2	DPKKEAGRGAQL*FQLLRFRKHETHLNPGG*GCSESRSHSSPPAGATK*NGVSKKK*Y*APKEERHPRPVLVEPRVPQVPSGSQTYRQDHSRPRV
11300	25201	A	11398	121	321	KKLYTHKSKSDVMIFLKIETVSWLYCPGWRVMAHCDLKLGLSSKPPTSAS*VAETSGTCHHARLIFL
11301	25202	A	11399	118	394	QALPQPIPVILLQFFFFFF*GTGFCFVAQIGGQGGHYG*LEPPIRGLKPSSRRTL RGGWD*GGHHNAQLILGFFEKTGSCFVVQAGLKALA
11302	25203	A	11400	273	379	AEPGVVAHSYNPGTLGCRGGGIT*AQEFYTSLGNM
11303	25204	A	11401	360	38	KIFGQARWLTVPVPAFWETEVDGSPVEGRSRPA*PS
11304	25205	A	11402	254	404	GPAGHDFHMITPSKSTETGLGAVAHVCN PSTLGGRGWII*RQDLETSLA
11305	25206	A	11403	161	3	ILTPTLQYIKINLRGQAWWFTHVIPALWKAK*SGGLELRSLRPAWVIEGDL
11306	25207	A	11404	1	170	MGVSLSPRLECNVISAHCNCHLL*FTFK*FSCLSLPSSWYRCVPPCLATTFIY
11307	25208	A	11405	249	3	NAKSRIQVISIWVFTVKFFHLYLNCNFSQ*NEMAGGQSIFRKKHLDFSLEHSGMMTTHCSLDLPGSSDPNSASSVGGTRH
11308	25209	A	11406	70	401	CGKHGVNLIITHSFLNHLKYLQLLQMANL



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FISQFLLTCVSEPLLF*YCHQITKVGRL HEVKQMRGTTKKQEKMFPPYWNNDKNVCPG VPAHACNPPTVGG*GGWIT*GQEFNT
11309	25210	A	11407	257	389	GGSLQLQKYLRLVAFLLFSFFFFFSFETES *SVVRLECNMISAHG
11310	25211	A	11408	364	420	SQPFGRPRQADCLSSG*AQWLTPVVPAL WEAKAGRLLELRLR
11311	25212	A	11409	312	413	TSGMGPGVVAHACNPITLGGQGGWIT*G REFETS
11312	25213	A	11410	283	425	HGHKDYVHWLGAVARACGPSILGGRGMW IS*GQEFETSLANMVKPCL
11313	25214	A	11411	389	3	CRIDGLFFNLVFLRLVVKF*VIFFLSY FSFLVILQLTYMLNCTFF*QILNLF ILVLLTKILNTLLSTENYCHFSLLYCLE FWFHPILKHMYNLFLI*FILIFILRQS LARSRLKYSGTISIH
11314	25215	A	11412	267	3	QBFQQEDTSELDLEIRSLCKRKGGLKQG DTKDNLKRVVETDKGKAAWPGAVTH ACNPSTLGGQGGWIT*GQEFETTLNRC PRV
11315	25216	A	11413	3	281	GAWSCRIPGEGSLASQAIQPFSLYPVN PQ*ISLSARKKKKKKKKKKKKKKKKKKK KKKGGGGVLKKIYFPPRGEKKFFFFWGP PKKTGGGGF
11316	25217	A	11414	275	2	KTAHFQLFNSDFKFPGRSNPGQSWSPRA KQSFCTQALLKYFLK*NMENKLNKSRSG AVARTCNPSTLGGQGGWIT*GQEFETSL ANMAKPR
11317	25218	A	11415	319	1	RNLGVQVYEVVLVYKCVSSNNMKMN KRDLLVI*VPGIVIHLYRIKENPELY ISLFIYSMRSLKLTYPGAVAHACNP TLGGRGGWIVCSQEFETSLGNM
11318	25219	A	11416	121	428	LSCDKWGNRDMTKMLSKELKKKKKKKK KKKKKKKKKKKKKLGDDEEDKE*QSSW GGGGALIKNIFPSRAAGFFLSLLKYK KLGAAYIILGEKTIWL
11319	25220	A	11417	79	253	KIFNFQFSNMLENNSHTRINNYFPGRE RWLTPVIPPLWEAKAGRSLEVR*RPSC P
11320	25221	A	11418	180	4	EVGFMPKGLCGVFLEAGSHSVALTIVQW CDLGSPQHPLGSRDPPP*ALQIVGNTR RVP
11321	25222	A	11419	154	3	STLKDKENQKLSIQPDTMAHVCNPSTLG GRGGWIT*VQEFETSLNNMVKP
11322	25223	A	11420	436	478	AIPLPH*RKILHAALFFFLKGSFVLS PRLECSTKIWAHCSLPPNINSPASSS QEGGTT
11323	25224	A	11421	143	398	AAFGFWFVLIRFLRQLALSPRLDCFFA KSASCQPRPP*FKRVCWLSLPKSWDYRF DLLCAAGLVWVYLSVSRHLHINEKNQPPP P
11324	25225	A	11422	1	138	MVFHRVQDGLDLLTS*SAHLGLPKCWD YRHEPPRPAHSYFLLHK
11325	25226	A	11423	2	390	LELPILLNTLILFLFLILYIYLVFSPN AFRILFITIVLESFSFILLVPSKPWKYS LILSNAFVLCMMISSPPFPLFSLSTTRI NKKLDFWLGAHAHYNPSTLGSQGGWII *GQEFETSLTNMAKPHL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11326	25227	A	11424	267	414	VFQITFCIKNFWPQVVAHACSPSTLGG* GGRIT*AQEFETSLGNMVKPC
11327	25228	A	11425	189	73	HQDGLDLLTS*STRGLPKCWDYRHKPP RSARPNWVAP
11328	25229	A	11426	318	33	KKTISSHARGRKLGSFKTAAPFFFFF*T GSCSLAQAGVKWCSHSSMQPRPGLK*F SASGSAGIIGMSHHTRIAGFLLAKLKK KSNSTGYGGAHV
11329	25230	A	11427	291	393	DRVSLCLPGWSAVLPS*LTAQISWAQV IFLPQP
11330	25231	A	11428	51	399	KRVARQNPPNGQGFQWCS CSPILYQSR AQGENIYKLLGSGEWPQGLIIDVEREQL EDWRQGD LGRGMWMTKARVHKGPGLVAG TCNPSTLGGGRWIT*GQEFENSLANMV KPCF
11331	25232	A	11429	242	420	VKKKKRGGRFKGSKFTSACLQGISFFKG APKLNSRAGF*QRWEGKNLGV PQFNRF G AHP
11332	25233	A	11430	77	405	TKRGDSSFCLYRIWIIDSVMKWNQSKAA AAAAFFFFLRTLLFLRLKGVGASVI *NFCLRGWGGSPASPSKEVGMGACHNS GLFFVFLEKRRFPLVGQEFKTTTRAN
11333	25234	A	11431	121	439	LPLPTSGPEDPLALSFKPTFPFSTLSGM IYTGHPSP EHTSHLMPAPPVNNKACRF FKT*KKKKKKKKKKKKKKKKKKGGPL KKKKIFAPPGGEIFFFFWGP KK
11334	25235	A	11432	109	283	LTPWNLDSRCEIKGNKGPQENHLNLGGG GCSEPKSHHCTPAREKRQNSVSKK*INK IK
11335	25236	A	11433	296	1	FLKKPSKGFSKLP HLPQN LNFPPK*K CPRAKKIDPPPSF*KISSLFGE*GFTG SRPPSLNLENPPKRIFFFFFLDRVSHC RPGWSAMASSCPRV
11336	25237	A	11434	385	418	QSETLSQKQKTK*E*SWLGAVAHACNPS TSGGRGGWIT*GWEFENSLTNMVKPCL
11337	25238	A	11435	3	405	LLHQGRMLGQWGNRTKTL MRENVGK FPAEPSCSALGVWLQALACYPGLVRRQ* ANHWEKKKKKKKKKKKKKKKKKSGG G
11338	25239	A	11436	221	3	KHEFQTIQMESMK*NTSIKICIYAS*IQ DCLRYQWRPAAVAQAITEHFGRPQAD HLRSGVSDQPGQHGET
11339	25240	A	11437	288	366	KMFFSWA*WLMPIIPELWEAKAGGSL
11340	25241	A	11438	160	370	LWYHYFPVRDGLTILVTYQLKAI RRLLT LKSRSGAVAHTCNLNTLGGRGWIT*GR EFETSLANMEKPHL
11341	25242	A	11439	230	404	MQHGQVGIYSQGGGW RVPDKKNSQLGTV AHTCNLITLGGRGWIT*GQEFKTSLTN MV
11342	25243	A	11440	302	54	LSGVWFLTPPPKGGGFPT*NGGAPGFF PPPPFKNPPPEGKLGPKKKKNFPPPGG EKLVLKGAPPPPPPPPPPPPPPPFL
11343	25244	A	11441	271	416	KRTLSTELQYMCCLLIKSKSIFK*KKKK KKKKKKKKKKKKKKKNPPSLP
11344	25245	A	11442	254	392	SVTGMTIMTSSCCYKTKQCKTIQKLARH GGTCL*SQLLRRLRQENS
11345	25246	A	11443	390	150	LLKNQKTLGGPARNPPLGGFNGGVPKA GNWGP PPGPGT PFFFKNQKITPGGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						P*FPPLRGGGPGNPLYPGGQGCH
11346	25247	A	11444	122	1	PAPLFFFFFFFETQSCSVA*AGVQWRNLGSLQPPPPDDGTRL
11347	25248	A	11445	272	403	RPKVDKTKMGRNQSRKAENSKNQSSASSPPKDHNSSPAME*SWM
11348	25249	A	11446	70	397	LCHCAPAWATERDPVLGEKKRTMMSYCHPPMRMVEKKIVGDIKC*GYGETGFLTHC*WECKMVQIL*NIV*QCLKNLVHSPYELAIVLLGIYPREMKTYIFTKKTSM
11349	25250	A	11447	3	401	HASAHASAHASAYYRLCAYPKSSFLYPSFLLVVSNFPLNILDITIGPKATETLFIKHVMHDVISMQLKSKTFYNYFFLLSLNVFYFVLSCKRRKRSQLGMVSHICNPSTLGGGRWIT*GQEFETSLANMA
11350	25251	A	11448	333	1	KSGCIPPKGQVLFLLQKTAKIGSPKPVSPPRGKGQFFPQGLRGFY*FLPPPPGVP EIFFFFFF*DSSHSVTLSPRLEYSGMNTAHCSSLHLPSSSNPASDSHIAGSTGTCHH
11351	25252	A	11449	104	402	VVCRPLLGGVSQLGYMGVMDPFKEAVCLFSELKHCAGRTTALFRAVRQGCLSLKNFLLPFFQLCPAHRGGVL*RQ*ALLSCGGLHPVRASRPLCLPTQA
11352	25253	A	11450	198	2	KYKFMAGLGGSC*SHHFARPRQDGLSPGV*NQPGQHGETPSLQKKVSWAWWHASVEAEAGEQP
11353	25254	A	11451	171	3	TPPPRATSLFFFF*TESHSVSQECNGTISAHCNCLCPGSSDSPASASRVAGITGA
11354	25255	A	11452	177	461	PMTGGKYISNSTCSKPNLSPLPLKTKQTKNMEHFGRLTRGDCLSPGV*DQPGQRGKTLQLLQKISQALWDVTAHAWVVPGLPTRERRRSLSFPTG
11355	25256	A	11453	247	3	EGECCGIESR*ILHLKGRICWHINYLKTKIKN*VILKKMYKQLRPGAVAHAYNP SALGG*GGRIARAQELBTRLGNIVR
11356	25257	A	11454	328	57	EVHSNICATLSTHQMILTKGTRHQHIS*GFF*EGEVLTLSKLECSGVIMAHCNLNLGGSSDPLALVSQVAETRGASYLLLAICPKVKNK
11357	25258	A	11455	70	435	ATRAKLHLKKKKEGRKKEFFPHWQGOPTPALVFPQPRTHFIFKVSIFSLKKNREQLPYTVQTQSLLPLNSHWGQVA*AGVQWRNLRFSCSLSPSSWDY
11358	25259	A	11456	112	401	KCWDYRRERPCPAPNICF*LTFFFLGKLKNQSFFFFLKGSVLVPPRLKGGGAF LFN*NLTLOQKNNSPASPS*RAETLGLGPHAKLWFVFLKK
11359	25260	A	11457	198	3	EKTSVKQSGDSNKKAWLEMTNKKSLKR*GVVAHACNPSTLGGRGGWIS*GREFETSWTNMEKP
11360	25261	A	11458	179	1	FFHMYNHIVCEYTTITLSVNINSQGGPRAHAYNPSTSEDRWIP*AQEFKTSANMVKPH
11361	25262	A	11459	210	5	RLIHYFFKNNLPSGGGGSTA*GQEFETRLDNTVRPHFLKK*KISQVWVCMVVVSATQ EVEVGNGLSPGV
11362	25263	A	11460	139	2	RILALSKLFFFFFKQESHFFLPMLECSGVISAHCNL*LLGSSDLS
11363	25264	A	11461	388	272	S*KKKKRGGRFKCSMFLSPAGQGNPFFM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GPLKSISLAVV*QRREGKNLGAPHITRLGAHPLFAGWHKTQGAEF
11364	25265	A	11462	2	387	CVWKSNNKKAPPCVAALRFWRKDDMDDEM APGKHWGGTTSKVQSGGLMGRYTGPLTK TENSILLKNPYFEAGHSGSRL*HQHLGR PRWEDYLRPGGQGCSEL*SSHCTFT*VT EGDPVSKKLKRTIFGG
11365	25266	A	11463	325	398	SLPTWAVCAPRPSG*GSGIPELKTMLAG VILEDYLDIKNFGAKVVGLSCTLATGST LFLGKVGPFVHLSVMIAAYLGRVRTTI GEPENKSKQNE
11366	25267	A	11464	174	2	YLEILFFFTGSRSTQAGVQWSHPGSL QTPTPPCPSNSPASA*VAHASADAWADA W
11367	25268	A	11465	105	411	TDVELLLMDE*RKWFLELETPGEDDVN IVKMTTKDFGYSINLVDKAVSEFKRIHS YFERGSAVGKVLSHSIVC*GEIFHERKS PLMQQISLLTFILFYFSE
11368	25269	A	11466	291	404	SQEGVKIKRQGTVAHTCDPSTLGG*GGR IT*GQEFKTS
11369	25270	A	11467	64	236	THASGLDLLTS*SSCLGLPKCWDYRHEP PRPARFSSFYSGSLLNYLAKIIKRDAFC I
11370	25271	A	11468	278	416	NPQISCLQHVWGAHAHCNPSTSGG*G GRIT*GQELKTIILVNMVK
11371	25272	A	11469	178	325	RPEVKDQGASCRDQPHRVGGLLPVCSDE RVPQKKKKKKKKKKKKKKKKKKKKKK KKASSGGARF*KKKKKKKKKKKKKKKK
11372	25273	A	11470	264	60	DINHQSWSLGRWTPLSWVSISQREDRR GFSASIYIYIYIYIYIYIYPIHIYIHT YT*SYHFNQNT
11373	25274	A	11471	95	399	DFPHLLFLPLSQFCTACCPVPENRCFM YFFLIIFSALCWEMNSRISHSNTARVEQC CKVFKILLQMKSVLGQVQLTPVIPALWE AEAS*LPEIRSRNQPGQ
11374	25275	A	11472	139	2	NHVSTELSLHTMAHTCNPSTAGGQGGQ IT*GQEFKTSLATMAKP
11375	25276	A	11473	179	3	RARWNPQVFC*GFLPVFEKILPIWPLRK GVFPFPNFFFFFFLRLVSLCHPHWSAVERS RL
11376	25277	A	11474	282	12	KYIRNE*IVLFVIYFCRNRISWCCPGWS *TPELKRSSCLCLPSCWDYRHEPLCPAE MNKLDRNLNKMDDTTKWIQQKKKNHRTQRO DNKII
11377	25278	A	11475	145	3	VCMQLRTDFQPGAVAHACNPSTLRC*GG WIT*GREFKTGLNNMEQPC
11378	25279	A	11476	61	397	PQTPRLKQSYHVSPLPSSWDYSWIYHERL VNPGRETDWATCYSGGNIQLQENKLNTP TDSTLWVSLCCPRLECSSAIPADCSLNL PG*SDPPTSTSHVAETTGACHYAQLIFG
11379	25280	A	11477	156	3	FIFLKSSQNSYI*KCWPGAVAHACNLDT LGG*GGWIT*GHRFKPTRRPRV
11380	25281	A	11478	224	383	CWVCLIHRAFLAPRPVLGCQ*QKKKKKK KNKKKKKKKKKDSRGGG
11381	25282	A	11479	339	58	NFKNKLFCFASGYLDSKDSQHYIIFFIR WSLALLPRLRWEDCLNPGGGGCSEPRSY HRTPAWVIE*DPVSKK*IK*NKIK*KQQ DWLRLHDKIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11382	25283	A	11480	244	407	SFGKKIGFLFGPKKFNNGSSYGNYKINR RFFFPILGEGFSPHVYF*NLETRTTGGG LLETTKTTTFNLLGRKLGSLGPRSLTAA PTGTTIKLTGGFFQFWGKVFPRMYIFW KDEWKKGF
11383	25284	A	11482	308	30	SPQKNPPTYSGFKNLSASPGQKAKPRF FLKNQFLPGIMGGGRQFPLLRVRPPNC FNFPGGKRCN*QKLGPCPPGPKETVSKK KKKRERQQ
11384	25285	A	11483	226	407	NHWNKK*FWPKVAHTYNLSALGGQGRI T*GQEFETSPSNMRPHAS
11385	25286	A	11484	10	411	QPFIYFLSLRISLFWVFHINGIIQYVAI CVWLVSCHNFSRFICVAACDQDFIVFLW LNNIPLCGYNILCIHSICPNWRTTGLFP LLAI I I K L * T F V K K K K K K K K K K K K K K K R
11386	25287	A	11485	184	1	TDEELLPMDEQRKWFLEKKPTSGEDAVN IFEMTRKDIECYVH*VDKAAAMYERIDS NFLSN
11387	25288	A	11486	435	222	AKNLNRHFSKKVI*MASRHIKRCSISLT IRET*IKSIIR*HVIPGQMTFIQKTGDM FGSVSPLKSHHLKL
11388	25289	A	11487	317	408	FRPGTVAHACNPSTLGGQGGWIT*GKEF KT
11389	25290	A	11488	340	469	GKGDTKCHLWLGTVVHACDPNTLGGQGR RIA*GQEFKTSLSNM
11390	25291	A	11489	38	389	KRPTSLKKSNFCSLQGGFFFGLSQKPGK SNRSPGKKKNPFFSGGKAP*KG*KIPL SPGLGGSPQKPHLLGGLGEKNYLTLEKG GCRDPK*CPCFPPWAGECNPFSSKKKQK FPPFG
11391	25292	A	11490	235	2	FVLMWLMPKLIHIPVTEFRRILFAPEFL* FLFCFVLSYFVLLETGSHYVTYAECSGA ISVHCSSLNLPSSDPPTSVLV
11392	25293	A	11491	25	417	GTLCLRIGFINISHHCMLKENSLSFFFF WETKFYFAPQADGRGPNLG*WNPPSPG* RGSPGPTSRKRNGGGGPPGPVIFGFLR KNGVPPGGLKGPKSLAPGIGPPGPPKDR GLRGGPPAPGLLKKNPKW
11393	25294	A	11492	234	438	MVVI I A Q Q C D C T E C H Y * L K M A K M I N F M L F I F Y H T H T H T H T H T H T R E R G P S Y I Y G K V S F K L T H L
11394	25295	A	11493	344	477	CFTMFIS*IKT*KFNISQLVAHTCNPSI LGGQGGRIIT*GQEFKT
11395	25296	A	11494	35	482	GIPGFHHVGQNGLDLTS*SIHLGLPKC WHYRPGPPRPAISITPST*AYLLGNQKI GVTHFLAILALFFSGTKAMISPKYVCII FYLLVEEHLGCFYFLAINTATCVCVYKL FDTYMYQVESATHETISYFFKILCSL SIRLYAVLL
11396	25297	A	11495	307	484	LSPSERHELKCVLWPGAVAHAYNQSTVG GRGRQIT*GPEF
11397	25298	A	11496	487	349	FLIKTEFHPIGQEGFDFTL*FARLGLP KGWDYKGEPLRLAFWHPF
11398	25299	A	11497	224	417	ASGASALKVELCSFSRYKIYPRHKRRYA RTDGKVF*FLSAKCEGITFFLSFFFFFL EVLFCSPG
11399	25300	A	11498	17	411	KRLVFGGRGRTDRFISQYV*AEVVSINL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIIFLTKKKKKKKKKKKKRGGALKKKKP WGGQNKTEGKKKNFFFLRGKKKPWGDF KKKNFFWGGENWGKPPPKKTPWGKKKI FKGKGGKTPPYFCFLKMG
11400	25301	A	11499	117	370	VSESADLAWSLGICFFIEFPSDADVAGL ETAFFLGGWTGSCSVQPGV*WCNHSSL QPRPSGPRQSSCLSLPSSWDYKYMPPCL
11401	25302	A	11500	244	1	EELFECYSCSPTFSSDPLTTPLLIIT* LLPLTIMASQRHLSSEPLSRKKLYLSIL ISLQISLIITFTATELIIFYIFET
11402	25303	A	11501	130	55	RFVCSSTIKVLRDLSSDRNPGRFLSTSN SSLKKKKKKGRPF*RDNSAILF
11403	25304	A	11502	186	421	SERLKIAGTIGVHHCTWLVLILNLVLL K*ITFALKIMMFSKYSDIGQAQGLMPVI PALWEADAGGSLQPRSLSLGNK
11404	25305	A	11503	1	213	GELLFLYIFA*WLFLLPKLLKFVIVCLC ELQFNERFIMVLCIIILGVGGFFLFCF LL*FCFDFFFFFFWRG
11405	25306	A	11504	82	6	AGVQWPRSWLRIP*LFFTQVLMIFPPPF YHQNFFFP*KGFFFLGGLSHFFPPPNKG FFFNYPQGFFFSPLKKKFFFSPIFL APPGIFL*GEPRFFFFFFFF*EGVSL CHLGWSAVAAILAPPAGFTPSSCLSLPS S
11406	25307	A	11505	245	440	WAPCIG*QLLKDPQVLFAGYKVPHPLEH KIIIRVQTPDYSPQEAFTNAITDLISE LSLLEERFR
11407	25308	A	11506	256	370	GKLM*GHHVGGAGLKLTTSSDPPALASR SAGITGVNRHAPPRLNVTLYTKGQTIL YHNQYNQ
11408	25309	A	11507	1	149	GCMWPRTVLFQFQHKFVNFLKTLGDFGQ VQWLMRVIPALWEAEAGKLPEARRWRPP *PRTVLFQFQHKFVNFLKTLGDFGQVQW LMRVIPALWEAEAGKLPE
11409	25310	A	11508	316	420	YTYIYEPG*VQWLTPVIPALWEAKAGGS LEVRSRLR
11410	25311	A	11509	136	2	LDNRLWPGAVAHACNSRTLGDQSGWIT* GQEFETSLANMMKPHL
11411	25312	A	11510	167	420	PTPRSGNTALQPPHHTHTHTHTHTHR HTHTHTHTHTTRACI*KVRVRALFSPKKK PLFCLSVSQIYVGRCLLKRLLFIPLYRH
11412	25313	A	11511	124	415	IYISVANTILIFIAIHVLAISFFFFKK EVLFLPPRREGGAF*VN*NLCFWG*GN FPA*PSLKKGITGALYTPGLFFVFLKKT GFRHVGQAWLDFL
11413	25314	A	11512	121	1	PPVKFWAPFFFFFF*IGSPSVAQAGVQWN NLSSLQSPPSCL
11414	25315	A	11513	245	13	VLFILSGFFGPINYPSTPPPLPFPASG NHPSTLYLHEFNCFYFYFLFIYFF*DRV SLCRPGWSAVERSQLLVPSDS
11415	25316	A	11514	434	2	RPPFFPVWGSPPPPFFFGEGIWQEER KGASSPPVVRGILRGGGPGGPGAPPT PLKKPPLFFFLAPPFLGVFPFRFFSPTV FPLPFFVCPKKREALGVKGPFRFFFR SFLFFFSGD*VSLCRPGWSAVERSQTLE SLAS
11416	25317	A	11515	247	390	QGLRIYSQDFFFFFFLETKSRFVAQAGEQG GNLG*LEPPPPS*SDFMASP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11417	25318	A	11516	269	368	FFFERESCSVTRAGVQWHRLLSSL*PLPPAFRRF
11418	25319	A	11517	256	404	NILKIFYLRI*KKKNQLGVVAHACNLRTLGGRGGWITRGQ*FKTSKEKMKVK
11419	25320	A	11518	211	404	YLCFTRCSVHSHLK*VFLHKCVI*MYRPHI*HT*GTL*CMQVHTHTHTHAHTHTHTP LSQGGDCI
11420	25321	A	11519	41	232	ESVEPRRRRVPRQAQITPLHCSLGDRA RCL*SQLLKLRLHENLLNPGGAGCREPRS HHCTAAWATEQDPV*KKKSLNFKTVRA INLKMGLALISFHLFLWGIWF
11421	25322	A	11520	146	2	LIDQQGVNQLPRMECSGAITAHCCLELP GSSDPLTSAS*VAGRPTRP
11422	25323	A	11521	297	437	TDHFWNRILSSCGDTFRDTWLGVP PHAYNPSTLGGRARRIT*AQEFE
11423	25324	A	11522	244	460	NCATITNSRIFLQLQKHCTKWLSLSI SWQSLISF**ICFVLFFETNLAVSLRLE CSGAILAHCNLCLLSS
11424	25325	A	11523	222	1	ESKDLDFRCQLAPRNSSCFVLFCFVFP LEIGSCSVAQAGQWCNHSLSLQPPPIA SAS*VAGTTNVRHYVQLF
11425	25326	A	11524	308	424	ITFLTMTFKIYVLQFDPATPLLGIY PKDY*SCCYKDTCTRM
11426	25327	A	11525	98	2	NIGGRPGAVAHAYNPSTLGGRGGQIT* GQEFE
11427	25328	A	11526	113	399	LDRFLTLLPRLRREDCLSPGGQGCSEP* SHRCVPWATE*DLLSKKKKGVLEKPF LPPPSVGKPPFPSPPERLFFFILRPPLGG VFPSPSKIIIS
11428	25329	A	11527	280	3	PKYCQI*VLQCIAQLFKLSIYNTYTH THSLSLSLSLPPPKVNKLMSSEFTLTF KMYTFGPGRVTHTCNPSTLGG*GGWIT* GQEFETNL
11429	25330	A	11528	284	2	FWGPQKKNFSFPPPGKLGISFKRAPPPF FFFFETKCSVTQAGVRWCDLGLQPLA WATERD*LNK*IKGMSKKLHT*VCMFRT RGRTRGRTRG
11430	25331	A	11529	134	2	DTLLPRLECNGTITAHCSLKLPGSGDPP ASAS*IAGTGMCSHA
11431	25332	A	11530	104	1	GRGFFFFFFFFF*EVESCSVAQAGVQWL NLGSIQ
11432	25333	A	11531	157	373	CVFYTSTSQLRCYIFIGNTRSVFRCHE IYT*KNRFWASTVAHTCNFSTLGRGKW II*G*EFMTSLANVVR
11433	25334	A	11532	237	389	ICKCKSTGFG*DFQEFETSLGNIVR PCFYRKIKASQV*WHAPITVATWEAE
11434	25335	A	11533	259	122	HISPSVQRHFFLFYF*TKPHLVAAQAGVQ WCNLSSLQSPPPGFKRF
11435	25336	A	11534	164	1	SSVVSQALILLFLKKTCFWPGAVAHACN PCTLGGRGERIT*GQKFETSLASINL
11436	25337	A	11535	106	310	GGDKGTVDTLHFFDQKRLDHNKDHWM TIHAELPHELSA*CYAFKKECISGIGSI *AEKEYKIQFDG
11437	25338	A	11536	167	378	ASFFGTTITYKTILVYVYMFEEKFTIYIH MYTF*RQGLVLSKLECSNVIIGHCNLKH LGSSNLPTSASRVA
11438	25339	A	11537	101	396	VNNLKQRIGLSKRGEKLLVLISGFGGG FPGAGWIKKGKPPPGFPGGLGP*KRGP

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						GKKGNFNKMGFNPKTLVFNQNFPGGA KPGTPGVRGELGDL
11439	25340	A	11538	18	361	QIGPRLY*DNGETPSLLKIQKKKIPGF GGGPKLSQLLGGGLGWENH*NPGGGGCRD PK*PQGLPPWGTNQNPFVKKKEGGREKGT EGRKEGGGEKKKTLPGKIGALNLGGLLT SP
11440	25341	A	11539	134	365	PGFQNKKTGGGGPFRPKTKTNFKVF*KY LKICFGFWPKRPPPPGFFILETRSLFFI FFLGFFF*ETKRSVTRLECSGVILAH NPLVGSSSHYP
11441	25342	A	11540	2	318	TTERFIYRITFGPKETEVDNLPGAPSEP VAALRLEARSFILKL*SFSLVDFDFFLP F*KTGSCLSPLRECRGEITIVHCSREL S*SHPPTSASQSSSGSGFHLG
11442	25343	A	11541	294	409	GTISFFRTCRGLMVAHTWNPSTLGGQGG *II*GQEFQT
11443	25344	A	11542	1	123	GKQRQEPALSYDHATVLLTS*SAHLGLP KCWDYRSDPPCLA
11444	25345	A	11543	69	350	VGAHWHIMDTKIETADPGNYYSGERGK RPRAEKLPVCYYALYLNGIICNPKPPC CWKGHDFIYIYVCGHIYIHIYICTHIYI YFF*DGGLLC
11445	25346	A	11544	103	340	LFCAFFLSPSKLDIFYHLSFYV*TLFLKD LISLAFFFLFWEAGSCSVTQAGVQGPNS THCNLCPLGSNNPSTASQAAGT
11446	25347	A	11545	256	354	PYPFGKPKRGDHWGLGV*NQPGQQGETP SLLKI
11447	25348	A	11546	196	335	EIVARLKRSVPVGRQWLPVIPALWKAK ESGSPEVRSS*VKKITCRPGTVAHACNP STLEGQGWIT*GQEFKTSANMVK
11448	25349	A	11547	202	377	TIHTKGMVGNFILVIFYQNFKTF* D KILGWARWMPPLIPAFWESEMGLLEPK SL
11449	25350	A	11548	396	26	PPRIKKEKRSPNGAFYPPFCWNF*KKKN LSLAKRFRDSVFFVSW*GSYLPPTFL QLLRWYVLTSHIAVSFKHLCEPHKNFTL QHSIPYLYIIEIEVYSYFINRNTIYKIN MDFSIVGFVFL
11450	25351	A	11549	232	371	REVPFENIKIGVQWLTLIIPALWEVKA GGSLEARSL*KYQNWPGAVAHAYNPSTL GGQGGRIA*GQKFEISPANMAKP
11451	25352	A	11550	174	381	NRDEGFRYADRAEVQRLTGTILEHCGL QRPL*RSSCFTLPCGWDRH*SPSHVA GTTGISHTRLIKKAFFSQTVSSC
11452	25353	A	11551	262	359	DYSNLGLVWLTTVIPALWEAKAGRSSE VRSS*PALWEAKAGRSSEVRSS
11453	25354	A	11552	70	380	LHKCSFIYINHCNNTIYGLISLYPKQLF SYENFKDFCNKI*P*IPNFELKTSTP*L EKL*NWAMARHGGSL*SQHFGRRRAD HMRSGVPGQPGQGESPT
11454	25355	A	11553	319	56	TFFLGPPGFF*KIFFSVGPPLIFFLPKK FIGEQKNAPGKNFFGFSLFFFFLL TLSSALECSGAMSAHDNLCLPGSSNSPA SAF
11455	25356	A	11554	230	399	MMGEIINQANIISVCQIIRRLRHESHLI PGGRGYSELRSYHCTSTWVTE*DSCLKK
11456	25357	A	11555	376	396	F*IFWRDGVSPCCPGWSQILRLQOSTCL



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLPKCWDYRPPHPDATAASCPYFYHYVLL KIWRYSFDLSCLWNLVVWGLAFG
11457	25358	A	11556	176	384	KAWPNVRNNYR*NFFFQCCINNFRKRLK CFRCGADKFGKTGFSCLYALKPTNWGR EQWLTVNPTNFGK
11458	25359	A	11557	295	391	PYKLLITHTHTHTHTHSRTHTI*HTTSL LYTF
11459	25360	A	11558	1210	1753	NTWCMERLAVAFGSFNRRNSPLRGWALWL TPIILALWEAEAGGPLEPQEFETCLGNM VKHCLYKNLKNVSGV*DLPGQHGETLSL QKFKKCVRRGGTCL*SQRLRRLSWEDCL SQGGQGCSEP*SHQCVPAWVTELDPSK KTKTKKFFGLPSPFLFVCFLTHIYVKE YAFVLAEEASGKTTSKLTMVTSRNLGK TKKFFGL
11460	25361	A	11559	172	3	KQKFFFPFPPSHQIKIFGGGAPEMPPFFF FFRKESRFVA*AGVQWRNLSSLHPPPHP
11461	25362	A	11560	143	1	GQAQWFMPVIPVLWEAKG*SLEARSSR PVCATATPPQLIPK*YEGL
11462	25363	A	11561	84	2	KPLDTLGGQGGCIT*GQEFETSLANMV
11463	25364	A	11562	12	387	QGILLPCFMSSEERGRIYSNTFSFFFF FGKGGQINPQGGGQATEPRLREPSPSGL TLQGGPGNGGPPPPGQNFFFKKGGYPG GAGGVLPNPGPKGNTPPGPPKARKKRGGP PGPGQKFL*NPKG
11464	25365	A	11563	230	375	RAKGKLLSESLLSIQSFKKPSVHTCNPS TLGG*GRWIT*GLETTSLA
11465	25366	A	11564	287	55	PDGRVQWLTVPVPGWLWEAKEGGSLKSR SS*SQINPVGSVPYSLRVLR
11466	25367	A	11565	115	411	FFFFFFFFLGENSFFSFRGGPRGGHIFW NFPFPG*GVFPPPPPPGGGNKGGAPPPG FFFFFFP*KTGFPPPLGPGGPPPLFGPPP FPPPKGYNFRDPPP
11467	25368	A	11566	139	356	CLLIGWYNTGCITQGSTRKIGTTFFLRQ SSSVAQAGVKCSGMILCYRNLRLPGSSN LPDSAS*VAGTTATYP
11468	25369	A	11567	101	410	FLFFFFFFFFLKKIFFPPRGGGGGN*K KQTPPLGGKKNFPPPPKRGGGTTPPP PLLFLVF*GEGGFPGGAGGKKTPKGNP PPPPKGGEMGRGPPPRGG
11469	25370	A	11568	417	56	EDCLRTGVRDLLPNPHNLQIAGRDGAR L*SQLQEHHLSPGFRGYSEL*SCHCSPA WATE*AYRKQNKTKQNYRSSLHLHYTP MATAWIKIAFLRAGDIFLSVLSFLPNSY PLFSHPSQ
11470	25371	A	11569	301	443	EDTTFVCFEVESCSVAQATDSPASAS*I AGIIGVCHHARLIFVFLVE
11471	25372	A	11570	44	408	RGRGHGPHSPWRRRRRLRVVEGRKATES KRRAYKYPALLCSHQWKPNWELDSQI KIPTGL*LK*PSFIFIFIYLFWKQGLS LAPMLECRGAVLAH*HLRLPRSSLSHAS ASQVAVTTG
11472	25373	A	11571	201	1	AERPVTGPPVYAEPGLQGRQG*KNMFKN MQHPRWADHLRSGVQDQPGQYGETPVST KNTKITQAQCI
11473	25374	A	11572	343	1	FGLLFAFTLEYKLYESINHFHACCVCRF SSGTLHVVCNRRHPNKLDEWNSGGGGRQ DLTLTPRLGCSGVIMAHCNLVLLGLSNP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VSAS*VAGTTGAHSHAWIDKLFVKTGPLY
11474	25375	A	11573	209	3	VGPPPKSLPGGFPPFFFCPKCFPRLLKKKKK KKPGLVAYTCNLNTSGVRGKKIT*AQEF KKSPSNIVKPWY
11475	25376	A	11574	312	430	QRYARPGPVVHCYNSSSTVGGRSRGIV*A QEFATSLCNMT
11476	25377	A	11575	125	3	NSLGPVVHACNPRSLGG*GGRITSAQEF ETSLGKIRRLPY
11477	25378	A	11576	190	362	CVNNYID*EKKKKKKKKREREKKKKKKKK KKKKKK*GGGAPKKKKKFTPGGGKNEFF L
11478	25379	A	11577	231	340	KRITRVNQDGLDLLTS*SAPLGLPECWD YTMKPCLY
11479	25380	A	11578	60	3	RMQVSV*ITFPMSLQAYLIYSSSVAAGA QSGIEECKYQFAWDRWNCPERALQ
11480	25381	A	11579	285	406	KKGNWPGAMAHTCNPSTLRGRGGWIA*G QEFETNVGDMAK
11481	25382	A	11580	121	1	NLNCPGPVAHASNPNTTGG*CRPIV*GQ EFYTRIANTVKP
11482	25383	A	11581	199	384	KKTPPGGIFFCPKEAGPAPPL*TPFC*T PLFFSPAPFKPKRALKFPLKPKRGFFQI PFFFF*DGVS LCHPGWSTVARSCPRV
11483	25384	A	11582	677	934	YGSRHCI CFLQAISEILFLKNPARHGGS QVQDQPGQQSKTLTLRKSK*ARHNGSC LSSQNFGRLRQEGHLSPGG*GCSEL*PR HC
11484	25385	A	11583	104	2	KKIGGGPPLFFFFETESCSVARLE*SCA ISAHCN
11485	25386	A	11584	349	9	GGRSLGPRKTRVQWGIPFPPPLHLGGKA KPCFPKPKKKKKVKGLNKHYSKEDIQMVN RYMKKCSSTSLPRERIKITIMRYHFPsir MAIRKIKDKPDQ*GCIEKGGSVVRPMY L
11486	25387	A	11585	163	1	TAVRIKHNSYTLTPCLRHSRYLINVTCW PGPVAHACNPSTLGGGRGWIT*GQEF
11487	25388	A	11586	192	41	SKSKYHTYGDALQKSTVYKWITHPKKG *DDVKDKAHSTRLSMSICEEKE
11488	25389	A	11587	30	374	GWSPEDLFPGLSPALKGFGSGEGG*PFL PFQKKRGGGGSSPPFVLKVRPENRL YPGGGGFR*PKQGCPSAWGAEPDSLK KKKGFGQKKKKKKVLKEKT
11489	25390	A	11588	66	245	SLCFFVFFVFF*TESCSVTQGV*WYNL GSLQPPPPKKNKIKQKKKINWGRGFK RRL
11490	25391	A	11589	243	402	FLHLKKKKKKKKKKKKKKKN*KDAG
11491	25392	A	11590	205	3	IRLLGIKNPTPAHCQ*K*KTGEPLW*V VW*FFRRLHTELSYDPAIPLLCINSTE VWAPGIPPRFR
11492	25393	A	11591	404	152	MGFHVSQDGLDLLTS*STLLSLPKCWD *CWDYTRRELCPGHFAISFNKVVLT VVLYFYLIILHCTYCPYKLLFLFFFYIY
11493	25394	A	11592	311	386	TVYPPLAGNLAHAGA*AGIVGTALSILI RAELGQPGALLGDDQIYNVIVTAHAFVI IFFIAIPIIIGGFGN*LVPLIIGAPDIA FPRINNISF*LLPPSFLLLASSIVEAG AGTG*TVYPPLAGNLAHAGASVDLTIFF LH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11494	25395	A	11593	39	397	EGCPLFFVFFVFFVFFFGKKIFFPPPRG GGGAPHKIPGPPPPGGNFFPPPPPLRG GKRGPppppgffff*KKGGVSLFPRGG VFFFSFWRGGRGGFPPPPQKKIFLKGP PPFYKKK
11495	25396	A	11594	243	46	GILSCCFHDSLNLNSL*CD*VWISLCLS YLVSIELGQCGLIFFIKRESFWLLLLK MYLQPLSFLS
11496	25397	A	11595	327	2	PRAILRIQFLWPMRPYVWMSQPCSLCF CHTAKTVPTSRPLLLGFFSLPGIAHISM WLVLSYGLGFSSKVTLPWGPVVAHCNPS TLGG*GGWIT*GWEFKTSLANMVK
11497	25398	A	11596	292	384	LGTVAHTCNPSTLGGQDGWIT*IQEFET SLR
11498	25399	A	11598	125	2	PFQQRSGGTRGPGAVAHTYNPSTLEG* GGRIT*GQEFETS
11499	25400	A	11599	302	408	TGGWLGVAHACNPSILGGRGRQIT*GQ ELETRLA
11500	25401	A	11600	409	131	GRSGGVPKSGVLKPPGPPGTPFFFKKP KITRGGGQPLFPLLRVRPENCLSLGS GGCH*TKLPPCPSTWGAQ*KLVSKKKKC EGGGRIYS
11501	25402	A	11601	196	330	HHCMLAWVTGRPYLNIYICIIYADIYIHI YICIIYIYTHRVYIYLAI*YIYVYMR YIYIYIYVYIYTHTHGYIYIY
11502	25403	A	11602	41	252	TPGRARGQLGHSSSTGLDLLTS*SACLS LPKCWDYRREPPRAEDIKFMF*AILSE TILVRGVRSRATPS
11503	25404	A	11603	271	440	KKKKRGGRFKESKFTSAGLQGNIFFIGP PKLIPRAAV*QRGDWKNLGVTLNRLCH
11504	25405	A	11604	429	2	FSSFFAEKGCHCVSQAGFKLLSSRDLP SAPHLGIRLLGRLRQEDPPSPGV*GCSE LQSRCLTPAWITKRDPVS*KFKKQKTKT HTH*RKPTKGQDHQYHCLPPPHVMPKV FRGSNVHGAVRTGRSGRSIPELSHAVPH AP
11505	25406	A	11605	113	2	TEATHLVCTYKN*KLGAWWIMPVIPAL WEAEVGRLL
11506	25407	A	11606	301	3	WVMVCSVKNIALGHACGKFHYEGRGKPA EHPSWVLLVLESLQKKLFLSYFLFTFL QPPSPRLT*PVFRFFFRDRIMLCCPGW SAVVPERVGRAGNSE
11507	25408	A	11607	117	431	SCDFCLSFSLSLFFVFFFRKGIFFLGPRG ENKGGNKIKWTLGPGGKGNRSPSPKGG GKRGGPPPGANLDF*KKTGFPQGGRGGE KPPPPGGRAGGAPQRGKPGAG
11508	25409	A	11608	277	88	RRTTSSWLARNCIQGPAGYHTGS*TPDL KGSACLSFPKCWDYRWRLDL
11509	25410	A	11609	200	27	VRLKPGDSRDPDMQWYI*ENRPARCGG SLL*S*HFGRKRKADHLRLGVQDTRSSA R
11510	25411	A	11610	17	414	TVWLVMQDPENEWIVSGWGGKEEPRYF MCEARSSMDRVFFFF*KKTLLFFPPGGG GGAKIWNIGIPPPQGSPLSVAYPLGVWE KKGPPHHPKKRVPPV*PGGVLFSEPGN PPPGPPKGVGKRSSPPSPVL
11511	25412	A	11611	296	428	RIYENWRGTVAHACNPSTLGGQGGWIT* GQSLKTSTGTVAKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11512	25413	A	11612	20	362	NFVRGVARGSRGGATRCCEWVGLRPVGMAYGRSPSWLL*VKPSAASHRPPLPRAADTPGTAPAPTPTPAPAAAPALTPSSGPGSALTLLEELQEAIRRAQRWGLTMLPRLASNS
11513	25414	A	11613	158	2	LMLSRTPQLQL*YTLLELELPRL LAPDL LSNGLSLKDLKWTSHSNYRASKETK
11514	25415	A	11614	3	410	RSEVYGLVLTWYQVNRVPWTHKAAFTRVSRWARPRSKI ESECYWLPQAHRTKS*PLVRTLSGLCSLLGFHPLFLSLLATDLVPLPSFALLLLELFFLPMPKLPAP*SPTKRSFSFYFFRDRVLLCCPGWSQTP
11515	25416	A	11615	189	397	YKVLFLVEKNGFFFLFFETKPCCVAPTGVQGNFNG*LQAPPPGLPLFSALAAPEVGTNGTPPPPPRFFF
11516	25417	A	11616	158	1	KGKPTPKTFFCQKQIFFLVFFF*TESHSVARAGVQWRDLDSLQAPPPGFPTPR
11517	25418	A	11617	319	425	KVWLYSQAV*KVWLYSQAVAHYTNPNLTGGQGWRIA*AYEFKTSL
11518	25419	A	11618	94	2	CLTISWLGTVAHV CNPSTLGG*GGHITRSR
11519	25420	A	11619	381	9	FFPLPLPLPTVSLFPRSPSDAEPKLDCTAAISAHCNLP*FSCSLPSACNCRRAPRLTASASRGAGIADGVST*QCSMVPRLECSGVISAHYNLHLPATSLGLPKCRDCSLCPDEIVDPRI
11520	25421	A	11620	144	431	IVNVIVGKGEKGRKIPE*LIRCNGWN*SWDRWVAEDHVLREPS ENRRLARVRLTPVSQHFGRRRRLDHEVRSRIPACATWRNSVSTYNTKSGWAC
11521	25422	A	11621	174	449	VFSLPLLGGASQLGYLEV RDPLEEA VCPFSDLKPHAGRTTTLFKAIRQGHLSLQRFLLPFVWLCPAPRGGVYRGRQASLS*GGLHPVRASRP
11522	25423	A	11622	316	412	GGPSAVAHACNPSALGGRGGRIS*GQEFKTSL
11523	25424	A	11623	183	2	PKQVYLRNGLLSHSHKCNKIHHINRLKREKIOPGVVAHAYNANTLGGQGRWIT*GQEFENE
11524	25425	A	11624	355	168	DLIVCYDPNAINL*SLLLRRLKWEDCLSPGG*GYSEPRSCHSPAWAAEPDPVSKKDRNVEFIYCC
11525	25426	A	11625	154	3	TADVLFLLGQAGRGNFVVMKKNCRPGTVAHACNPSTLGGRRG*ITRGLEFK
11526	25427	A	11626	412	3	IFFPPPKKDKRTRGGQKNIPPAPPNRLGRGGNFPPQKPFPPPLF*IFPRPP*CKGSIPPFLFPLCFQKKKTPSFFFLPNGPSPICEKIFLFPKKGFLKFKPRFLKKGKPPFFFFGNAVLLCQPGWSAVAQSQ
11527	25428	A	11627	290	423	VFEYFFKFFKKNNSWPGVVAHTYNPSSLGGQGGWIT*SQVLRPP
11528	25429	A	11628	213	3	LSGIYSGNRRLVRYSKSVSVIHHINRLKKNHIIISIDGKPLEQIQNSFMT*KRNKLKWDHLRPADA
11529	25430	A	11629	152	2	FQKNRDLPSKAGWPGMVAHACNPSTLGARGGQIT*GQEFETSMVMNVKP
11530	25431	A	11630	422	189	PLSGFCPSTWGAQRALSKKKRSEAGHSGSCL*SQYLGRLKQKDHPSPGGRGFSE

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						LLNCTPAWVAKQDPVPKKRLK
11531	25432	A	11631	239	424	KEDNNRVFVIGPLGGLNELAHDKAFKTO NHHWLGVGHAACNPSTLGGQGRWTT*GQ EFTTSL
11532	25433	A	11632	343	401	AREHEKSAACQ*GMERSVIKCHVATE *EREQKRERQKERASEKERQESERDSK RERARESERERESTRAQLVRKIVNQIS
11533	25434	A	11633	125	371	FQGCACIKLTNTLLPYAHGYLIWRHDGK GCHCKMTAKIHSCKLSPDAL*SQLGVP L*THTHTHTHTHTHTHTFSEKKGLVP
11534	25435	A	11634	235	433	AALTSFSGPFSFCSYLINTLGNFNPHE ISTT*FTLQRL*KIIFWPGMVAHACNPS TFGGQGRWIT
11535	25436	A	11635	93	385	FTLKSEERRKHSVPQGGKQNKIKLLSPDC KLENKRFGWARWLTVPVIPAL*EAKAGES PEGNGEREEATEPFGSIIILGFFFTQIA HLHRSDYEPNEDS
11536	25437	A	11636	190	398	NTKKSQKAFKTKQKPPPLDPKKKASKK TKFFLPKKISTRKFRTGPWRGTNFSCLK AKKNLGKTRKKIFP*RPFFPSISLFWP FFFFLFF*KDKVPLCHRGWSAVVQSQLT ATSIISQMY
11537	25438	A	11637	190	380	TPKKWPKAFFKTKGKPSFFHPRKKALRK TKFFLPQKFP*NPLSPLIPALFWPFFFF FFF*KDKVPLCHRGWSAVVQSQLTATSI SQMY
11538	25439	A	11638	261	91	EKTLWAGHGGTCL*SQLGLRLRWENHLN LGGRG*RSRHCTPAWVTERDSVSNK*IN K
11539	25440	A	11639	1	334	FRANRTVKDAHSIHGTNPQYLVERTIRT RIYESKYWKEECFGLTAEVLVDKAMELR FVGGVYGGNIKPTPFLCLTLKMLQIQPE KDIIVEFIKNEDEFK*VQCSLANIRGMY
11540	25441	A	11640	193	457	DGILLCGPGWSAVAPSQLCSGTISAYCN LCLPGSSESPVSAP*YGLQACAHAPLM FVFLVYTGTCLPLSAHHSRAANSSHFS YPLL
11541	25442	A	11641	257	373	NTISCFRSLRPVAHTCNPSTLGG*DGQI T*AQEFETCLG
11542	25443	A	11642	211	367	DTTSHPFEWL*FKKSRK*RVLDRIWGN* MLVHCWWEHKMVQLL*KTVWWLFK
11543	25444	A	11643	112	367	LQIKTIRYHHILTRMAKIQNTDTNKCYQ ECGATGTLIHCWWEFKIIPVIPALWEAE VGGLLEVRSSRPAPWTRENPIFTKLIK Y*KYKNTPYIIR*LQIKTIRYHHILTRM AKIQNTDTNKCYQECGATGTLIHCWWEF KIIPVIPALWEAEVGGLLEVRSSRPAPW TRENPIFTKLIKNY
11544	25445	A	11644	310	335	YHLIAGSLGDIERLSML*IGKAVCHNKY **GCGEFGFLHCWWEWMVQSL*KIVC QILQT
11545	25446	A	11645	143	455	KRKGPSLWLLGKSMGGIRFF*KKVFFSG FKSLWFFFWPLWKPLERLN*IKISFYPP AKKKGQRKAQFFFFFPFSFSLAGCSG SISAHCNLCILGLSDSPTS
11546	25447	A	11646	182	458	SRGGIRFF*KRVFFSVIKSIWFFFWPLL KPLGRVN*IKISFNPPAKKRGWERKAQF FFFFLPRSFSLAGCSGISAHCNLCILG

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						LSDSPTS
11547	25448	A	11647	319	3	RSTKYSPRGWEPSMWFLFLHVFSLPFRS ILGPPLLGTPLRGSPPPPPFFEGKGFIY GLTFFFF*EPPCEIFFFFFLDRVLLYCP GWSAVVQSAHCSLELKDVCVI
11548	25449	A	11648	165	2	DQSGRPRKILCAHTHTAHMHTSLGQT* QDPV*THHTHTHTHTPLAAAAQRIN
11549	25450	A	11649	290	3	SKQNTTHTWATLKSYYPSQFWRLGSPSS RWQLDGLFVLRALFLVCRQPPSLRLITWW EKTEERKREREREK*DRERERNEIERNERE RERERETQRMV
11550	25451	A	11650	220	2	TPTLPGKTGLTALDRIPGRDPGPRRAGR PF*AGVAAENCPDPAEGGSTRPLGAPGR GSAPP*RHPGPAGGR
11551	25452	A	11651	29	387	FLIFDVTIVIDLACHEPHSYKMAHLINV VCVLTAPPTSYPFPIISFLGPPYSLRHNDI EIRPINNPTRTSQCSERKSHTSLTLNQ KLEMTTLSKDGMSKAKTG*EPGL*C*TV SQAVNAK
11552	25453	A	11652	267	2	KFFFFVFSTSKLNFYPTFPPLFLFSFF FFFFFFFMREGFAVTWVPAGAVAPAVIA HCSLELVGSGKPPISAS*GAGTTGMHYH TRMY
11553	25454	A	11653	50	411	EAVAGGMEKSMNNLPKGPDTLCFDKDEF MNEDFDVDHFVSDCRNRGQLEELRDNFQ LYYKLLKTAMVELINKDYADFNLSDDL VGMEQALNQLSVPL*QLREEVLSL*SFV IERISPSS
11554	25455	A	11654	303	403	VRNMVEWLGVAHAACNPSTLGGQGEQIT *GQEF
11555	25456	A	11655	356	653	SVSPCFPPGPASTLSFLVADFRRRGVDV SQVAWQSKGDTTPSSCCIINNSGNRTIV LHDT*GPRASPCYNPPIISWLNQFPHSP WASQLPPSVASVYQK
11556	25457	A	11656	442	2	GRPILMRPAVL*SEPRTPACVDIQQQIM TIIDEVVKACAKVQTLAPINSASRMQS IRHVVIYLDSSARPAGKGAIGFIKVG YKKLFVLDDREAHNEVEPLCILDPIIHE SVQRHGHGRELFQYMLQKERVEPHQLAI DRPSLV
11557	25458	A	11657	109	474	DINMCGRVVLAERM*KRKRDKYNYEET E*VL*KKVRHSQLOKENVAQNAPVVQNA AYIDQPSPAHVGGQGLSKLPSRPGDQGV EPQNLRTLQGRSVIRSATNTTLPHMLMS QRVIAPNPAQLQGQRGPPKHGICRTTTP NMNPANV
11558	25459	A	11658	342	3	ENQLKNGEHSKSSQASAPPNDHNTSLAR A*KWAGAEAEIALLTEAGFRWVIMNFA ELKEHVVTQCKEAKVHDKTTQELIAGFE RNITYLM*LKITTREPHIAITSINSRMA
11559	25460	A	11659	204	17	STCTPLPTA*SQSRPHPPPTPTPPAPWR SSNGPLSRGSSSRNSTSSWSIALATGPW THRSEL
11560	25461	A	11660	505	514	GS*GNHFNPDGASHGGPDSDRTGPRGP CLPSPWGAQILRDWYPQEEGMTLGKQ
11561	25462	A	11661	80	374	FLFDIYNRCYLIFINIT*YLSNFD*IF IIYLVAIYRLCLGLFRAPRQCKHPRP QFSFNKIGTKR*AWPGAMAHTCNPNTLG